STIC Search Report
Biotech-Chem Library

USPTO

| TO: **Malgorzata Walicka**	From: **Edward Hart**
Location: **cm1/10d06/10d01**	Location: **Biotech-Chem Library**
Art Unit: **1652**	**CM1-6B02**
Wednesday, October 15, 2003	Phone: **305-9203**
Case Serial Number: **10/054295**	**edward.hart@uspto.gov**

Search Notes

Examiner Walicka,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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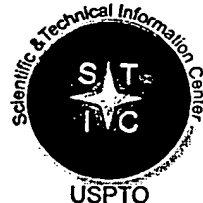
STIC SEARCH RESULTS

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* [ ]   *Example: 1610*

➤ *Relevant prior art* **found**, *search results used as follows:*

☐ 102 rejection

☐ 103 rejection

☐ Cited as being of interest.

☐ Helped examiner better understand the invention.

☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

☐ Foreign Patent(s)

☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art* **not found:**

☐ Results verified the lack of relevant prior art (helped determine patentability).

☐ Results were not useful in determining patentability or understanding the invention.

Comments:

sira
Search and Information
Resources Administration

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:       October 15, 2003, 02:25:19 ; Search time 897 Seconds
                                          (without alignments)
                                          6449.057 Million cell updates/sec

Title:        US-10-054-295-224
Perfect score: 4015
Sequence:     1 GCAGCGCTGCGTCCTGCTGC..........TTTTTCAGTTTTGAAAAAAA 4015

Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0

Searched:     1827256 seqs, 720399070 residues

Total number of hits satisfying chosen parameters:        3654512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Pending_Patents_NA_New:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	4015	100.0	4015	1	PCT-US03-19844-1	Sequence 1, Appli
2	4015	100.0	4015	1	PCT-US03-19844-1	Sequence 1, Appli
3	4008.6	99.8	4037	5	US-09-721-456-343	Sequence 343, App
4	3849.2	95.9	4029	5	US-09-721-456-292	Sequence 292, App
5	3641	90.7	3855	5	US-09-721-456-4	Sequence 4, Appli
6	2205.2	54.9	3451	5	US-09-721-456-721	Sequence 721, App
7	2200.8	54.8	3396	5	US-09-721-456-639	Sequence 639, App
8	2196.6	54.7	3396	5	US-09-721-456-638	Sequence 638, App
9	1960.4	48.8	2176	5	US-09-721-456-3	Sequence 3, Appli
10	1877.2	46.8	2171	5	US-09-721-456-266	Sequence 266, App
11	1862.2	46.4	3396	5	US-09-721-456-642	Sequence 642, App
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13	1670.6	41.6	4170	1	PCT-US03-19844-5	Sequence 5, Appli
14	1600.8	39.9	3426	1	PCT-US03-19844-3	Sequence 3, Appli
15	1542.2	38.4	3396	5	US-09-721-456-640	Sequence 640, App
16	1515.8	37.8	4335	6	US-10-674-836-6	Sequence 6, Appli
17	1515.8	37.8	15418	6	US-10-674-836-1	Sequence 1, Appli
18	967	24.1	1758	1	PCT-US03-19844-7	Sequence 7, Appli
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21	442.4	11.0	2855	1	PCT-US03-19844-11	Sequence 11, Appli
22	385.8	9.6	389	5	US-09-721-456-8	Sequence 8, Appli
23	182	4.5	182	5	US-09-721-456-9	Sequence 9, Appli
24	97.6	2.4	240	5	US-09-721-456-697	Sequence 697, App
c 25	67.6	1.7	90	5	US-09-721-456-669	Sequence 669, App
c 26	67.6	1.7	9795	7	US-60-501-821-44	Sequence 44, Appl

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c 37	64.4	1.6	90	5	US-09-721-456-653	Sequence 653, App
c 38	64.4	1.6	90	5	US-09-721-456-699	Sequence 699, App
c 39	64.4	1.6	90	5	US-09-721-456-703	Sequence 703, App
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c 44	62.8	1.6	90	5	US-09-721-456-669	Sequence 669, App
c 45	62.8	1.6	90	5	US-09-721-456-711	Sequence 711, App

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                            ALIGNMENTS

RESULT 1
PCT-US03-19844-1
; Sequence 1, Application PC/TUS0319844
; GENERAL INFORMATION:
;   APPLICANT: Geron Corporation
;   APPLICANT: Majumdar, Anish Sen
;   APPLICANT: Ferber, Iris
;   APPLICANT: Frolkis, Maria
;   APPLICANT: Wang, Zhuo
;   TITLE OF INVENTION: Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase R
;   TITLE OF INVENTION: Transcriptase
;   FILE REFERENCE: 086/200
;   CURRENT APPLICATION NUMBER: PCT/US03/19844
;   CURRENT FILING DATE: 2003-06-24
;   PRIOR APPLICATION NUMBER: 60/393,295
;   PRIOR FILING DATE: 2002-06-27
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 4015
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US03-19844-1

Query Match             100.0%;  Score 4015;  DB 1;  Length 4015;
Best Local Similarity   100.0%;  Matches 4015;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy    301 CCGAGTGCTGCCAGAGGCTGTGCGAGCGGCCGGCCGAAGAACGTGCTGGCCTTCGC 360
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Qy  1441  CGGCTTCGTGCGGGGCTGCCTGCGCGGGCTGGTGCCCGGCCTGGTGCCCGGCCTCCAGGCA  1500
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Qy   361  GCTGCTGGACGCGGGGGGGCCCCGCGGGGGCGCCCCGAGGCCTTCACCACCAGCTGCGCAGCTA  420
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Db   361  GCTGCTGGACGCGGGGGGGCCCCGCGGGGGCGCCCCGAGGCCTTCACCACCAGCTGCGCAGCTA  420

Qy   421  CCTGCCCAACACGTGACCGACACTCGGGGGGAGCGGTGGGGCGTGGGGCGTGCTGCTGCGG  480
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Db   421  CCTGCCCAACACGTGACCGACACTCGGGGGGAGCGGTGGGGCGTGGGGCGTGCTGCTGCGG  480

Qy   481  CCGCTGGGGCGACGACTGCTGTTCACCTGCTGGCACGCTGCGCGCGCTCTTTGTGCTTGT  540
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Qy   541  GGCTCCCAGCTGCGCCTACCAGGTGTGCGCCCGCGCTGCCACCAGTGTGGGCGGCTGCCAC  600
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Qy   601  TCAGGGCCCGCCCACACAGCCTAGTGACCCCGAAGGCGTCTGGGATGCGAACGGGC  660
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Qy   841  GCGCTGGACGAGTGACCGTGGTTTCTGTGGTGTCACTGCAGCCACTCCCACTCCCAGCGAAAGC  900
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Qy   901  CACCTCTTGGAGGGTCGCCTCCACATCGCGGCCACCCATTCACATCGGGACGCCTTGTCC  960
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Qy  1021  CCCGGTGTACGCGGACGACCAGACGACACCACTTCCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1080
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Db  1381  CACAGACCCCGTCGCTGCCTCGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGCGTGTA  1440
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RESULT 2
US-09-721-456-1
; Sequence 1, Application US/09721456
; GENERAL INFORMATION:
    APPLICANT: Cech, Thomas R.
        Lingner, Joachim
        Nakamura, Toru
        Chapman, Karen B.
        Morin, Gregg B.
        Harley, Calvin B.
        Andrews, William H.
    TITLE OF INVENTION: Human Telomerase Catalytic Subunit
    NUMBER OF SEQUENCES: 727
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Townsend and Townsend and Crew LLP
        STREET: Two Embarcadero Center, Eighth Floor
        CITY: San Francisco
        STATE: California
        COUNTRY: USA
        ZIP: 94111-3834
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC Compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/721,456
        FILING DATE: 22-Nov-2000
        CLASSIFICATION: <Unknown>
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/08/974,549A
        FILING DATE: 19-NOV-1997
        APPLICATION NUMBER: US 08/724,643
        FILING DATE: 01-OCT-1996
        APPLICATION NUMBER: US 08/844,419
        FILING DATE: 18-APR-1997
        APPLICATION NUMBER: US 08/846,017
        FILING DATE: 25-APR-1997
        APPLICATION NUMBER: US 08/851,843
        FILING DATE: 06-MAY-1997
        APPLICATION NUMBER: US 08/854,050
        FILING DATE: 09-MAY-1997
        APPLICATION NUMBER: US 08/911,312
        FILING DATE: 14-AUG-1997
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APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
    NAME: Apple, Randolph Ted
    REGISTRATION NUMBER: 36,429
    REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 4015 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    MOLECULE TYPE: cDNA
    FEATURE:
        NAME/KEY: CDS
        LOCATION: 56..3454
        OTHER INFORMATION: /product= "hTRT"
            /note= "human telomerase reverse
            transcriptase (hTRT) catalytic protein
            component"
    SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-721-456-1

Query Match      100.0%;   Score 4015;  DB 5;   Length 4015;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 4015;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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(Sequence alignment — Query (Qy) vs Database (Db), positions 1–1680)

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Db    1  GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGCGCCCCGCCACCCCCGGCGATGCC   60

Qy   61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  120
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Qy  121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG  180
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Qy  241  ACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGC  300
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Qy  541  GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC  600
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Qy  601  TCAGGCCCGGCCCCCGCCACACGCTAGTGACCGGCGTGGGATGCGGGCTGGAACGGGGC  660
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Db  841  GCGTGGACCGAGTGACCGTGGTTTCTGTGTCACCTGCCAGACCCCGCCGAAGAAGC  900

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Db  2821 GCCGGCCCACGGCCTATTCCCCGTGCGGCGGCCGCTGCTGTCGTCGATACCGGACCCTGGAGGT 2880

Qy  2881 GCAGAGCGACTACTCCAGTATGCCGGACCTCCATCAGAGCCAGTCTCACCTCACCTTCAACCG 2940
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Db  2881 GCAGAGCGACTACTCCAGTATGCCGGACCTCCATCAGAGCCAGTCTCACCTCACCTTCAACCG 2940

Qy  2941 CGGCTTCAAGGCTGGGAGAACATGCTGTCGCAAACTCTTGGGGTCTTGGGGTCTTGCGGCTGAAGTG 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 CGGCTTCAAGGCTGGGAGAACATGCTGTCGCAAACTCTTGGGGTCTTGGGGTCTTGCGGCTGAAGTG 3000

Qy  3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACATGGACGTGTGTCACCAACATCTA 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACATGGACGTGTGTCACCAACATCTA 3060

Qy  3061 CAAGATCCTCCTGCGTGCAGGCGTACAGGTTTCACGCATGTGTCGTGCGTCCCATTTCA 3120
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Db  3061 CAAGATCCTCCTGCGTGCAGGCGTACAGGTTTCACGCATGTGTCGTGCGTCCCATTTCA 3120

Qy  3121 TCAGCAAGTTGGAAGAACCCCACATTTTCCTGCGCATCTCTGACACGGCCTCCCT 3180
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Db  3121 TCAGCAAGTTGGAAGAACCCCACATTTTCCTGCGCATCTCTGACACGGCCTCCCT 3180

Qy  3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGAGGATGTCGCTGCGGGGACCGCCGG 3240
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Db  3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGAGGATGTCGCTGCGGGGACCGCCGG 3240

Qy  3241 CGGCCCTCTGCCCTCCGAGCCGTGCAGTGGCTGGTGCCACCAAGCATTCTGCTCAAGCT 3300
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Qy  3301 GACTCGACACCGTGTCACCTACGTGCCACCTCCGGGGTCACTCAGGACAGCGCA 3360
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Qy  3361 GCTGAGTCGGAAGCTCCCGGGGACGTGCCCTGCCCTGAGGTGAGTGTTGGCGAGGCCTG 3420
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Db  3361 GCTGAGTCGGAAGCTCCCGGGGACGTGCCCTGCCCTGAGGTGAGTGTTGGCGAGGCCTG 3420

Qy  3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCCGCCAGGCCGA 3480
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Qy  3481 GAGCAGACACCAGCAGCCCGTCTCACGTGTCCCAGGCTCCAGGAGGGAGGGCGGGCC 3540
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Qy  3541 CACACCCAGGCCGCCCGCCACCACGCGCCAGCCAACCCCGGAGTCTGAGTGTTGGCGAGGCCTG 3600
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Db  3541 CACACCCAGGCCGCCCGCCACCACGCGCCAGCCAACCCCGGAGTCTGAGTGTTGGCGAGGCCTG 3600

Qy  3601 CATGTCCGGCTGAAGGCTGAGTGTCGGCTGAGTGTCGGCTGAGCGTGGCCGAGTGTCCAGGCCAAGGGCT 3660
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Qy  3661 GAGTGTCCAGCAGCACACCTGCCGTCTTCACTTCCCACCAGGCTCCGGCTCGCGGCTCCACCCCCA 3720
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Qy  3721 GGGCCAGCTTTCTGGATGATTTCTTGTTGGTGACACCTCACCTCCCACATAGGAATAGTCCATCC 3780
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Db  3721 GGGCCAGCTTTCTGGATGATTTCTTGTTGGTGACACCTCACCTCCCACATAGGAATAGTCCATCC 3780

Qy  3781 CCAGATTCGGCCATTGTTCACCCCTGCCTTTGCCTTCACCTCTTTGCCTTCACCCCACCATCC 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 CCAGATTCGGCCATTGTTCACCCCTGCCTTTGCCTTCACCTCTTTGCCTTCACCCCACCATCC 3840
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Qy   3841  AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG  3900
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Db   3841  AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG  3900

Qy   3901  CCCTGTACACAGGCGAGGAGGACCCTGCACCTGGATGGGGGTCCCCTGGGTCAAATTGGGGG  3960
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Db   3901  CCCTGTACACAGGCGAGGAGGACCCTGCACCTGGATGGGGGTCCCCTGGGTCAAATTGGGGG  3960

Qy   3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA  4015
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SEQUENCE CHARACTERISTICS:
  LENGTH: 4037 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
  NAME/KEY: CDS
  LOCATION: 56..3454
  OTHER INFORMATION: /note= "refined sequence of hTRT cDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 343:
US-09-721-456-343

Query Match   99.8%;   Score 4008.6;   DB 5;   Length 4037;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 4008; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Qy    1  GCAGCGCTGCGTCCTGCTGCGCACGTGGAAGACCCTGGCCCCGGCACCCCGGCCATGCC   60
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Db    1  GCAGCGCTGCGTCCTGCTGCGCACGTGGAAGACCCTGGCCCCGGCACCCCGGCCATGCC   60

Qy   61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCAGCCACTACCGGAGGTGCT  120
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Db   61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCAGCCACTACCGGAGGTGCT  120

Qy  121  GCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCGCCCAGGGCTGGCGCTGGTGCACGCGCG  180
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Db  121  GCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCGCCCAGGGCTGGCGCTGGTGCACGCGCG  180

Qy  181  GGACCCGGCGGCTTTCCGGCGCGCGCTGGTGGCCCAGCATGTGCGTGTGCGTGCCCTGGGACGC  240
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Db  181  GGACCCGGCGGCTTTCCGGCGCGCGCTGGTGGCCCAGCATGTGCGTGTGCGTGCCCTGGGACGC  240

Qy  241  ACGGACGCGCGCCCCGCCCCCCTCCTTCCGCGCGCAGTGTCCTGCCAGGTGTCCTGAAGGAGCTCGTGGC  300
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Db  241  ACGGACGCGCGCCCCGCCCCCCTCCTTCCGCGCGCAGTGTCCTGCCAGGTGTCCTGAAGGAGCTCGTGGC  300

Qy  301  CCGAGTGCTGCAGAGGCGTGCGACGCGCGCGGAAGAACGTGCTGGCCTTCGGCTTCGC  360
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Db  301  CCGAGTGCTGCAGAGGCGTGCGACGCGCGCGGAAGAACGTGCTGGCCTTCGGCTTCGC  360

Qy  361  GCTGCTGGACGGGCGCCCGGGCGGGCCCCCCGAGGCCTTCACCACCAGCGTGCCGCAGCTA  420
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Db  361  GCTGCTGGACGGGCGCCCGGGCGGGCCCCCCGAGGCCTTCACCACCAGCGTGCCGCAGCTA  420

Qy  421  CCTGCCCAACACGGTGACCGACCACTGCGGGGGCTGTGGGCTGCTGCTGCGCG  480
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Qy  481  CCGGCGTGGACGACGTGCTGGTTCAACCTGGCTGCACGCTGCTGGCACCGCTGGCACCGCTGCGCGTCTTTGTGCTGGT  540
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Db  481  CCGGCGTGGACGACGTGCTGGTTCAACCTGGCTGCACGCTGCTGGCACCGCTGCTGGCACCGCTGCGCGTCTTTGTGCTGGT  540

Qy  541  GGCTCCCAGCTGCGCGCTACCAGGTGTGCGGGCCCGCGCTGTACCAGCTCGGCGTCGCCAC  600
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Db  541  GGCTCCCAGCTGCGCGCTACCAGGTGTGCGGGCCCGCGCTGTACCAGCTCGGCGTCGCCAC  600

Qy  601  TCAGGCCGGCCCGCCCACCACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAAACGGGC  660
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Db  601  TCAGGCCGGCCCGCCCACCACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAAACGGGC  660

Qy  661  CTGGAACCATAGCCTCAGGAGCCGCCGAAGTCTGCCGTTGGGCACGGGGTCCTGGGCGTGCGCGAG  720
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Db  661  CTGGAACCATAGCCTCAGGAGCCGCCGAAGTCTGCCGTTGGGCACGGGGTCCTGGGCGTGCGCGAG  720

Qy  721  GAGGCGCGGGGGCAGTGCGACGCCCGTTGGGCACGGGGTCCTGGGCCACCCGGTGCGGGCGGC  780
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Qy  781  TGCCCCTGAGCCGCGAGCCGAGCCGCGACGCGCCCGTTGGGCAGGGGGTCCTGGGCGGTCCTGGGGGCAGGAC  840
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Db  781  TGCCCCTGAGCCGCGAGCCGAGCCGCGACGCGCCCGTTGGGCAGGGGGTCCTGGGCGGTCCTGGGGGCAGGAC  840
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RESULT 3
US-09-721-456-343
; Sequence 343, Application US/09721456
; GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
  Lingner, Joachim
  Nakamura, Toru
  Chapman, Karen B.
  Morin, Gregg B.
  Harley, Calvin B.
  Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Townsend and Townsend and Crew LLP
  STREET: Two Embarcadero Center, Eighth Floor
  CITY: San Francisco
  STATE: California
  COUNTRY: USA
  ZIP: 94111-3834
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/721,456
  FILING DATE: 22-Nov-2000
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/974,549A
  FILING DATE: 19-NOV-1997
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US 08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US 08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US 08/911,312
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US 08/912,951
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US 08/915,503
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: WO PCT/US97/17618
  FILING DATE: 01-OCT-1997
  APPLICATION NUMBER: WO PCT/US97/17885
  FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph Ted
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:

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Qy  1921 CTTCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGATCGTCTGGGAGC 1980
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Db

Qy  1981 CAGAACGTTCCGCAGAGAAAAGAGGGCGCGAGCGTCTCACCTGAAGCCACTGTT 2040
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Db  1981 CAGAACGTTCCGCAGAGAAAAGAGGGCGCGAGCGTCTCACCTGAAGGCACTGTT 2040

Qy  2041 CAGCGTGCTCAACTACGAGCGGCGGCGGCGGCGGCCCCGGCCTCTGGCGCCTCT 2100
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Qy  2641 GCTCCTGGCGTTTGTTGGTGATGATTCTTGTTGGTGACACCTCACCTCACCACGCGAAAC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 GCTCCTGGCGTTTGTTGGTGATGATTCTTGTTGGTGACACCTCACCTCACCACGCGAAAC 2700

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Db
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Qy   841 GCGTGGACCGAGTGACCGTGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCTGAGAAGC 900
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Qy  1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCGGGAAGCATGCCAA 1560
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Db  1561 GCTCTCGCTGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGCCGACTGCGCTGCGCAG 1620

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Db  1621 GAGCCCAGGGGTTGGCTGTGTTCCGGGCCCGAGAGCACCGTCGCGGAGATCCTGGC 1680

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Qy  1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGCCGAGTCTCTGGAA 1800
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Db  1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGCCGAGTCTCTGGAG 1800

Qy  1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAGAGGGTGCACTGGCAGGCTGTCAAACTCTTTGGGGTCTTTGCGGGTGAAGTC 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 GCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAGAGGGTGCACTGGCAGGCTGTCAAACTCTTTGGGGTCTTTGCGGGTGAAGTC 1860

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Db  1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCCCCTGCTGACGTCCGACTCCG 1920

Qy  1921 CTTCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGATCGTCTGGGAGC 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db
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Db  3001 TCACAGCCTGTTTCTGATTTGCAGGTGAACAGCTCCAGACGGTGTGCACCAACATCTA 3060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGTCGTGCAGCTCCCATTTCA 3120
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Db  3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGTCGTGCAGCTCCCATTTCA 3120
Qy  3121 TCAGCAAGTTTGGAAGAACCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180
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Db  3121 TCAGCAAGTTTGGAAGAACCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180
Qy  3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGATGCGCCTGGGGGCGCAAGGCGCCGC 3240
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Db  3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGATGCGCCTGGGGGCGCAAGGCGCCGC 3240
Qy  3241 CGGCCCTCGCCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAGCATTCCTGCTCAAGCT 3300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CGGCCCCTCCGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAGCATTCCTGCTCAAGCT 3300
Qy  3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360
Qy  3361 GCTGAGTGCGGAAGCTCCCGGGACGACCCTGACCTGCCTGGAGGCCGCCAACCCGGC 3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 GCTGAGTGCGGAAGCTCCCGGGACGACCCTGACCTGCCTGGAGGCCGCCAACCCGGC 3420
Qy  3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGAGCCACCCGCCCACAGCCAGGCCGA 3480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 ACTGCCCCTCAGACTTCAAGACCATCCTGGACTGATGAGCCACCCGCCCACAGCCAGGCCGA 3480
Qy  3481 GAGCAGACACCAGCAGCCCTGTCACGCCGGCTCTACGTCCCAGGAGGAGGGCGGCGGC 3540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GAGCAGACACCAGCAGCCCTGTCACGCCGGCTCTACGTCCCAGGAGGAGGGCGGCGGC 3540
Qy  3541 CACACCCAGGCCCGCCACCGGCCGCCACCCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTG 3600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCGAGTGTCCAGCCAAGGGCT 3660
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Db  3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCGAGTGTCCAGCCAAGGGCT 3660
Qy  3661 GAGTGTCCAGCACACCTGGCGCTTCACTTCCCCACCAGCTGGCGCTCGGCGTCCACCCA 3720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GAGTGTCCAGCACACCTGCCGTCCTTCACTTCCCCACCAGCTGGCGCTCGGCGTCCACCCCA 3720
Qy  3721 GGGCCAGCTTTCCTCACCAGGAGCCCCGCTTCCACTCCCACATAGGAATAGTCCATCC 3780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GGGCCAGCTTTCTTCACCAGGAGCCCCGCTTCCACTCCCACATAGGAATAGTCCATCC 3780
Qy  3781 CCAGATTCGCCATTGTTCACCCGTCTTCACCTGCCTTCACCCCCACCATCC 3840
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Db  3781 CCAGATTCGCCATTGTTCACCCYTCGCCCCTCGCCYTCCTTGCCTTCACCCCCACCATCC 3840
Qy  3841 AGGTGGAGACCCTGAGAAGGAGGACCCTGGGAGCTCTGGAGTTGGAGTGACAAAGGTGTG 3900
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Db  3841 AGGTGGAGACCCTGAGAAGGAGGACCCTGGGAGCTCTGGAGTTGGAGTGACCAAAGGTGTG 3900
Qy  3901 CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960
Qy  3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA 4015
              ||||||||||||||||||||||||||:|||||||||||||||:||||||||||||
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RESULT 4
US-09-721-456-292
; Sequence 292, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin B.
;   Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/721,456
;   FILING DATE: 22-Nov-2000
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/974,549A
;   FILING DATE: 19-NOV-1997
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997
;   APPLICATION NUMBER: US 08/854,050
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: US 08/911,312
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/912,951
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/915,503
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: WO PCT/US97/17618
;   FILING DATE: 01-OCT-1997
;   APPLICATION NUMBER: WO PCT/US97/17885
;   FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph Ted
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-0026100US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 292:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4029 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: -
;   LOCATION: 1..4029
;   OTHER INFORMATION: /note= "preliminary sequence for
;   human TRT cDNA insert of
;   plasmid pGRN121"
; SEQUENCE DESCRIPTION: SEQ ID NO: 292:
US-09-721-456-292

Query Match   95.9%; Score 3849.2; DB 5; Length 4029;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 3955; Conservative 0; Mismatches 53; Indels 9; Gaps 8;

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Qy      1 GCGAGCGCTGCGTCCTGCTCGCGCAGTGGGAAGCCCTGGCCCCCGGCCACCCCCGCGATGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCGAGCGCTGCGTCCTGCTCGCGCAGTGGGAAGCCCTGGCCCCCGGCCACCCCCGCGATGCC 60

Qy     61 GCGGCTCCCCGTGCCGGAGCCGTGCGCTCCTCCTGCCGCAGCCACTACCGCGAGGTGCT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGGCTCCCCGTGCCGGAGCCGTGCGCTCCTCCTGCCGCAGCCACTACCGCGAGGTGCT 120

Qy    121 GCGGCTGGCCAGTTCGTGCGGGGCCCAGGGCTGGGCGGCTGGCCGTGCAGCGCGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCGGCTGGCCACGTTCGTGCGGGGCCCAGGGCTGGGCGGCTGGCCGTGCAGCGCGGG 180

Qy    181 GGACCCGGCGGCTTTCCGGCGCGCTGGTGCCCAGTGCGTGGTGCCCTGGGACGGC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db    181 GGACCCGGCGGCTTTCCGGCGCGCTGGTGCCCAGTGCGTGGTGCCCTGGGANGCN 240

Qy    241 ACGGCGNGCCCCCCGCCCCGGCCCCCCTCCTGCCCAGTGTCTGCCTGAAGAGCTGGTTGGC 300
          |||| ||||  ||||||  |||||||||||||||||  || |||||||||| || 
Db    241 ANGCNGNCCCCCCGCCCCGCCCCCCTCCTTCCTGCCCAGTGTCCTGCCTGAANGANCTGGTGGC 300

Qy    301 CCGAGTGCTCGCAGAGGCTGTGCGAGCGGCGCGGCGGCTGGGCGGCGGGTGCCGCTTCGC 360
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Db    301 CCGAGTGCTGCANANGCTGCGANCGGCGGCGGCGGCTGGGCGGCGGGTGCCGCTTCGC 360

Qy    361 GCTGCTGGACGGGCCCGCGGGGGCCCCCCCGGGGGGCCTTCACCACCAGCGTGCCGCAGCTA 420
          ||||||||||||||||  ||||||||||||||||  ||| |||||||||||||||||||||
Db    361 GCTGCTGGACGGGCCCGCGGGGGCCCCCCGGGGGGCCTTCACCACCAGCGTGCCGCAGCTA 420

Qy    421 CCTGCCCAACACGGTGACCGACGACGTGCTGGTTCACCTGCTGCGCCGTCGGGGCGTGGCGG 480
          ||||||||||||||||||||||  |||||||||||| |||||||||||||  |||||||||
Db    421 CCTGCCCAACACGGTGACCGACGACGTGCTGGTTCACCTGCTGCGCCGTGCGCGGGGCGTGGCGG 480

Qy    481 CCGAGTGGGCGACGACGTGCTGGTTCACCTGCTGCGGCGCGCGCCTCTTTTGTGCTGGT 540
          |||||||||||||||||||||||||||  ||| ||||||||||||  || ||||||||
Db    481 CCGAGTGGGCGACGACGTGCTGGTTCACCTGCTGCGGCGCGCGCCTCTTTTTCACCGNTNTTTGCTGGT 540

Qy    541 GGCTCCAGTGCGCCTACCAGGTGCGGCGGCGCCGCGCTTACCAGCTCGGCGCGCTGCCCAC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db    541 GGNTCCAGTGCGCCTACCAGNTGCGGCGGCGCCGCGCTTACCAGCTCGGCGCGCTGCCCNAC 600

Qy    601 TCAGGCCCGGCCCCACCACGCTAGTGGACCCCCGAAGGCGTCTGGCGATGCCGAACGGGC 660
          |||||||||||||||||||||  | |||||  ||||||||||||||||  | 
Db    601 TCAGGCCCGGCCCCACCACGCTANTGGA-CCCGAANGCGTCTGGCGAT-CCAACGGGC 658

Qy    661 CTGGAACCATAGCGTCAGGGAGCCCGTTCCCGGGCCCCAGCCCCGGGTGCGAG 720
          ||||||||||||||||||||||  ||||  ||||||||||||||||||||||
Db    659 CTGGAACCATAGCGTCAGGGAGCCCGTTGGGG-CTGCCCAGCCCCGGGTGCCGAG 717

Qy    721 GAGGGCGCGGGGGGCAGTGCCAGCCGGAGTCTGCCGGGTGCCCAAGAGGCCCAGGGCGTGGCGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db    718 GAGGGCGCGGGGGGCAGTGCCAGCCGGAGTCTGCCGTTGCCCAAGAGGCCCAGGGCGTGGCGC 777

Qy    781 TGCCCCTGAGCCGGCGGACGGCGCCCGTTCAGGGGTCCTGGGGCCAGGCACCCCGCAGGAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    778 TGCCCCTGAGCCGGCGGACGGCGCCCGTTCAGGGGTCCTGGGGCCACCCCGCAGGAC 837

Qy    841 GCGTGACCGAGTCAGGGGCAGTCGTGTTTCTGTGTGGTGTGTGTCGCGTGACCGACTCCTTACTCTCTTACCTCTCTGTCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||  || || 
Db    838 GCCTGACCGAGTCAGGGGCAGTCGTGTTTCTGTGTGGTGTGTCGCGTGACCGACTCCTTACTCTGTCC 897

Qy    901 GCACCGCGGGGCCCCCCATCCAGCACATCGCGGCGCCACCACGTCCTGGGGGCCGCCA 960
          ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db    898 GCACCGCGGGGCCCCCCATCCAGCACATCGCGGCGCCACCACGTCCGTGGGGCCGCCCA 957

Qy    961 GCACCGCGGGGCCCCCCATCCAGCACATCGCGGGACACGCCTTGTCC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    958 GCACCGCGGGGCCCCCCATCCAGCACATCGCGGGACACGCCTTGTCC 1016

Qy   1021 CCCGTGTACGCCGAGACCAAGCACTTCCTTACTCCTACCAGCGACAAGGAGCAGCTGCG 1080
          ||||||||||||||||||||||||  |||||  || 
Db   1017 CCCGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTACCAGCGACACAGNA--CACTGCG 1074

Qy   1081 GCCCTCCTTCCTACTC-AGCTCTCTGAGGCCCCAGCCTGACTGGCCGTCGGAGGCTCGTGG 1139
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Db   1075 NCCCTCCTTCCTACTCAATATATCTGAGGCCCCTGGATCGCGGCCTGGCTGGCCGTTCGGTGG 1134
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Qy   1140 AGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCGAGGTGCT 1199
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Db   1135 GAGACANTCTTTCTGGTTCCAGCCTTGGTGGATGCCA-GGATTCCCGCCAGGTTGCCGCCGCC 1193

Qy   1200 TGCCCCAGGCACTACTGGGGCGCCCTGTTTCTGGAGCTGCGGCGGGTGCGGTTGGAACCACGCGC 1259
          ||||||||||||||||||  |||||  || |||||||||||||||||||||||||||||||
Db   1194 TGCCCCAGCGNTACTGGCAAATGCGGGCCCTGTTTTCTGGAGCTGCGGCGGGTGCGGTTGGAACCACGCGC 1253

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Db   1254 AGTGCCCTACGGGGTGTCCTCAAGACGCACTGCCCCTGCCGAGCTGCGGTGCACCCCAG 1313

Qy   1320 CAGCCGGTGTCTGTGCCCCGGGAGAAGCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGG 1379
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1314 CAGCCGGTGTCTGTGCCCCGGGAGAAGCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGG 1373

Qy   1380 -ACACAGACCCCGTGCTGCCTCCGCCGCTGCTGCCGCAGCAGCCCCTGGCAGTG 1438
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1374 AACACAGACCCCGTGCTGCCTCCGCCGCTGCTGCCGCAGCAGCCCCTGGCAGTG 1433

Qy   1439 TACGGCTTCGTGCGGGCGGGCCTTCACCACCAGCCCTCTGGGGCTCCAGG 1498
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Db   1494 CACAACGAACGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCC 1553

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Db   1554 AAGCTCTCGCTGCGAGGAGCTGACGTGGAAGATGAGCGGGACTGCGCTTGCGGCGC 1613

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1614 AGGAGCCCAGGGGTTGGCGTGTGTTCCGGCGCCGCAGCACCGTCTGCGTGAGGAGATCCTG 1673

Qy   1679 GCCAAGTTCCTGCTACTGGCTGTACGTCGTGCTCGAGCTGCTCTTTCTTT 1738
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Qy   1739 TATGTCACGGAGACCACGTTCAAAAGAACACAGCTCTTTTTCACCGGAAGAGTGTCTGG 1798
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Db   1794 AGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTG 1853

Qy   1859 TCGGAAGCAGAGGTCAGGCAGCATCGGAGCAGCAGCCCGGGCGCGCCGTCCAGACTC 1918
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Db   1854 TCGGAAGCAGAGGTCAGGCAGCATCGGAGCAGCAGCCCGGGCGCGCCGTCCAGACTC 1913

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1974 CGCTTCATCCCCAAGCGTTCCGGAGAAAGAGGGCGCGGCCGATTGTGAACATGGACTACGTCGTGGGA 1973

Qy   1979 GCCAGAACGTTCCCAGAGAGCTGCACCTGCTCCTGAGGGTGAAGGCACTG 2038
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1974 GCCAGAACGTTCCCAGAGAGCTGCACCTGCTCCTGAGGGTGAAGGCACTG 2033

Qy   2039 TTCAGCGTGCTCAACTACGAGCGGGCCGCCTCCTGGGCGCCTCCTGTGCTGG 2098
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2034 TTCAGCGTGCTCAACTACGAGCGGGCCGCCTCCTGGGCGCCTCCTGTGCTGG 2093

Qy   2099 GGCCTGGACGATATCCACAGACGTCGTGCTGCGGGCGGTGTGCCCAGGAC 2158
          ||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2159 CCGGCGCCTGAGCTTGTACTTTGTCAAGGTGGATGTGACGGGCGCGCTGACCATCCCCCC 2218
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Db   2159 CCGGCGCCTGAGCTTGTACTTTGTCAAGGTGGATGTGACGGGCGCGCTGACCATCCCCCC 2218
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RESULT 5
US-09-721-456-4
; Sequence 4, Application US/09721456
; GENERAL INFORMATION:
;   APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin B.
;   Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/721,456
  FILING DATE: 22-Nov-2000
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/974,549A
  FILING DATE: 19-NOV-1997
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US 08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US 08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US 08/911,312
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US 08/912,951
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: US 08/915,503
  FILING DATE: 14-AUG-1997
  APPLICATION NUMBER: WO PCT/US97/17618
  FILING DATE: 01-OCT-1997
  APPLICATION NUMBER: WO PCT/US97/17885
  FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph Ted
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 3855 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  FEATURE:
    NAME/KEY: -
    LOCATION: 1..3855
    OTHER INFORMATION: /note= "nucleic acid sequence with an
      open reading frame encoding a delta-182
      variant polypeptide"
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 56..2479
    OTHER INFORMATION: /product= "delta-182 variant
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  SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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US-09-721-456-4

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Query Match      90.7%;  Score 3641;  DB 5;  Length 3855;
Best Local Similarity  95.5%;    Pred. No. 0;
Matches 3833;  Conservative  0;  Mismatches  0;  Indels  182;  Gaps  1;

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Db      1 GCAGGCGTGCGTCCTGCTGCCAGCCGTGCGCTCCCTGGGAAGCCCGCACCCCCGCGATGCC 60

Qy     61 GCGGGCTCCCGCGTGCCGAGCCGTGCGCTCCCTGCGCCGCCAGCCACTACCGCGAGGTGCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGGGCTCCCGCGTGCCGAGCCGTGCGCTCCCTGCGCCGCCAGCCACTACCGCGAGGTGCT 120

Qy    121 GCCGGCTGGCCACGTTCGTGCGGCGCCTGGCGGCGCCCCAGGGGCTGGCGGCTGGTCAGCGGGG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCGGCTGGCCACGTTCGTGCGGCGCCTGGCGGCGCCCCAGGGGCTGGCGGCTGGTCAGCGGG 180
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Qy   181 GGACCCGCGGCTTCCGCGCGCTGGTGCGCTGCCCAGTGCCTGGTGTGCCCTGGGACGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACCCGCGGCTTCCGCGCGCTGGTGCGCTGCCCAGTGCCTGGTGTGCCCTGGGACGC 240

Qy   241 ACGGCCGCCCCCGCCGCGCCCCTCCTTCCGCCAGGTGTCCTGCCTCCAGGTGTCCTGCCTCCAGGTGGTGGC 300
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Db   241 ACGGCCGCCCCCGCCGCGCCCCTCCTTCCGCCAGGTGTCCTGCCTCCAGGTGTCCTGCCTCCAGGTGGTGGC 300

Qy   301 CCGAGTGCTGCAGAGCTGTGCGAGCGGCGCCGAAGAACGTGCTGGCCTTCGGCTTCGC 360
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Db   301 CCGAGTGCTGCAGAGCTGTGCGAGCGGCGCCGAAGAACGTGCTGGCCTTCGGCTTCGC 360

Qy   361 GCTGCTTGGACGGGGCCCGCGGGGGCCTTCACCACCAGCGTGCGCAGCTA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCTGCTTGGACGGGGCCCGCGGGGGCCTTCACCACCAGCGTGCGCAGCTA 420

Qy   421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCCGGGGCGTGGGGGCTGCTGCGCG 480
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Db   421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCCGGGGCGTGGGGGCTGCTGCGCG 480

Qy   481 CCGCGTGGGCGACGAGCTGCTGGTTCACCTGCTGGCACGCTGGCCGCTCTTGTGCTGGT 540
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Db   481 CCGCGTGGGCGACGAGCTGCTGGTTCACCTGCTGGCACGCTGGCCGCTCTTGTGCTGGT 540

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCTCCCAGCTGCGCTACCAGGTGTGCGGGCCCGTGTACCAGCTCGGCGCCTGCCAC 600

Qy   601 TCAGGCCCGGCCCCCGCCCACACGCTAGTGACCCCGCCAGAGGCGTCTGGGATGCGAACGGGC 660
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Db   601 TCAGGCCCGGCCCCCGCCCACACGCTAGTGACCCCGCCAGAGGCGTCTGGGATGCGAACGGGC 660

Qy   661 CTGGAACCATAGCGTCAGGGAGCCGGGGCCGCTGCCCTGGGCCTGCACGGCCTGCCAGTGCCGGAG 720
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Db   661 CTGGAACCATAGCGTCAGGGAGCCGGGGCCGCTGCCCTGGGCCTGCACGGCCTGCCAGTGCCGGAG 720

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Qy   781 TGCCCCTGAGCCGGAGCGGACCCCGTTGGGCAGGGTCCTGGGCCCACCCGGCCAGGAC 840
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Db   781 TGCCCCTGAGCCGGAGCGGACCCCGTTGGGCAGGGTCCTGGGCCCACCCGGCCAGGAC 840

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Db  1081 GCCCTCCTTCCTTACTCAGCTCTCGAGGCCCAGCTGGCGTCGACTGGCGTCTGCTGGAGGCTCGTGGA 1140

Qy  1141 GACCATCTTTCTGGGTTCCAGGCCTTGCCCAGCCACTACCGCGAGGTGCT 1200
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Db   3299  GAGCAGAACACCAGCAGCCCTGCACGCCCGGCTCTACGTCCCAGGGAGGGAGGGCGGCC  3358

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Qy   3601  CATGTCCGGCTGAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT  3660
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Db   3419  CATGTCCGGCTGAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT  3478

Qy   3661  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCACCAGGCTGGCGTCCGGCTCCACCCCA  3720
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Db   3479  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCACCAGGCTGGCGTCCGGCTCCACCCCA  3538

Qy   3721  GGGCCAGCGTTTTCCTCACCAGGAGCCCGGCGTTCCACTCCCCACATAGGAATAGTCCATCC  3780
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Db   3719  CCCTGTACACAGGCCAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGGTCAAATTGGGGG  3778

Qy   3961  GAGGTGCTGTGGGAGTAAAATACTGAAATATGAATATATGAGTTTTTCAGTTTTGAAAAAA  4015
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RESULT 6
US-09-721-456-721
; Sequence 721, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin B.
;   Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/721,456
;   FILING DATE: 22-Nov-2000
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/974,549A
;   FILING DATE: 19-NOV-1997
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
;   APPLICATION NUMBER: US 08/844,419

;   FILING DATE: 18-APR-1997
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997
;   APPLICATION NUMBER: US 08/854,050
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: US 08/911,312
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/912,951
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/915,503
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: WO PCT/US97/17618
;   FILING DATE: 01-OCT-1997
;   APPLICATION NUMBER: WO PCT/US97/17885
;   FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph Ted
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 721:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3451 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   FEATURE:
;   NAME/KEY: -
;   LOCATION: 1..3451
;   OTHER INFORMATION: /note= "hTRT sequence employing codon
;   distribution preferentially used by
;   highly expressed genes in E. coli
;   containing SacI and XhoI sites"
;   SEQUENCE DESCRIPTION: SEQ ID NO: 721:
US-09-721-456-721

Query Match   54.98%;   Score 2205.2;   DB 5;   Length 3451;
Best Local Similarity 78.0%;   Pred. No. 0;
Matches 2654;   Conservative 0;   Mismatches 748;   Indels 0;   Gaps 0;

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Qy   56  ATGGCCGCGCGCTCCCGCTGCCGAGCCGTGCGCCCTGCTCCCACTACCGCGAG  115
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Db   28  ATGGCCGGTGGTGCTTCCCGCTGCCGTGTTCCGTTCCTGCTCGTTCCCACTATCGCGAA  87

Qy  116  GTGCTGCCGCTGGGCCACGTTCGTCGCGCCCTGGCGGCCCCAGGGCTGGCGTGGTCAG  175
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Db   88  GTTCTGCCGCTGGCTACCTTGGTTCGTCGCGCTCTGGGTGGTCCGCAGGGTTGGCGTCTGGTTCAG  147

Qy  176  CGCGGGACCCGCGGCGGGTTTCCGCGGCTGGTGGTGGCCAGTGCTGGCTGGTGCCCCTGG  235
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Db  148  CGTGGTGACCCGCGGTGGTTTCCGTCGTCTGGTTGGTGGTGCTCAGTGCTGGCTGGTTCCGTGG  207

Qy  236  GACGCACGGCCGCGCCCCCCCGCGCCCCTCCTTCCGCGACGTGTCCGCCAGTGTCCTGAAGGAGCTG  295
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Db  208  GACGCGCTGGCCGTCCCGCCGCGCCCTCCTTCCGTCCGTGGTTTCCTCCGTCCAGGTTTCCTCGTCGTGAAAGAACTG  267

Qy  296  GTGGCCCGAGTGCTGCAGAGGCTGCTGCCGGGCGGCGAAGAACGTGCTGCCTTCGGGC  355
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Db  268  GTTGCTCGTGTTCTGCAGCGTCTGCTGCCGGGTGCGAACGTGTGCTAAAAACGTGTCTGGCTAAAAACGTGTTCTGGCTTTCGGT  327

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Db  328  TTCGGCCTGCTGGACGGTGTCGTGGTGGTCCGCGAAGCATTCACCCACCTCCGTCGT  387

Qy  416  AGTACCTGCCCAACACGGTGACCGACGCACTGCGGGGAGGCGGGGCTGTGGGGCTGCTG  475
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Db   448 CTGCGTCGTGTTGGTGACGACGTTCTGGCTTCACCTGCTTGCGCTTCGCCGT   507

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Db   688 GCTGCTTGGAACCACTCCGTCGGTGGTGTGTTTCCGCTTCCGGTTCCGGTCGTCGT   747

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Qy   956 CGCCAGCACCACGCGGGGCCCCATCCACATCGCGGCCAGCAAGCACTTCCTCTACTCCGGAGACACGCCT   1015
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Db   928 CGTCAGCAGCTGGTCCGTCCGGTTACGCTGGACCATCCACAGGGTCCACCACGTCCGGTCCGGT   987

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Db   988 TGCCCGCCGGTTTACGCTGAAACCAAACACACTCCTGTACTCCTCCGGACAAAGAACAG   1047

Qy   1076 CTGCGGCGCCTCCTTCACTCAGCTCTTCGAGGCCCAGCGTGCGCGCCTGGTCGGAGGGCTCTGTTCGTCTG   1135
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Qy   1136 GTGGAGACCATCTTTCTGGGGTTCCAGGGCCCTTGGATGCCAGGGGACTCCCCGCAGGTTGCCC   1195
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Db   1168 CGTCTGCCGCAGCGTACTGGCCGTTGAATGCGTCCTGTTCCTGGAACTGCTGGGCAACCAC   1227

Qy   1256 GCGCAGTGCCCCTACAGGGGTGCTCTCGAAGACGCCAGCACGTGCGGGTCACC   1315
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Db   2128 GACCCGCCGCCGGAACTGTACTTCGTTAAAGTTGACGTTACCGGCGGTACGACACCATC   2187

Qy   2216 CCCCAGGACAGGGTGACCGTGGAGGTCACGCGGAGCATCATCCAGCATCATCCAGATCGC   2275
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Db   2488 CGTGGTAAATCCTACGTTCAGTTCCAGGAGGTTCCCATCCTGTCCACCCCTG   2547

Qy   2576 CTCTCAGCCGTGCTACGGCCCTGTCGTTTGTGCGGGATTCGGCGCGGGAC   2635
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Db   2548 CTGTGCTCCGTGCTGCTACGGTGACATGGACATGGACATCCGTGCGTGAC   2607

Qy   2636 GGGCTGCTCCTGCCGTTGGTGGATGATTCTTGTTGGTGACACCTCACCCACGCG   2695
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Db   2636 GGGCTGCTCCTGCCGTT

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00261OUS
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 639:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396
OTHER INFORMATION: /note= "hTRT-encoding sequence employing
alternative codon distributions for
enteric bacteria (high expressing
genes)"
SEQUENCE DESCRIPTION: SEQ ID NO: 639:
US-09-721-456-639

Query Match   54.8%;   Score 2200.8;   DB 5;   Length 3396;
Best Local Similarity 78.0%;   Pred. No. 0;
Matches 2649;   Conservative 0;   Mismatches 747;   Indels 0;   Gaps 0;

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Qy   56 ATGCCGGCGCTCCCGCCGCAGCCGGCTCCCTGCTGCGCAGCCACTACCGGCGAG 115
           ||||||| ||||| ||   |||| ||  |||||| || |||||||||||||||||
Db    1 ATGCCGGCGTGCTCCGGCGTGTCCGGCGTTCCCACTACCGGTGAA 60

Qy  116 GTGCTGCCTCGGTGCCACGTTCGTGCGCGCCGCCCTGGGGGCCCCAGGGCTGCGGCGTGTGCCAG 175
           |  |||||  || ||   ||| || | |||| ||| || ||||||| | |||||| ||
Db   61 GTTCTGCCTGCGTCACCTTCGTCGTCGTCTGGTCCGCAGGTGCTCCTGGTTCTCGGTTCAG 120

Qy  176 CCGCGGGGACCCGGCGTTCCCGGCCTGGTCGGCCCAGTGCCCTGG 235
           |  || ||||||||| ||||| ||||||| ||| ||||| ||||||||||| |||
Db  121 CGTGGTGACCCGGCTGCTTTCCGTGCTCGTTCCTGGTGCGCTCAGTGGTTCCGTGG 180
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Db 2608 GGTCTGCTGCTGCGTCCTGGTTGACGACTTCCTGCTGCTGGTTACTCCGGCACCTGACCCACGCT 2667
Qy 2696 AAAACCTTCCTCAGGACCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACTTG 2755
           ||||||| | |||||  | |||| || || ||| |   ||| |||| |||  || | ||
Db 2668 AAAACCTTCCTGCGTACCCTGGTTCGTGGTGTTCCGGAATACGGTTGCGTGTAAACCTG 2727

Qy 2756 CGGAAGACAGTGGTGAACTTCCCTGGTAGAGACGAGGCCCTGGGTGGCACGGCTTTTGTT 2815
           || || || || ||||| |||||  ||  |||| ||||| ||||||||| ||  ||||||
Db 2728 CGTAAAACCGTTGTTAACTTCCCGGTTGAAGACGAAGCTCTGGGTGGCACCGCTTTCGTT 2787

Qy 2816 CAGATGCCGGCCCACGGCCTATTCCCGTGCGCCTGCTGCTGATACCCGGGACCCTG 2875
           ||||| |||| |  ||| ||| || || || || |||  | ||  ||||  ||||||
Db 2788 CAGATGCCGGCTCACGGTCTGTTCCCGTGCGCCTGCTGCTGGACACCCGTACCCTG 2847

Qy 2876 GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC 2935
           ||  ||||| || |||||||| |||| || |||||| |||| || ||||||  ||| ||||
Db 2848 GAAGTTCAGTCCGACTACTCCTCCTACGCTCGTACCTCCATCCGTGCTTCCGTGACCTTC 2907

Qy 2936 AACCCGGCTTCAAGGCTGGGAGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG 2995
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Db 2908 AACCGTGGTTCAAAGCTGGTCGTAACATCGTCGTAAACTGTTCGGTGTTCGTGCGCTG 2967

Qy 2996 AAGTGTCACAGCCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGCGCACCAAC 3055
           || || ||||| || ||||| ||||| ||||| ||| || |||| || ||||| ||||||
Db 2968 AAATGCCACTCCCCTGTTTCCGGACTGCAGGTAAACTCCCTGCAGACCGTTTGCACCAAC 3027

Qy 3056 ATCTACAAGATCCTCCGCTGCTGCAGGGCTACAGGTTCAGCTGCTCGCAGCTCCCA 3115
           ||||||||||  |||||||||||| || ||||  |||   |||||  |||| ||| |
Db 3028 ATCTACAAAATCCTGCGCTGCTGCAGGCTTACCGTTCCGTTTCCAGCGTCTGCAGCTGCCG 3087

Qy 3116 TTTCATCAGCAAGTTTGGAAGAACCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC 3175
           ||| || |||||| ||||| ||| ||| ||  ||||| ||| || || ||||| || ||
Db 3088 TTCCACCAGCAGGTTTGGAAAAACCCGACCTTCTTCCTGCGTGTTATCTCCGACACCGCT 3147

Qy 3176 TCCCTCCTGCTACTCCATCCTGAAAGCCAAGAAGCCAAGAACGCAGGGATGTCGCTCGGGGGC 3235
           || ||  | || || ||||| |||||  || || ||  ||||| | || |||| ||| |||||
Db 3148 TCCCTGTGCTACTCCATCCTGAAAGCTGGTGAAGCGTGGTATGTCCCGGCTGCTAAAGGT 3207

Qy 3236 GCGGCGGGCCCCTCTGCCCTCCGAGGCGTGCAGTGGCCGTGTGCCAAGCATTCCTGCTC 3295
           || ||||||| |||| |||| ||| ||| || || ||||| |||| |||  |||| |||
Db 3208 GCTGCTGGTCCGTCCGGCGTTCCGAAGCTGTTCAGTGGCTGTGTGCCACCAGGCTTCCTGCTG 3267

Qy 3296 AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG 3355
           ||||| |||| || ||||| | |||||  |||| ||| || || |||| ||||| ||||
Db 3268 AAACTGACCCGTCACCGTGTTACCTACGTTCCGCTGCTGGGTTCCCTGCGTACCGCTCAG 3327

Qy 3356 ACGCAGCTGAGTCGGAAGCTCCGGGACACGTCCCGGGACGCCGCAGCCGCAGCCAAC 3415
           || || |||| ||| || ||||| || || ||| ||||| |||| ||||||| |||
Db 3328 ACCCAGCTGTCCCGTAAACTGCCGGGTACCACCATCTGACCCGTGCTGCTGCTAAC 3387

Qy 3416 CCGGGACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGG 3457
           |||||| |||| |  |||| |   ||||||| |||||||||||
Db 3388 CCGGCTCTGCCGTCCGACTTCAAAACCATCCTGGACTAATGG 3429
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RESULT 7
US-09-721-456-639
; Sequence 639, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin B.
;   Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California

```
Qy  1316 CCAGCAGCCGGTGTCTGTCCCGGGAGAAGCCCAGGGCTCTGTGCGGCCCCCAGGAG 1375
              || || ||||||| |  || ||  | ||  ||| |  |||| ||| ||| |||| |
Db  1261 CCGGCTGCTGGTGTTTGCGGTCGTGAAAAAACCGAGGGTTCCGTTGCTGCTGCTGCCGGAAGAA 1320

Qy  1376 GAGGACAGAAGACCCGGC 1435
              || |||  |  ||| |
Db  1321 GAAGACAACCGACCCGGTCTGCTGCTGTCTGTTCAGCTGCTCAGCGACTCCTCCCCGTGGCAG 1380

Qy  1436 GTGTACGGCTTCGTGCGGGGCCTGCCTGCGGCCTGGTGCCGCGTGGTGCCTGGGCCTCC 1495
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Db  1381 GTTTACGGTTTCGTGCGTGTCGTGCTGCCTGGTTCGTTCGTCGTGTGTGGGGTTCC 1440

Qy  1496 AGGCACAACGAACGCCGCTTCCTCAGGAACAACCAAGAAGTTCATCTCCCTGGGAAGCAT 1555
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Db  1441 CGTCACAACGAACGTCGTTTCCTGCGTAACAACCAAAATTCATCTCCCTGGGTAAACAC 1500

Qy  1556 GCCAAGCTCTCGCTGCGAGGAGCTGACGTGGAAGATGAGGGTGCGGGGACTGCCGCTTGGCTG 1615
              || ||||| | ||||| || |||| | |||  ||  | || |||| || | ||| |||||
Db  1501 GCTAAACTGTCCCTGCAGGAACTGACCTGGAAAATGTCCGTTCGTGCGGTTCTTGGCTG 1560

Qy  1616 CGCAGGAGCCCAGGGGTTGCGTGCTGTTCCCGGCCCGCTGGTGCCGCGTGCTGCTGCGGGATC 1675
              ||  ||  |||| |  | || |  |||||||  || || | |  | ||||| |||| | ||
Db  1561 CGTCGTTCCCCGGGTGTTGGTGTTGTTCCGGTTCGTTCGTCGTGTGTGGCGTGCTGCTGAAGAAATC 1620

Qy  1676 CTGGCCAAGTTCTTGCACTGGCTGACTGTGTTACGTCGTGTGCTGCTCAGGTCTTTC 1735
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Db  1621 CTGGCTAAATTCCTGCACTGGCTGATGTCCGTTTACGTGGAACTGCTGCGTGTCCTTC 1680

Qy  1736 TTTTATGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTTCTCACCGGAAGAGTGTC 1795
              || |||| || || ||||| || |||| | |   | || |   || | | | ||  | ||
Db  1681 TTCTACGTTACCGAAACCACCTTCCATCGTGTTCGTCGTCTGTTTCTCTACCGTAAATCCGTT 1740

Qy  1796 TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGGAG 1855
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Db  1741 TGGTCCAAACTGCAGTCCATCGATCCGTCAGCGACCACCCTGAAACGTGTTCAGCTGCGTGAA 1800

Qy  1856 CTGTTCAGGCGAAGCAGGAGTCAGGCAGCATCGGGAAGCGCCGCGCCTGCTGACGTCCAGA 1915
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Db  1801 CTGTCCGAAGCTGAAGTTCGTCACCGTTTACGTTGGAAGCTGCGTTGCTGCTGACCTCCCGT 1860

Qy  1916 CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGCGGCCGCGATTGTGAACATGACTACGTCGTG 1975
              || || ||||| |  ||  | ||| |  |  ||  |  || | ||  | | ||| ||  | |
Db  1861 CTGCGTTTCATCCCGATCCGGAAACCGGACGTCTGCGTCCGATCGTTAACATGGACTACGTTGTT 1920

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Db  1921 GGTGCTGTCGTACCTTCCGTGTGAAAAAACGTGCTGACCTCGACCTCCCGTTAAAGCT 1980

Qy  2036 CTGTTCAGCGTGCTCAACTACGAGCGGGACGGCGCCGGCGCGCCCTCTGTG 2095
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Db  1981 CTGTTCCGTGTTCTGAACTACGAACAGGACGGTGCTGGTGCGCCGTCCGTT 2040

Qy  2096 CTGGGCCTGACGATATCCAACCCGCCGCTTCGTGCTCGCGGGCCGCCAG 2155
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Db  2041 CTGGGTCTGGACGACATCCACCCGTTGCGTACCTTCGTTCGTGTGTCTCAG 2100

Qy  2156 GACCCGGCGCTGAGCGTGACTTTGTCAAGGTGACGGCGCGCGTACGACCATC 2215
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Db  2101 GACCCCGCCCTGAGCTGAACGTGTTACTTCGTTAAAGTTGACGTTACCGACCATC 2160

Qy  2216 CCCAGGACAGAGCTCACGGAGGCCTCGGATGCCAGCATCATCCCAGACACGTACTGC 2275
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Db  2161 CCCAGGACCGTGACCTGACCGAAGTGTATCGCTTCCATCATCCCAGCAGAACCACCTACTGC 2220

Qy  2276 GTGGCTCGGTATGCCGTGGTGTCCAGAAGGCCGCTTCGCGGCCTTCAAG 2335
              || | |   || || || |  | ||| || | | || | || ||| |||
Db  2221 GTTGCGTCGTACGCTGTTGTGTTCAGAAGTGCTCACGGTCACGTTCGTAAAGCTTTCAAA 2280

Qy  2336 AGCCACGTCTCTACCTTGACAGACCACGCACTGCCGAGCTGCGTTCGTGCTCACCTG 2395
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Db  2281 TCCCACGTTTCCACCCTGACCGACCTGCGTGACCTGCAGTTCGTTCGTGTGCTCACCTG 2340

Qy  2396 CAGGAGACCACCAGCCCGTCGAGGATGCCCGTCATCGACGCAGAGCTCCTCGTCAATGAG 2455
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Qy   236 GACGCACGGCCGCCCCGCCCCCTCCTTCGCCCAGTGTCCTGCCTGAAGGAGCTG 295
              |||||| | |||||| || | |||||| | | ||||||| ||||||
Db   181 GACGCTGCTCCCGCCGCCGGCTCCGTCCGTTCCTGCCTCAGGTTTCCTGCCTGAAAGAACTG 240

Qy   296 GTGGCCCCAGTGCTGCAGAGGCGTGCGCGGGCGCCCCCCGAGGGCCTTCACCACCAGCGTCGC 355
              || |||||||| ||| || ||||| || | || || || ||||| | || ||||| |||
Db   241 GTTGCTGCTGTTGCTGGCAGGTGTGTGCGGGAACGTGTGTAAAAACGTGTTTCGGT 300

Qy   356 TTCGCGTGCTGACAGGGGCCCCGCGGGGGCCTTCACCACCAGCCGTCGCGC 415
              || | ||||| | || |  || | |||| || || |||| |||| |   |
Db   301 TTCGCCTGCTGGACCACCTCCGTCGTGGTGCTCGTTCACCTGTCTTTCACCGTTCCTT 360

Qy   416 AGCTACCTGCCCACACGGTGACCGACGACCACATCGGTTCTGCTCTGTTTGTTGCGGATGCGCA 475
              |||| || | ||   || | ||| ||  | || |  |  | ||||| || | |  ||   || ||
Db   361 TCCTACCTGCCGAACCACCGTGACCACCATCGGTGTTCCGGTGTTCACCTGGTTTGGGGTGCT 420

Qy   476 CTGCGCCGCGGTGGGCGACGACGTCTGGTTCACCTGGTTCACGCCTGGCCTGCCCGCTCTTTGTG 535
              ||| || | | | ||| || || |  | || ||| || | | | | |  | ||| | |||  ||
Db   421 CTGCGCCCAGGTCTGGGTGACGACCTCCTGTTCTGCTTCACCTGGTTCGTTGTTGCGCTGTTCTT 480

Qy   536 CTGGTGCTCCCAGTCGCGCTTCCTACCAGTGTGCGGGGGCCTTGCGGGGCTGTACCAGCTGCGGCCT 595
              || |||  |  ||   ||| | || |||| | || | |  | | || || |  | ||||||| | ||
Db   481 CTGGTTGCTCCCGGTTCGTCCGTTACCAGCGTTGCGGGTGTTCCGCCGTGTACCAGCTGTGGCT 540

Qy   596 GCCACTCAGGCCCGGGCCCCACACGCTCAGTGGACCCCGCGAAGGCGTCCGTCGGGGGATGGCGAA 655
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Db   541 GCTACCCAGGCTCGTCCGGGAGTCTGGTTGGTGTCGTCCGGTTCCTGGCTTCACCTGGGTTGCCGAA 600

Qy   656 CGGGCCTGGAACCATAGCTCAGGGAGGCCGGGGTCCCCTGCCCAGCGACCCGCCGAA 715
              || | || |||  | | || || || ||  |  | |||  | |  ||||| | ||| |
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Qy   716 GGCAGGAGGCCGGGGAGTGCAGCCGAAGTCTGCCCAGAGGCCCAGGCGT 775
              |  |||||| | || ||  | ||| | | | ||| |||| ||||||| ||
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Qy   776 GGGGCTGCCCTGCCAGCCGGACGGCGACCGGTGGGCAGGGGTCCTGGGCCCACCCGGGC 835
              || || | || |||| ||| || ||  || | |  ||| |  || || |  ||| |||
Db   721 GGTGCTGCTGCTGGTGCCGGAACCGTACCTCCGGTTCCTGGCTTCACCTGGGTTCACCCGGGT 780

Qy   836 AGGACGCGCTGGACCGAGCTGGTTTCTGTGTGTGCGGTCGCGCGACCGCCGCCGAA 895
              || || | |||| || || ||| | | || |  |  || | |  |  ||| ||||||
Db   781 CGTACCCCGGTTCGTGGTTCGTCGGTTGTTTTCCCGGCGTCCGGGCTGCGTCCGCGAA 840

Qy   896 GAAGGCCACCTCTTTGGAGGGTGCGCTCTGCACGCGGTCGCCACTCCACTCCTGGGC 955
              ||| | |||| | | || ||  |  || ||| |  |  | ||| ||| ||| | |||
Db   841 GAAGCTACCTCCCCTGAAGGTGCTCTGTGCTGCGTTCCGTCACTCCACTCCGGTTGGT 900

Qy   956 CGCCAGCACCGGGGCCCCCCATCCACATGGGCCACCACAGCCTCCTGGGACACGCCT 1015
              || ||||| ||  ||  |  | || |  |  | || ||  | |  |||||  | |
Db   901 CGTCAGCACCACCGTCCGGTTCCGGTCCGTTGGGGGACACGCCTTCCTGGGACACCCCG 960

Qy  1016 TGTCCCCGGTGTACGGCCGAGACCCGAGAGCGCTGACTGGCTGCCTCTCAGGCAGAAGGAGCAG 1075
              |  | | || ||||| || ||  | |||||| | | | ||| | | | |   |||| |||| ||
Db   961 TGCCCGCCGGTTACGCTGACGTGGTTCGTCCTGTGTACTGGCTGGTTCTTCCGGGTGACAAAGAACAG 1020

Qy  1076 CTGCCTGGCGGCCCTCAGCTGCTCTCGAGGCCGAGGCGCTGCCTGCGGGCCAGAGTGCGGAGCTC 1135
              || ||||| | | | ||| || ||  | |  | |  ||| | || | || | | | |||| ||
Db  1021 CTGCCTGGTGCTGCGTCCGGTTCCTGGTCCGTGCTCGGACGTGCCTGCGTGTCCGGTTGGTCGCTG 1080

Qy  1136 GTGGAGACCAGCTTTCTGTGGGGTTCCAGGCCCTGGATGCCCGTCCCCCGAGGTTGCCC 1195
              || |||||||  | | |||  | || || | | |||  | || |||   || ||||| |
Db  1081 GTTGAAACCATCTTCCTGTGGGTTCCTGGATGCCGGTGAAGCCGTACCCCGTGGTTGCGC 1140

Qy  1196 CGCTGCCCAGCGCACTGGCAAATGCGGCCCTGTTTCTGGAGACCTGTGCTTGGGAACCAC 1255
              || |||||||| ||| || |  | ||||| | ||||| || || || || ||||| | ||
Db  1141 TGCCTGCCCAGCGTTACGGCTGAATGCGGTCCGTCTGTTCCTGGAACTGCTGGTAACCAC 1200

Qy  1256 GGCCAGTGACGTCCCCTCAGGTGCTGCCCCTCAAGAGACGCACTGCCGAGCTGCGGTCACC 1315
              || |||| | | ||   ||| ||| | || || |  ||  | | |  ||| ||| | ||||
Db  1201 GCTCAGTGACGGTGTTCTGCGTGTTCTGCCGGTGAAAACCCACTGCCGTGCTGCTGTGTGTTTACC 1260
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US-09-721-456-638

; Sequence 638, Application US/09721456

GENERAL INFORMATION:

    APPLICANT: Cech, Thomas R.
        Lingner, Joachim
        Nakamura, Toru
        Chapman, Karen B.
        Morin, Gregg B.
        Harley, Calvin B.
        Andrews, William H.

    TITLE OF INVENTION: Human Telomerase Catalytic Subunit

    NUMBER OF SEQUENCES: 727

    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Townsend and Townsend and Crew LLP
      STREET: Two Embarcadero Center, Eighth Floor
      CITY: San Francisco
      STATE: California
      COUNTRY: USA
      ZIP: 94111-3834

    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.30

    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/721,456
      FILING DATE: 22-Nov-2000
      CLASSIFICATION: <Unknown>

    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/08/974,549A
      FILING DATE: 19-NOV-1997
      APPLICATION NUMBER: US 08/724,643
      FILING DATE: 01-OCT-1996
      APPLICATION NUMBER: US 08/844,419
      FILING DATE: 18-APR-1997
      APPLICATION NUMBER: US 08/846,017
      FILING DATE: 25-APR-1997
      APPLICATION NUMBER: US 08/851,843
      FILING DATE: 06-MAY-1997
      APPLICATION NUMBER: US 08/854,050
      FILING DATE: 09-MAY-1997
      APPLICATION NUMBER: US 08/911,312
      FILING DATE: 14-AUG-1997
      APPLICATION NUMBER: US 08/912,951
      FILING DATE: 14-AUG-1997
      APPLICATION NUMBER: US 08/915,503
      FILING DATE: 14-AUG-1997
      APPLICATION NUMBER: WO PCT/US97/17618
      FILING DATE: 01-OCT-1997
      APPLICATION NUMBER: WO PCT/US97/17885
      FILING DATE: 01-OCT-1997

    ATTORNEY/AGENT INFORMATION:
      NAME: Apple, Randolph Ted
      REGISTRATION NUMBER: 36,429
      REFERENCE/DOCKET NUMBER: 015389-002610US

    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 576-0200
      TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 638:

    SEQUENCE CHARACTERISTICS:
      LENGTH: 3396 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear

    MOLECULE TYPE: DNA

    FEATURE:
      NAME/KEY: -
      LOCATION: 1..3396
      OTHER INFORMATION: /note= "hTRT-encoding sequence employing
      alternative codon distributions for
      E. coli (all genes)"

    SEQUENCE DESCRIPTION: SEQ ID NO: 638:

US-09-721-456-638

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Qy   2341 |||||  |||  |||      |||||||  ||  |||  ||  |||||  |||      ||||||||||||  || 2400
Db        CAGGAAACCTCCCGCTGCGTGACGCTGTGTTATCGACAGTGCTCCTCCCTGAACGAA

Qy   2456 GCCAGCAGTGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCCATC 2515
Db   2401 GCTTCCTCCCGGTCTGTTCGACGTTTTCCTGCGTTTCATGTGCCACCACGCTGTTCGTATC 2460

Qy   2516 AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCCCACGCTG 2575
Db   2461 CGTGGTAAATCCTACGTTCAGTGCCAGGGTATCCCGCAGGGTTCCATCCTGTCCACCCTG 2520

Qy   2576 CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCCGGAC 2635
Db   2521 CTGTGCTCCCTGTGCTACGGTGACATGGAAAACAAACTGTTCGCTGGTATCCGTCCGTGAC 2580

Qy   2636 GGGCTGCTCTCGCGTTGGTGGTGACATTCTTGTTGGTGACACCTCACCTCACCCACGCG 2695
Db   2581 GGTCTGCTGTCGCGTCCGGTTGGTGGTTGACACTTCCTGCTGGTTACCCCGCACCTCACCCAGCGCT 2640

Qy   2696 AAAACCTTCCTCAGGACCCTGGTCTCCGAGGTGTCCCTGAGTATGGCGCGTGGTGAACTTG 2755
Db   2641 AAAACCTTCCTGCGTACCCTGGTTCGTGGTGTTTCCGGAATACGGTTGCGTTGTTAACCTG 2700

Qy   2756 CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT 2815
Db   2701 CGTAAAACCGTGTTAACTTCCCGGTTGAAGACGAAGCTCTGGGTGGTACCGCTTTTCGTT 2760

Qy   2816 CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGATACCCGGACCCTG 2875
Db   2761 CAGATGCCGGCTCACGGTCTGTTCCCGTGTGTCGGCCTGCTGCTGGACACCCGTACCCTG 2820

Qy   2876 GAGGTGCAGAGCGACTACTCCAGCTATGCCCCGGACCTCCATCAGAGCCAGTCTCACCTC 2935
Db   2821 GAAGTTCAGTCCGACTACTCCTCCTACGCTCCGGACCTCCATCCGTCTCCGGACCTTC 2880

Qy   2936 AACCGCGGCTTCAAGGCTTGGGAGGAACATGCCGTCGCAAACTCTTTGGGGTCTTGCGGCTG 2995
Db   2881 AACCGTGGTTTCAAAGCTTGGGAAACTGTGTCGGTATCTGTCTGTCTCTG 2940

Qy   2996 AAGTGTCACAGCCTGTTTCTGGATTTGCAGTTGAACAGCCTCCAGACGGTGTGCACCAAC 3055
Db   2941 AAATGCCACTCCCTGTTCCTGGACCTGCAGGTTAACTCCCTGCAGACCGTTTGCACCAAC 3000

Qy   3056 ATCTACAAAGATCCTCCTGCTCGCAGCCGTACAGGTTTCACGGCATGTGCTGCAGCGTCCCA 3115
Db   3001 ATCTACAAAAATCCTGCTGCTGCGTTTCCACCGTTTCCGTGTTATCCGCACACCGCT 3060

Qy   3116 TTTCATCAGCAAGTTGGAAGAACCCCACATTTTCCTGCGGCGTCATCTCTGACACGGGC 3175
Db   3061 TTCCACCAGCAGGTTTGGAAAAACCCGGAAGCTAAAAACGCTGGTATGTCCCTGGGTGCTAAAGGT 3120

Qy   3176 TCCCTTCCGCTACTCCATCCTGAAAGCCAGAGACCAGGGGCATTCGCTCGCGGCCCAAGGGC 3235
Db   3121 TCCCTGTCGCTACTCCATCCTGAAAGCCTAAAAACGCTGGTATGTCCCTGGGTGCTAAAGGT 3180

Qy   3236 GCCGCCGGCCCCTCCGCCCTCCGAGGCCGTGCAGTGCCTGTGTCCACCAAGCATTCCTCGCTC 3295
Db   3181 GCTGCTGGTCCCGCTGCCGTCCGAAGCTGTTCAGTGCGTGTCCACCAGGCTTTCCTGCTG 3240

Qy   3296 AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGGTCACTCAGGACAGCCCCAG 3355
Db   3241 AAACTGACCCGCACCGTGTTACCTACGTTCCGCGTGTCTGGGTACCCGTCCAG 3300

Qy   3356 ACGGCAGCTGAGTCGGGACGTCCCGGGGGACGACGCGCTGGAGGGCCGCAGCCAAC 3415
Db   3301 ACCCAGCGTGTCCCGTAAACTGCCGGGTACCACCCCTGACCCGCTGCTGGAAGCTGCTGCTAAC 3360

Qy   3416 CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC 3451
Db   3361 CCGGCTGCCGTCCGACTTCAAAACCATCCTGGAC 3396
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RESULT 8

Query Match   54.7%;   Score 2196.6;   DB 5;   Length 3396;
Best Local Similarity 77.9%;
Matches 2646;   Conservative 0;   Mismatches 0;   Indels 749;   Gaps 0;

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Qy    56 ATGCCGGCGGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCGCTGCGCAGCCACTACCGCGAG  115
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Db     1 ATGCCGGCGGCCCCGCGCCGGTGCGCGCGGTGCGCTGCGCTGCGCCAGCCATTATCGCGAA   60

Qy   116 GTGCTGCCGCGACGTTCGTGCGGCGCCTGGGGCGCCTGGCGGCTGGTGTGCAG          175
         |||||||||| ||||||||| ||||||| ||||||||||||||||||||| |||
Db    61 GTGCTGCGCCTGGCGCACCTTTGTGCGCGCGCCCTGGGCGCGCCTGGCGCTGCGCAG     120

Qy   176 CGCGGGGACCGGGCGGCGGCGGGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGCCCTGG   235
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Db   121 CGCGCGGGCGGATCCGGCGCGGCGTTTCCGCGCGCTGGTGCGCAGTGCCTGCCCGTGG    180

Qy   236 GACCGCACGGCGCCGCGCCGCGCCCCGCGGCGCGCCTCTTCCGCCAGTGTCTGCCGAAGGAGCTG   295
         || || ||||| ||||||| ||||||| || ||||||| |||||||||||||||||||||
Db   181 GATGCGCGCCGCCGCCGCGGCGCGCCGAGCTTTCGCCAGTGAGCTGCCTGCCGAAAGAACTG    240

Qy   296 GTGCGCCAGTGCTGCAGAGGCTGTGCGAGGCGCGGAAGAACGTGCTGGGCCTTCGGC      355
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Db   241 GTGCGCGCGCCGTGCTGCAGCCGCGTGCGAACGCGGCGAAAAACGTGCTGGCCGTTTGGC   300

Qy   356 TTCGCGCTGCTGACGGGGCGCCCCCGAGGCCTTCACCACCAGCGTGCGC          415
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Db   301 TTTGCGCTGCTGGATGGGCGCGGCGCCCCGGAAGCGTTTACCACCAGCGTGCGC     360

Qy   416 AGCTACCTGCCCAACACGGTGCCCGACGACTGCGACGCACTGCGGGGCGTGCTG   475
         ||||||||||||| ||||| ||||| |||||||||||||||||||||||||||
Db   361 AGCTATCTGCCGAACACCGTGCGCGATCGCGACGCGCTGCGCGGCGTGGGGCGCG    420

Qy   476 CTGCGCCCGCGTGGGGACGACGTGCTGGTTCACCTGGTCTGGTGGGCGCCGCGCTCTTGTG   535
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Db   421 CTGCGCCCGCGTGGGGCGATGATGCGCTGGTCGCATGCCTGGCGCGCGCCTGCGGCTG     480

Qy   536 CTGGTGGCTCCCAGCTGCGCCTACCAGTGTGCGGGCGCGCTGTACCAGCTCGGCGCGCT   595
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Qy   596 GCCACTCAGGCGCCGCGCCCCCACACGCTAGTGGACCCGCGCGAGGCGTCTGGGATGCGGAA   655
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Db   541 GCGCCGCAGCCCCGCGCGCCGCGCCGCGCCGAGCGGACCCGCGCGAGGCGCGCCGGGCTGGAA    600

Qy   656 CGGGCCTGGAACCATAGCGTCAGGAGGCGGAGGTCCCCGAGTTCCAGCCCCCGGT   715
         || |||||||||||||| ||||| ||||||| |||||||||||||||||||||||
Db   601 CGGCCGGTGGAACCATAGCGTGCGCGAAGCGGCGGGCCTGCGCCGGCGCCCGGGGC    660

Qy   716 GCGAGGAGGCGGGGGGAGCAGTGCCAGCCGAAGTCTGCCGCGGCCCCCAGGCGT   775
         |||||||||||||||||||||||| || ||||||||||| |||
Db   661 GCGCCGCCGCCGGGGCCGGGCGGCAGCCGCGGCGCCCGGGCGAAACGCCCGCGCC    720

Qy   776 GGCGCTGCCCCCGTGAGCCGAGGGGACCCCGTTGGGCAGGGGGTCCCGGGCACCCGGGC   835
         ||| |||||||| ||||||||| |||||||| |||||||| ||||||||||||||||
Db   721 GGGCGCGGCGGCCCGGAACCGGACGCGCACCCCGGTGGGCGCATCCGGCGTGGGC    780

Qy   836 AGGACGCGGTGGACCGGAGTGACCCGAGTGTTCTGTGTGGTTCTGTGGTGTCACCTGGTGGGC   895
         ||||| ||||| ||||| |||| |||||||||| |||||||||||||||||
Db   781 CGCACCGCGGGCCGCGGAGCGGTGGGCGCGCCGCCACTGCGCCTGGGCGGC    840

Qy   896 GAAGCCACCTCTTTGGAGGTGCGCTCTGCGAGGACCAAGCCACTCCCACCTCCGGGC   955
         ||||| ||||| ||||| ||||| |||
Db   841 GAAGCGACCAGCCTGGAAGGCGGCGCGTGAGCGCTGACGCTGGAGCCGCGTGGGC    900

Qy   956 CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT   1015
         |||||||||||||||||| |||| |||||||||||
Db   901 CGCCAGCACATCGGGCCGCGCCGAGCACCACGCCCCCGCCGTGGGATACCCCCG     960

Qy  1016 TGTCCCCGGTGTACGCCCGAGACCACCAAGCAGCCTCCTCTACTCCTCCAGGCGGACAAGGAGCAG   1075
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Db   961 TGCCCGCCGGTGTATGCGCCGGTGTGGCGCGCAGCCAGCGGCAATCCGGGCGATAAAGAACAG    1020
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Qy  1076 CTGCGCGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCGTCGGCGGCCGGAGGCTC   1135
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Db  1021 CTGCGCCGCCGAGCTTTCTGCTGAGCAGTTCCAGGCCCGCCGGATGCCCAGGGACTGCCAGGAGGCTG   1080

Qy  1136 GTGGAGGACCATCTTTCTGGGTTCCAGGCGCCTGCGCTGCGCGGGACTTCCAGGGACTGCCCC   1195
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Db  1081 GTGGAAACCATTTTTCTGGGCACGCCGCGGCGGTGGCCCGGCCGCCACCCGCGGCTCGCCG   1140

Qy  1196 CGCCTGCCCCAGCGCTACTGCACTGCCAAATGCGGCGCCCTGTTTCTGGAGCTGCTTGGGAACCAC   1255
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Db  1141 CGCCTGCCGCAGCGCTATTGCGCAGATGCGGCGCCCGTGTTTCTGGAACTGCTGGGCAACCAT   1200

Qy  1256 GCGCAGTGCCCCTACGGGGTGCTGCTCCTCAAGACGACTGCCCGCTGCCAGCTGCGGTCACC   1315
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Db  1201 GCGCAGTGCCCGTATGCGGTGCTGCGCGCTGAAACCCATCCCGCTGCGCGGCGGCGTGACC   1260

Qy  1316 CCAGCAGCCGGTGTCGTGTCGTGCCCGGAGAGAAGCCCAGGGCTCTGTGCGGCGGCCCCCGAGGAG   1375
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Db  1261 CCGGCGGCCGGCGTGTCGTGCAGCCGCGAAAAAACCAGGGCAGCGGCGCCCGGAAGAA   1320

Qy  1376 GAGGACACAGACCCCCGCTTCGTGCGGGCCCTGCTCGCCCAGCACGCAGCCCCTGGCTGCCAG   1435
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Db  1321 GAAGATACCGATCCGCGCTTCGTGCGCGCGCTGCTGGCCCAGCAGCCGCGCGTGGCGGCAG   1380

Qy  1436 GTGTACGGCTTCGTGCGCCTGCCCTGGCCGTGGTGGCCCCGCAGGCCTTCTGGGGCTCC   1495
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Db  1381 GTGTATGCGTTTGTGCGCGTGCGCCTGCCGTGGCCGTGGTGGCGGCAGC   1440

Qy  1496 AGGCACAACGAACGCGCTTCCTCAGGAGAACCAAGAAGTTCATCTCCCTGGGAAGCAT   1555
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Db  1441 CGCCATAACGAACGCCGCTTTCTGCGCCAACACCAAAAAATTTATTAGCCTGGGCAAACAT   1500

Qy  1556 GCCAAGCTCTCGCTGCAGAGACTGACGTGGAAGATGAGCGTGCGCGACTGCGTTCGGCTG   1615
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Db  1501 GCGAAACTGAGCCTGCAGAGAACTGACCTGGCGAAAATGAGCGTGCGCGATTGCGTGCGGCTG   1560

Qy  1616 CGCAGGAGCCCAGGGGTTGGCTGCTGTGTTCCGGCCGCACCGTCTGCCTCTGAGGAGATC   1675
         ||||| |||||||||| || |||||| |||||| || || ||||| ||||| ||
Db  1561 CGCCCGCAGCCCGGGCGTGGGCTGCGTGCGCGCCGAAACATCGCCCTGCGCGGAAGAAATT   1620

Qy  1676 CTGGCCAAGTTCCTGCACTGGCTGGATGGACCCCGAAGGCGTCTGGGATGCCAGGTCCAGA   1735
         |||| ||||| || |||| ||| |||| || ||||| ||| ||||||| |||||
Db  1621 CTGGCGAAATTTCTGCATTGGCTGGATGAGCGTGATGGAACTGCTGCGCAGCTTT   1680

Qy  1736 TTTTATGTCACGGAGACCACGTTCAAAAGACACAGGCTCTTTCTCACCGGAAGAGTGTC   1795
         ||||| || ||||| ||||| ||||||| |||| || |||| ||||
Db  1681 TTTTATGTGACCGAAACCACCTTTCAGAAAAATCCGCCCCTGTTTTTTTATCGCAAAGCGTG   1740

Qy  1796 TGGAGCAAGTTGCAAAGCATTGGAATCAGACATCAGACGTGCAGCTGCGGGGAG   1855
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Db  1741 TGGAGCAAACTGCAGAGCATTGGCATTCGCCAGCATCGAAACGCGCAGCTGCCGAA   1800

Qy  1856 CTGTCGGAAGCAGAGGTCAGGCAGCAGCATCGGGAAGCCAGGCCCGCTGCCAGA   1915
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Db  1801 CTGAGCGAAGCGGAAGTGCGCCAGCATCCCGAAGCGCGCCCGGCGCTGCTGACAAGCGC   1860

Qy  1916 CTCCCGCTTCATCCCCAAGCCTGAACATGGAACATGCGTCTCACCTCGAGGGTGAACGGCA   1975
         |||| ||| || |||||| ||||||||
Db  1861 CTGGGCGCTTTATTCCGAAACCGGATGCTGTGAACATGGAACACATGGTGGTG   1920

Qy  1976 GGAGCCAGGAAGCGTTCCGCAGAGAAAAGAGGGCCCGGTCCTACCTCGAGGGTGAAGGCA   2035
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Db  1921 GGCGCGCCAACCTTTGCGGAAGCGGGCGGCAAAAACGGCGGGCCTCACCTCGACGGTGAAAGCG   1980

Qy  2036 CTGTTCAGCGTGCTCAACTACGAGCCGCCTGGGCACACCTCCTCTGTG          2095
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Db  1981 CTGTTTAGCGTGCTGAACTATGAACCGCCGTGGGATACCCCCG   2040

Qy  2096 CTGGGCCTGGACGATATCCACAGAGCCTGGCCCACCTTCGTGCGCGTGTCGCGGGCCCAG   2155
         |||||||||| ||||||||| ||| ||||||||||||||||||||||||
Db  2041 CTGGGCCTGGATGATATTCATCGCGCTGGCCGCGTGCGCGTGTCGCGCGCGCCCAG   2100

Qy  2156 GACCCGCGCGCCCTGAGCGTGTACTTTGTCAAGGTGATGTGACGGCGCGTACGACGACCATC   2215
Db
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RESULT 9
US-09-721-456-3
; Sequence 3, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin B.
;   Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/721,456
;   FILING DATE: 22-Nov-2000
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/974,549A
;   FILING DATE: 19-NOV-1997
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997
;   APPLICATION NUMBER: US 08/854,050
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: US 08/911,312
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/912,951
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: WO PCT/US97/17618
;   FILING DATE: 01-OCT-1997
;   APPLICATION NUMBER: US 08/915,503
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: WO PCT/US97/17885
;   FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph Ted
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-00261OUS
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200

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;
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2176 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: -
;     LOCATION: 1..2176
;     OTHER INFORMATION:  /note= "clone 712562"
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 23..802
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-721-456-3

Query Match      48.8%;  Score 1960.4;  DB 5;  Length 2176;
Best Local Similarity  92.1%;  Pred. No. 0;
Matches 2153;  Conservative  0;  Mismatches  3;  Indels 182;  Gaps  1;
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Qy   1678 GGCCAAGTTCCTGCACTGGCTGTGTACGTCGTCGATGAGTGTACGTCGTCGAGCTGCTCAGGTCTTCTT 1737
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGCCAAGTTCCTGCACTGGCTGTGTACGTCGTCGATGAGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT 60

Qy   1738 TTATGTCACGGAGACCACGTTCAAAAGAACAGAGCTCTTTTCTTTCTACCGGAAGAGTGTCTG 1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TTATGTCACGGAGACCACGTTCAAAAGAACAGAGCTCTTTTTCTTTCTACCGGAAGAGTGTCTG 120

Qy   1798 GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCT 1857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCT 180

Qy   1858 GTCGGAAGCAGAGTCAGGCAGCAGAGGAAGCCAGGCCCGCCCTGCGTCGACGTCCAGACT 1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTCGGAAGCAGAGTCAGGCAGCAGAGGAAGCCAGGCCCGCCCTGCGTCGACGTCCAGACT 240

Qy   1918 CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGTGACTACGTCGTGGG 1977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGTGACTACGTCGTGGG 300

Qy   1978 AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACT 2037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGCCAGAACGTTCCCCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACT 360

Qy   2038 GTTCAGCGGTGCTCAACTACGAGCGCGGGGCGCGGGGGCGGCGGCGGCCCGCCTCGTGCT 2097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTTCAGCGGTGCTCAACTACGAGCGCGGGGCGCGGGGGCGGCGGCGGCCCGCCTCGTGCT 420

Qy   2098 GGGCCTGGACGGATATCCACAGGGCCTCATCGGCCAGCATCAACATCAAACCCAGGCCCAGGA 2157
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGGCCTGGACGTGACATATCCACAGGGCCTGGCCACCTTCGTGCTGCTGCCCACCTTCGTGCTGCTGCCCACCTTCGTGCTGCTGCCCAGGA 480

Qy   2158 CCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGTAGCGTACGACACCATCCC 2217
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Db    481 CCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGTAGCGTACGACACCATCCC 540

Qy   2218 CCAGGACAGGCTCACGGAGGCTCATCGCCAGCATCATCAAACATCAAACACGTACTGCGT 2277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAGGACAGGCTCACGGAGGCTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGT 600

Qy   2278 GCGTCGGTATGCGGTGGTCAGAGAGGCCGCCATTGGGCACGTCGCAAGGCCTTCAAGAG 2337
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Db    601 GCGTCGGTATGCGGTGGTCCAGAGAGGCCGCCCATTGGGCACGTCGCAAGGCCTTCAAGAG 660

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Qy   2458 CAGCAGTGGCCTCTTCGACGCGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCCGCATCAG 2517
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Qy   2518 GGGCAAGTCCTACGTCCAGTGCCAGTGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCT 2577
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    719 CTGCAGCCTGCTGCTACGGCGACATGGAGCAACAAGCTGTTGCGGGATTCGGCGGGGACGG 778

Qy   2638 GCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGGAA 2697
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Db    779 GCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGGAA 838

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Db    839 AACCTTCCTCAGGACCCTGGTCCCGAGGTGTCCCTGAGTATGGCGTCGTGGTGAACTTGCG 898

Qy   2758 GAAGACAGTGGTGAACTTCCCTGTAGAGACAGAGGCCCTGGGTGGCACGGCTTTTGTTCA 2817
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    899 GAAGACAGTGGTGAACTTCCCTGTAGAGACGAGAGGCCCTGGGTGGCACGGCTTTTGTTCA 958

Qy   2818 GATGCCGGCCACGGCCTATTCCCGTGCGGCCTGCTGCTGGATACCGGACCCTGGA 2877
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Db    959 GATGCCGGCCACGGCCTATTCCCGTGCGGCCTGCTGCTGGATACCGGACCCTGGA 1018

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Db   1019 GGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCACCTTCAA 1078

Qy   2938 CCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGCGGCTGCGGCTGAA 2997
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 CCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGCGGCTGCGGCTGAA 1138

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Db   1139 GTGTCACAGCCTGTTCTGGATTTGCAGGTGAACAGCCTCCAGAGCAGCGGTGTGCACCAACAT 1198

Qy   3058 CTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGCTGCAGCTCCCATT 3117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1199 CTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGCTGCAGCTCCCATT 1258

Qy   3118 TCATCAGCAAGTTGGAAGAACCCACATTTTCCTGCGCGTCATCTGACACGGCCTC 3177
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Db   1259 TCATCAGCAAGTTGGAAGAACCCACATTTTCCTGCGCGTCATCTGACACGGCCTC 1318

Qy   3178 CCTCTGCTACTCCATCCTGAAAGCCAGGATGTCGCTGGGGCCAAGGGGCGC 3237
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Db   1319 CCTCTGCTACTCCATCCTGAAAGCCAGGATGTCGCTGGGGCCAAGGGGCGC 1378

Qy   3238 CGGCGGGCCCTGCCCTCGAGGGCCGTGCAGTGGCTGGCTGTGCCCACAAGCATTCTGCTCAA 3297
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Db   1379 CGGCGGGCCCTGCCCTCGAGGGCCGTGCAGTGGCTGGCTGTGCCCACAAGCATTCCTGCTCAA 1438

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Db   1499 GCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTCCTGAGGACCCCAGCCAACCC 1558

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RESULT 10
US-09-721-456-266

; Sequence 266, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT:
;   Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin B.
;   Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/721,456
;   FILING DATE: 22-Nov-2000
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/974,549A
;   FILING DATE: 19-NOV-1997
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997

;   APPLICATION NUMBER: US 08/854,050
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: US 08/911,312
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/912,951
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/915,503
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: WO PCT/US97/17618
;   FILING DATE: 01-OCT-1997
;   APPLICATION NUMBER: WO PCT/US97/17885
;   FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph Ted
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 266:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2171 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 22..1716
;   OTHER INFORMATION: /note= "EcoRI-NotI insert of
;   clone 712562 encoding 63 kDa
;   telomerase protein"
; SEQUENCE DESCRIPTION: SEQ ID NO: 266:
US-09-721-456-266

Query Match   46.8%; Score 1877.2; DB 5; Length 2171;
Best Local Similarity   91.5%; Pred. No. 0;
Matches 2140; Conservative   1; Mismatches   9; Indels 188; Gaps   7;

Qy   1679 GCCAAGTTCCTGCACTGGCTCGATGAGTGTGTACGTCGTCGTCGCGAGCTGCTCAGGTCTTTCTTT 1738
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Db   1 GCCAAGTTCTGCACTGGCTGATGAGTGTGTACGTCGTCGTACGTCGTCGCGAGCTGCTCAGGTCTTTCTTT 60

Qy   1739 TATGTCACGGAGACCACGTTTCAAAAGACACAGGCTCTTTTCTACCGGAAGAGTGTCTGG 1798
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Db   61 TATGTCACGGAGACCACGTTTCAAAAGACACAGGCTCTTTTTCTACCGGAAGAGTGTCTGG 120

Qy   1799 AGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTG 1858
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTG 180

Qy   1859 TCGGAAGCAGAGGTCAGGCAGCATCGGAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTC 1918
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCGGAAGCAGAGGTCAGGCAGCATCGGAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTC 240

Qy   1919 CGGTTCATCCCCAAGCCTGACGGCGTGCGGCGGCGATTGTGAACATGGACTACGTCGTGGGA 1978
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Db   241 CGGTTCATCCCCAAGCCTGACGGCGTGCGGCGGCGATTGTGAACATGGACTACGTCGTGGGA 300

Qy   1979 GCCAGAACGTTCCGCAGAGAAAGAGGGCCGAGCGTCTCACCTCGAGGTGAAGGCACTG 2038
          |||||||||||||||||||| ||||||||||||:||||||||||||||||||||||||
Db   301 GCCAGAACGTTCCGCAGAGAGAAAAGARGGCCGAGCGTCTCACCTCGAGGTGAAGGCACTG 360

Qy   2039 TTCAGCGTGCTCAACTACGAGCGGCGGCCCTCCGGCCCTCGTGCTG 2098
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TTCAGCGTGCTCAACTACGAGCGGCGGCCCTCCGGCCCTCGTGCTG 420

Qy   2099 GGCCTGGACGATATCCACAGGCCTGGCGCACCTTCGTGCTGCGGGCCCAGGAC 2158
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GGCCTGGACGATATCCACAGGCCTGGCGCACCTTCGTGCTGCGGGCCCAGGAC 480

Qy   2159 CCGCCGCCTGAGCTGACGTGTACTTGTCAAGGTGGATGGACGGGCCTACGACACCATCCC 2218
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   3538 GCCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGC 3597
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Qy   3778 TCCCCAGATTCGCCATTGTTCACCCCTCGCCCTCGCCCTTGCCTTCCACCCCCACCA 3837
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Qy   3958 GGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAA 4015
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Db   481 CCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCC 540
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Qy  2219 CAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGACACGTACTGCGTG 2278     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         |||||||||||||||||||||||||||||||||||||||||||||||||||           Qy 3299 CTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCGGTGTGGGAGACAGCCCAGACG
Db   541 CAGGACAGGCTCACGGAGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTG 600     Db 1436 CAGCGAGTCGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCGGTGTGGGAGACAGCCCAGACG 1495

Qy  2279 CGTCGGTATGCCGTGGTCCAGAAGCCCAGCCGGCCACGTCCGCAAGGCCTTCAAGAGC 2338              3359 CAGCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGAGGCCGGCAGCCAACCCG 3418
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Qy  2339 CACGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGTTCGTGCTCACCTGCAG 2398            3419 GCACTGCCCTCAGACTTCAAGACCATCTGGACTGATGGGCACCGCCACCCACCAGGCC 3478
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Db   660 CAC------ 662                                                         Db 1556 GCACTGCCCTCAGACTTCAAGACCATCTGGACTGATGGGCACCGCCACCCACCAGGCC 1615

Qy  2399 GAGACCAGCACCGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCC 2458       3479 GAGAGCAGACACCAGCACCCGTGTCACGCGGGCTC-TACGTCCCAGGAGGAGGAGGGCG 3537
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Db   663 ------- 662                                                           Db 1616 GAGAGCAGACACCAGCACCCGTGTCACGCGGGCTTATACGTCCCAGGAGGAGGAGGGCG 1675

Qy  2459 AGCAGTGGCCTCTTCGACGTCTTCCTACGCGTTCATGTGCCACCACGCCGTGCGCATCAGG 2518         3538 GCCCACCCAGGCCCGCACCGCTGGAGTCTGGAGGCTGAGGGCTGAGCGTGCCAGCCAAGG 3597
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Qy  2519 GGCAAGTCCTACGTCCAGTGCCAGTGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTC 2578        3598 CTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGGCTGAGCGTGCCTGAGCGTGCCAGCCTCCACC 3657
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Qy  2579 TGCAGCCTGTGCTGCTACGGCGACATGGAGACAAGCTGTTTCGGCGGACCGGG 2638               3658 GCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACGAGCCTGGCGCTCGGCTCCACC 3717
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Db   718 TGCAGCCGTGTGCTGCTACGGCGACATGGAGACAAGCTGTTTCGGCGGACCGGG 777           Db 1796 GCTGAGTGTCCAGCACACCTG-CGTTTTCACTTCCCCACGAGCCTGGCGGTTCGG-TCCACC 1853

Qy  2639 CTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCACCGCGAAA 2698         3718 CCAGGGCCAGCTTTTTCCTCACCAGGAGCCCGGGCTTCCACTCCCACATAGGAATAGTCCA 3777
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Db   778 CTGCTCCTGCGTTTGGTTGGTGGATGATTTCTTGTTGTTGGTGACACCTCACCTCACCACCGCGAAA 837  Db 1854 CCAGGGCCAGCTTTTTCCTCACCAGGAGCCCGGGCTTCCACTCCCACATAGGAATAGTCCA 1913

Qy  2699 ACCTTCCTCAGGACCCTGTCCGAGGTGTCCCGTGAGTATGGCGTGGTGGTGAACTTGCGG 2758        3778 TCCCCAGATTCGCCATTGTTCACCCCTGTCGGGGCCTTCACCCCCACCACCTTGCCCTTCCACCCCCACCA 3837
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Qy  2759 AAGACAGTGGTGAACTTCCCCTGAGAAGACGAGGACCCTGGGTGGCACGGCTTTGTTCAG 2818          3838 TCCAGGTGGAGACCCTGAGAAGGACCCTGAGAGAAGGACCCTGGGAGTTTGAGTGACCAAAAGGT 3897
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Db  1078 CGCGGGCTTCAAGGCTGGGAGGAACATGCGTCGCCAAACTCTTTGGGGCTTGCGCGCTGAAG 1137

Qy  2999 TGTCACAGACCTGTTCTGGATTTGCAGTGAACAGCCTTCGACGACCAACATC 3058
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Db  1376 GCCGGGCCTGCCCTTCCGGAGCCCGGTGCAGTGCAGTGCGGCTGTGCCACCAAGCATTCCTGCTCAAG 1435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/721,456
    FILING DATE: 22-Nov-2000
    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/974,549A
    FILING DATE: 19-NOV-1997
    APPLICATION NUMBER: US 08/724,643
    FILING DATE: 01-OCT-1996
    APPLICATION NUMBER: US 08/844,419
    FILING DATE: 18-APR-1997
    APPLICATION NUMBER: US 08/846,017
    FILING DATE: 25-APR-1997
    APPLICATION NUMBER: US 08/851,843
    FILING DATE: 06-MAY-1997
    APPLICATION NUMBER: US 08/854,050
    FILING DATE: 09-MAY-1997
    APPLICATION NUMBER: US 08/911,312
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: US 08/912,951
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: US 08/915,503
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: WO PCT/US97/17618
    FILING DATE: 01-OCT-1997
    APPLICATION NUMBER: WO PCT/US97/17885
    FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
    NAME: Apple, Randolph Ted
    REGISTRATION NUMBER: 36,429
    REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 642:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 3396 base pairs
        TYPE: nucleic acid
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        TOPOLOGY: linear
    MOLECULE TYPE: DNA
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        NAME/KEY:
        LOCATION: 1..3396
        OTHER INFORMATION: /note= "generic" hTRT protein encoding
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    SEQUENCE DESCRIPTION: SEQ ID NO: 642:
US-09-721-456-642
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Query Match        46.4%;    Score 1862.2;   DB 5;   Length 3396;
Best Local Similarity 71.8%;  Pred. No. 0;
Matches 2437;  Conservative  0;  Mismatches  958;  Indels  0;  Gaps  0;

Qy     56  ATGCGCGCGCCTCCCGCTGCCGAGCGTGCGCTCCCGTGCTGCGCCAGCCACCACCGCGAG  115
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Db      1  ATGCGCACGTGCCCCACGTGTCGTGCGTGCCGTGCGGTCTCGGTTCTCACTACCGTGAA   60

Qy    116  GTGCTGCGCCTGGCCACGTTCGTGCGGCCGCTGGGCCCCAGGGCTGCCCAGGTTGCGCC  175
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Db     61  GTTTTGCCATTGGCCACCTTCGTTCGTCGTTTGGGTCCAAGGTTGGCGTTTGGTTCGTTCAA  120

Qy    176  CGGGGGACCCGGGCGGCTTCCGGCGGCGTTCCGGCGCTGGTGGCCAGTGCCTGGTGCCCTGG  235
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Qy    296  GTTGCCCAGTGCTGCAGAGGCTGCGAGACCCCGGTGGAGCGCGGGCGAAGAACGTGCTGGCCTTCGGC  355
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(sequence alignment blocks continue — Query (Qy) / Database (Db) pairs)

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Db    301  TTCGCCCTTGTTGGATGTGCCCGTGGTGGTCCACCAGAAGCCTTCACCACCTCTGTTCGT  360
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Db    661  GCCCGTCGTCGTGGTGTTCTGCCTCGTCTTGCCATTGCCAAAACGTCCACGTCGT  720
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Qy    836  AGGACGGCTGGACCGAGTGACCGTGGTTCTGTGTGGTTTCTGTGTGTTTCTGTTTCTGTTTCTTCCAGCCCGCCGAA  895

Db    781  CGTACCCGTGGTCCATCTGATCGTGGTTTTTCTGTGTGTTTCTGTGTTCTTCCAGCCCGTCCAGCCGAA  840
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Db    901  CGTCAACACCACCAGCCGGTCCACCATCTACCTCCGTCCATCGTTGGT  960
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Db   1021  TTGGCGTCCATCTTCTCTTGTTGCGTCCATCTTTGACCGGTCCCGTCGTTTG  1080
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Db   1081  GTTGAAACCATTTTCTTGGGTTCGTCCATGGATGCGAAAATGCGGTCGTTTGCCA  1140
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Db   1141  CGTTTGCCACAACGTTACTGGCAAATGCGTCCATTGTTTCGGAATTGTTGGGTAACCAC  1200
Qy   1256  GGGCAGTGCCCCTACGGGGTGCTTCCGCCGCGGCTTGGTGGTGTCCGTGTCGCCCTGG  1315

Db   1201  GCCCAATGTCCATACGGTGTTTGTTGCCCGTGAAAAACCACTGTCGTTTCGTTGTCCATGG  1260
Qy   1316  CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCAGGGCTCGTGTGGGCGCCCCCGAGGAG  1375

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Qy 2576 CTCTGCAGCCTGCTACGGCGACATGGAGAACAAGCTGTGTTGCGGGATTCGGCGGGAC 2635
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Qy 2756 CGGAAGACAGTGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGTGGCACGGCTTTGTT 2815
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Db 2941 AAATGTCACTCTTGTTCTTGGATTTGCAAGTTAACTCTTGCAAACCGTTTGTACCAAC 3000

Qy 3056 ATCTACAAGATCCTCCTGCTGCGAGGCGTACAGGTTTCACGCATGTGTCTGCGAGCTCCCA 3115
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Db 3001 ATTTACAAAATTTTGTTGTTGCAAGCCTACCGTTTCCACGCCGTGTTTTGCAATTGCCA 3060

Qy 3116 TTTCATCAGCAAGTTTGGAAGAACCCCACCATTTTCCTGCGCCGTCATCTGACACGGCC 3175
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Db 3061 TTCCACCAACAAGTTTGGAAAAACACCAACCTTCTTCCGTGTATTCTGATACCGGCC 3120

Qy 3176 TCCCTCTGCTACTCCATCCTGAAAGCCAGGACGTCGGGGGGATGTCGCAGGGGC 3235
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Db 3121 TCTTTGTGTTACTCTATTTGAAAGCCAAAAACCGTATGTCTTTGGGTGCCAAAGGT 3180

Qy 3236 GCCGCCGGCCCTGCCCCTCGCCCGTGCAGTGGCGTGCCCAAGCATTCCTGCTC 3295
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Db 3181 GCCGCCGGTCCATTGCCATCTGAAGCCGTTCAATGGTGTGTCACCAAGCCTTCTGTTG 3240

Qy 3296 AAGCTGACTGCGACACCGTGCACCTACGTGCCACTCCTGGGGTCACTCAGGAGAGACGTACTGC 3355
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Db 3241 AAATTGACCCGTCACCGGTTACCTACGTTCCATTGTTGGGTTCTTTGCGTACCGCCCAA 3300

Qy 3356 ACGCAGCTGAGTCGGAAGCGTCCAGAAGCGCTGACTGCGGGAACGAGCGCAGCAGCCAAC 3415
              || ||| || || || ||| || ||| || || ||| || ||||| ||
Db 3301 ACCCAATTGTCTCGTAAATTGCCAGGTACCAGCGTGGAAGCGCCGGCCGCCCAAC 3360

Qy 3416 CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGA 3450
Db 3361 CCAGCCTTGCCATCTGATTTCAAAACCATTTTGGA 3395

RESULT 12
US-09-721-456-641
; Sequence 641, Application US/09721456
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.

Qy 1436 GTGTACGGGCTTCGTGCGGGGCCTGCCTGGTGCCCGGCTGGTGCCCCAGAGCCTTCTGGGGCTCC 1495
              || | ||||| ||||| | |||| || |||| || ||||
Db 1381 GTTTACGGTTTCGTTCGTGCCTTCGTTGCGTTCCACCAGGTTGTGGGGTTCT 1440

Qy 1496 AGGCACAACGACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCAT 1555
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Db 1441 CGTCACAACGAACGTGCTTTCTTGCGTAACACCAAAAAATTCATTTCTTTGGGTAAACAC 1500

Qy 1556 GCCAAGCTCTCCGCGCAGGAGCTGACGTGGAAGATGAGGGTCGGGGACTGCCTGGCTG 1615
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Db 1501 GCCAAATGTCTTGCAGAATTGACCTGGAAAATGTCTGTTGGTGATTGTGTCCTGTTG 1560

Qy 1616 CGCAGGAGCCCAGGGGTTGGCTGTTCCGGCCGCAGAGCACCGTGCGTGAGGAGATC 1675
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Db 1561 CGTCGGTTCTCCAGGTGTTGGTGTTGTTCCAGCCGCCCAACACCGTTTGCGTGAGAAATT 1620

Qy 1676 CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTGGAGCTGCTCAGGTCTTTC 1735
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Db 1621 TTGGCCAAATTCTTGCACTGGTTGATGTCTGTTTACGTTGTTGAATTGTTGCGTTCTTTC 1680

Qy 1736 TTTTATGTCACGGAGACCACCGTTCAAAGAACAGGCTCTCTTTTCTACCGGAAGAGTGTC 1795
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Db 1681 TTCTACGTTACCGAAACCACCGTTCAAAGAACCGGTTCTCTTTTCTACCGTAAATCTGTT 1740

Qy 1796 TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAG 1855
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Db 1741 TGGTCTAAATTGCAATCTATTGGTATTCGTCAACACTTGAAAAGGTGTTCAATTGCGTGAA 1800

Qy 1856 CTGTCGGAAGCAGAGGTCAGGCAGCATGGGGAAGCCAGGCCCCCCCTTGACGTCCAGA 1915
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Db 1801 TTGTCTGAAGCGAAGTTCGGTCAACACCGTGAAGCCGTTGACGTCCAGCCGTTGACCTCGT 1860

Qy 1916 CTCCGGCTTCATCCCCAGGCCTGACGGGCTGCGGATTGTGAACATGGACTACGTCGTG 1975
              || ||| || ||| || || ||| || ||||| |||| || ||||
Db 1861 TTGCGTTTCATTCAACAACCAGATGGTTGCGTCCAATTGTTAACATGGATTACGTTGTT 1920

Qy 1976 GGAGCAGAACGTTCCGCAGAGAAAAGAGGAGGCGTCTCACCTCGAGGGTGAAGGCA 2035
              || || ||| || || ||||| || || || || || ||| || ||
Db 1921 GGTGCCGGTCGTTCCGCGCAAAAAAGTGCCGAACGTTGCGTCTCGTGTTAAAGCC 1980

Qy 2036 CTGTTCAGCGTGCTCAACTACGAACGGGCGCGGGCGCCCCGGCTCGTGGGCCTCTGTG 2095
              || || || || || ||| || || ||| |||| || ||||| ||
Db 1981 TTGTTTTCTGTTTTGAACTACGAACGTGCCCGTGCCCCGTGTTGTTGGGTTCTTGTGTT 2040

Qy 2096 CTTGGGGCCTTGGACGCTATATCCACAGGGTTGGTCCGTGTGCGCACCTTCGTCGGGGCGCCAG 2155
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Db 2041 TTGGGTTTGGATGTATATTCACCGTGGTTGCGTCCGTGTTTGCGTGTTCGTGTTCGTCCAA 2100

Qy 2156 GACCCGGCCGCTGAGCGTGCTACTTGTGTCAAGGTGGATGGGATGACGGCGGCGGTACGACACCATC 2215
              || ||| || ||| || || || ||| || || ||| ||| ||||
Db 2101 GATCCACCACCAGAATTGTACTTCGTTAAAGTTGATGGTATGACCGCTGCTGTTCGTCACCATT 2160

Qy 2216 CCCCAGGACAGGCTGACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGC 2275
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Db 2161 CCACAAGATCGTTTGACCGAAGTTATTGCCTCTATTATTAAACCACAAAACACCTACTGT 2220

Qy 2276 GTGCGTCGGTATGCCGTCGTCCAGAAGGCCAGGTCCCGGCCAGGCCTTCAAG 2335
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Db 2221 GTTCGTCGTTACGGCGTTGTTCAAAAAGCCCGTTCGGGTCAATGGCCTTCAAA 2280

Qy 2336 AGCCACGTCTACCTTGGTGACGGTTCGGACAGTTCGTGGCTTGGCTCACCTG 2395
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Db 2281 TCTCACGTTTCTACCTTGCGTGATGGTTTCATGTGTTCATGTGTTACCACCAGGTTGCCACTTG 2340

Qy 2396 CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCCTGCCCTGAATGAG 2455
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Db 2341 CAAGAAACCTCTCCATTGCGTGATGCCGTTGTTATTGAACAATCTTCTCTTTGAACGAA 2400

Qy 2456 GCCAGCAGTGGCCTCTTCGACGTTGTTCGACGTTTGCGTTCTTCCACCACGCCGTGCGCATC 2515
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Db 2401 GCCTCTTCGTTTGGTTTTGTTCGATGTTTTCATGTGTTCATCCACCACGCCGTTCGTATT 2460

```
                   Morin, Gregg B.
                   Harley, Calvin B.
                   Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
   ADDRESSEE: Townsend and Townsend and Crew LLP
   STREET: Two Embarcadero Center, Eighth Floor
   CITY: San Francisco
   STATE: California
   COUNTRY: USA
   ZIP: 94111-3834
COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/09/721,456
   FILING DATE: 22-Nov-2000
   CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US/08/974,549A
   FILING DATE: 19-NOV-1997
   APPLICATION NUMBER: US 08/724,643
   FILING DATE: 01-OCT-1996
   APPLICATION NUMBER: US 08/844,419
   FILING DATE: 18-APR-1997
   APPLICATION NUMBER: US 08/846,017
   FILING DATE: 25-APR-1997
   APPLICATION NUMBER: US 08/851,843
   FILING DATE: 06-MAY-1997
   APPLICATION NUMBER: US 08/854,050
   FILING DATE: 09-MAY-1997
   APPLICATION NUMBER: US 08/911,312
   FILING DATE: 14-AUG-1997
   APPLICATION NUMBER: US 08/912,951
   FILING DATE: 14-AUG-1997
   APPLICATION NUMBER: US 08/915,503
   FILING DATE: 14-AUG-1997
   APPLICATION NUMBER: WO PCT/US97/17618
   FILING DATE: 01-OCT-1997
   APPLICATION NUMBER: WO PCT/US97/17885
   FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
   NAME: Apple, Randolph Ted
   REGISTRATION NUMBER: 36,429
   REFERENCE/DOCKET NUMBER: 015389-0026100S
TELECOMMUNICATION INFORMATION:
   TELEPHONE: (415) 576-0200
   TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 641:
SEQUENCE CHARACTERISTICS:
   LENGTH: 3396 base pairs
   TYPE: nucleic acid
   STRANDEDNESS: single
   TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
   NAME/KEY:   -
   LOCATION:    1..3396
   OTHER INFORMATION:  /note= "hTRT-encoding sequence employing
      alternative codon distributions for
      yeast (high expressing genes)"
   SEQUENCE DESCRIPTION: SEQ ID NO: 641:
US-09-721-456-641

Query Match     43.7%;  Score 1756;  DB 5;  Length 3396;
Best Local Similarity   69.8%;  Pred. No. 0;
Matches 2371;  Conservative  0;  Mismatches 1025;  Indels  0;  Gaps  0;
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Db     1 ATGCCGAGAGCTTCCAAGATGTGAGAGCTGTTAGAGATCTTTGTTGAGATCTCACTACAGAGAA 60
Qy   116 GTGCTGCCGCTGCCACGTTCGTGCGGCCGCCTGGGCCGCCTGGGCGTTGGTGCGAG 175
         || |||| ||| ||||| ||| |  |||||  -  || || |||| ||  |||| ||||
Db    61 GTTTTGCCATTGCTACTTTCGTTAGAAGATTGGGTCCACAAGTTGGATTGGTTCAA 120
Qy   176 CCCGGGACCCGGCGTTCCGCGGCTGGTGCCCAGTGCCTGGTGTGTGCGTGCCCTGG 235
         || |||| ||| || || ||| | |||||||  -  ||||||| ||||||| ||| ||||
Db   121 AGAGGTGACCCAGCTGCTTGGTTGCTCAATGTTTGGTTGTGGTTGTCCATGG 180
Qy   236 GACGCACGGCGCCCCCGCGCCCCCTTCCGCCAGTGTCTGCCTGAAGGAGCTG 295
         ||| || || ||||| ||| |||| |||| || ||  |  ||||  ||||||| |||||
Db   181 GACGCTAGACACCACCAGCTGCTCACATCTTTCAGACAAGTTCTTGTTGAAGGAATTG 240
Qy   296 GTGGCCCAGTGCTGCAGAGGCGTGCGAGGACGTGCGGCGGAGAACGTGCTTCGGC 355
         ||| ||| ||||| || |  ||| || |||| || ||||||  |||  ||| ||||
Db   241 GTTGCTAGAGTTTTGCAAAGATTGTGTGAAAGAGGTGTAAGACGTTTGGCTTTCGT 300
Qy   356 TTCGCGCTGCTGACGGGCCCGGCGGCCCCCGAGGCCTTCACCACCAGCGTGCGC 415
         || ||  || || || || |||  | ||||| ||||||||||  | |||||| ||
Db   301 TTCGCTTTGTTGGACGGTGCTAGAGGTGGTCCACCAGAGAGCTTTCACTACTTCTGTTAGA 360
Qy   416 AGCTACCTGCCCAACACGTGACCGACCACTGCGGGGAGCCGGGGCCTGCTG 475
         ||| || || ||  || ||  |||  |||||  |||| ||||| || |||||
Db   361 TCTTACTTGCCAAACACTGTTACTGACGCTTTGACGGTTCTGGCACGCTGCGGGTTTGTTG 420
Qy   476 CTGCGCCGCGTGGGCGACGACGTGCTGTTCACCTGGCGCTGCGCTCTTTGTG 535
         || ||  ||||| || |||  || ||  || ||  |||| |   |||  || ||
Db   421 TTGAGAGTTGGTGACGACGTTTTGGTTCACTTGGTTTGTGTCTTTGTTCGTT 480
Qy   536 CTGGTGCTTCCCAGCTGCGCGCTTACCAGTGTGCGGGCCGCTGTACCAGCTCGGCGCCT 595
         || ||  || ||  ||||||  | | ||| ||||| || ||  | ||| || ||||  |||
Db   481 TTGGTTGCTTCCATCTTGTGCTTACCAAGTTGGTGGTTGTCCACCATTGTACCAATGGGTGCT 540
Qy   596 GCCACTCAGGCCCCGGCCAGGTAGTGACCCCGAAGGCGTCTGGGATGCCGAA 655
         || || ||  ||||| ||  |||| |||   |||||| || ||||| || ||
Db   541 GCTACTCAAGCTAGACCACCACCACGCTTCTGGTCTCAAGAAGAAGATTGGGTTGTGAA 600
Qy   656 CGGGCCTGAACCATAGCGTCAGGGAGCCGGGGCGGGGCCTGGCCCCGGGT 715
         || ||||| ||| |  || |||| |||| || ||||||| ||||| ||| ||
Db   601 AGAGCTTGGAACCACTGTTTGAAGAGCTGGTGTTGCCAGTGGGTTGCCAGTGTCCAGGT 660
Qy   716 GCGAGGAGGCGGGGGAGCCGAAGTCTGCGTTGCCAGCGGAGGCCCCAGCGCT 775
         ||| ||||| |||| |||| | ||||  || ||  ||||||| | |||| || ||
Db   661 GCTAGAGAAGAGAGTGGTTGCTGCTTCTAGAATCTTTGCCATTGCCAAAGAGACCAAGAGA 720
Qy   776 GGGGCTGCCCTGAGCCGAGCGGAGCGGACGCCCGTTGGGCAGGGCCCACCCGGGC 835
         ||||| ||||| ||| ||  ||| ||| || ||||| ||   |||  ||||||| ||
Db   721 GGTGCTGCTCCAGAACCAGAAGAACTCCAGTTGGTCAAGGTTCTTCCAGCTCACCCAGGT 780
Qy   836 AGGACGCGTGGACCGAGTGACCCGTGGTTTCTGTGTGGTGTCACCTGCCGCCGCCGAA 895
         ||||| || ||| || || || | ||||| |  ||| || ||  |||| || || || |||
Db   781 AGAACTAGAGGTCCATCGACAGAGTTTCGTGTTGGTGTTGTTGTCCACGCTGCCAGCTGAA 840
Qy   896 GAAGCCACCTCTTTGGAGGTGCGCTCTCTGCGGCGGCCCCATCCGTCCCGGGC 955
         || || || || || ||  ||||| |||||| |||  | ||  || ||| |||
Db   841 GAAGCTACTTCTTTGGAAGTGCGTTCTTGTCTGGTAGACACTCTCACCATCTGTTGGT 900
Qy   956 CGCCAGCACCAGCGGGGCCCCCATCCGGCCACCAGTGCTCCCTGGGACACGCCT 1015
         |  ||| ||  ||||||| |||  || ||| ||  |||  ||| ||| ||| ||||
Db   901 AGACAACACCACCACGCTGGTCCACCATCTACTTCTAGACACCACCAAGACCATGGGACACTCCA 960
Qy  1016 TGTCCCCGGTACGCGAGCCTGGTCTGTGACACTTCCTACTCCTCAGGCGACAAGGAGCAG 1075
         ||| || || || || ||||| | |||| |||||  |||| || |  |  ||  | ||
Db   961 TGTCCACCAGTTACGTGAAACTGAAACTAAGCACTTTGTACTCTTCTGGTGACAAGGAACAA 1020
Qy  1076 CTGCGGGCCCTCCTTCCTACTCAGCTCTTCGAGGCCTGACTGGCGCTCCGGAGGCTC 1135
         || || || |||  ||   |   | |||| |  || || ||  ||| || ||||| ||
Db  1021 TTGAGAGCCATCTTTTCTTGTTGTCTTTGAGAGACCATCTTTGACTGGTGCTAGAGAATTG 1080
Qy  1136 GTGGAGACCACCATCTTTCTGGTTCCAGGCCTGATGCCAGGGAGTCCCAGTTGCCC 1195
         || || ||  ||||| |||| || |||| ||| ||| |  |  || ||||| ||||
Db  1081 GTTGAAACTATTTTCTTGGGTTCAAACTAAGGATGGTCCGAGCAGCCACTACCGCGAG 1140

Qy    56 ATGCCGCGCTCCCCGCGTCCGCAGCGTGCGTCCCCGCTGCGCGAGCCCTACCCGGAG
         ||||| | ||||| ||||  || || ||||  || ||| || ||||  |||||| ||
                                                                      115
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Qy   2276  GTGCGTCGGTATGCCGTGGTCCAGAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAG  2335
            ||  |    ||     |||||                     |||  |    ||||| ||||||
Db   2221  GTTAGAAGATACGCGTGTGTTCAAAAGGCTGCTCACGGTCTCAGGCGTTAGAAAGGCTTTCAAG  2280

Qy   2336  AGCCACGTCTCTACCTGACAGACCTCCAGCGTTCCAGCCGTACATGACAGTTCGTGCTCACCTG  2395
            |||  |  ||   ||| ||  ||||| |||   ||||||| ||| ||   |||||| ||||||
Db   2281  TCTCACGTTTCTACTTGACTGACTGCAACCATGACATGACAGCAATCTTCGTTGCTCACTTG  2340

Qy   2396  CAGGAGACCAGCCGTCGAGGGATGCGTCATCGAGCAGAGCTCCTCCCTGAATGAG  2455
            ||  | |  |  ||    ||| |||||   |||  ||||| |||| |||||||
Db   2341  CAAGAAACTTCTCCATTGAAGACACGTGTTGTTATTGAACAATCTTCTTGAACGAA  2400

Qy   2456  GCCAGCAGTGCCCTCTTCGACGTCTTCTACGCTTCATGTGGTGGCCACCACGCCGTGCCCATC  2515
            |  |  |  ||||| ||  ||   ||| ||||   ||||||| |||||  ||||||| ||
Db   2401  GCTTCTTCTGGTTGTTCGACGTTTTTGAGATTCATGTGTCACCACGCGTTAGAATT  2460

Qy   2516  AGGGGCAAGTCCTACGTCCAGTCCGCAGGGGATCCCGCAGGCCTCCATCCTCCACGCTG  2575
            ||  ||||  |||| || ||| |  ||||| ||  | |||  ||| ||| ||||| |
Db   2461  AGAGGTAAGTCTTACGTTCAATGTCAAGGTATTCCACAAGGTTCATTTGTCTACTTTG  2520

Qy   2576  CTCTGCAGCCTGTGCTACGGCGACATGAGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC  2635
            ||  || ||| ||||  ||||| |||| |||  ||   |||| ||   ||| ||||||||||
Db   2521  TTGTGTTCTTTGTGTTACGGTGACATGAGTGAAAACAAGTTGTTCGCGTATTAGAAGAGAC  2580

Qy   2636  GGGCTGCTCCTGCCGTTGGTGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCG  2695
            |||  |||| |||  ||||| |    ||| ||||| |||| |||| |  |  |||| |||
Db   2581  GGTTTGTTGTGAGATTGGTTGACGACTTCTTGTGTTTACTCCACACCTTGACTCACGCT  2640

Qy   2696  AAAACCTTCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGGTGGTGTGAACTTG  2755
            |||   || || || ||   |||   ||||  |||| ||| |  |||||| || |||||
Db   2641  AAGAGTTTCTTGAGACTTTGGTTAGAGGTGTTCAGAATACGGTGTGTTGTTAACTTG  2700

Qy   2756  CGGAAGACAGTGGTGAACTTCCCTGTAGAGACGAGGCCCTCGGGGTGCACGGCTTTGTT  2815
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Db   2701  AGAAAGACTGTGTTAACTTCCCAGTTGAAGACGAAGCTTTGGGTTACTGCGTTTCGTT  2760

Qy   2816  CAGATGCCGCGCCACGGCCTATTCCCCTGGTGCGGCCTGCTGTGTGGATACCCGACCCTG  2875
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Db   2761  CAAATGCCAGTCCACGGGTTGTTCCCATGGTGTTGTTGGTTGTTGTTGGACACTGAGACTTTG  2820

Qy   2876  GAGGTGCAGAGCGACTACTCCAGGTTGAAGAGGGTGCAGCTGCGGGAG  2935
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Db   2821  GAAGTTCAATCTGACTACTTCTTCTTACGGTAGAGCTTCATTAGAGCTTC  2880

Qy   2936  AACCCGGCTTCAAGGCTGGAGGAACATCGTCCAAACTCTTGGGGTCTTCGCGGCTG  2995
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Qy   2996  AAGTGTCACAGCCTGTTTCTGTTCTGGATTTGCAGGTGAACACAGCCTCGACCAGGTGTGCACCAAC  3055
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Db   2941  AAGTGTCACTCTTGTTGTTCGTCAAGTTGCAAGGTTAACTGTTGTTACTAAC  3000

Qy   3056  ATCTACAAGATCCTCTTCACGGATGTCGCGTTCACCTTG  3115
            || |||| |  ||  |||  | ||  | ||||| |||| ||
Db   3001  ATTTACAAGATTTTGTTGTTGCAAGTTCTTACCGCTTTC  3060

Qy   3116  TTTCATCAGCAAGTTGGAAGAACCCCACATTTTCCTGCCGTCATCTCTGACACGTGTG  3175
            ||   ||   ||||| ||||| || || || |||  || | |||| ||  | |  |||
Db   3061  TTCCACCAACAAGTTGGAAGAGTTGCAAGTAATCTTCGACACTGCT  3120

Qy   3176  TCCCTCTGCTACTCCATCCTGAAAGCCGAAAGAACGCAGGAGATGTCGCTGGGGGCCAAGGGC  3235
            ||   |  ||  |||| |||| ||| || ||||| | || |  ||||||||| ||
Db   3121  TCTTTGTGTTACTCTATTTTGAAGGCTAAGAACGGTAGGTTCTTTGGGTGTCTTAAGGGT  3180

Qy   3236  GCCCGGCCGCCTGAGTGTACTTTGTCAAGGTGGAtGTGCCACCAGCATTCCTGCTC  3295
            ||   | || ||||| | |||  |||| |||| || ||  ||||  |||||  |||
Db   3181  GCTGCTGGTCCAATCGCCAGCTGTTCAATGGTTGTGTCACCAAGGTTGTGTCTGTGTG  3240

Qy   3296  AAGCTGACTGACACCGTGTCACTCACGTGCCACTCCTGGGCTCACTCAGGACAGCCCCAG  3355
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Db   3241  AAGTTGACTGACAACAGAGTTACTTACGTCCCATTGTTGGGTTCCTTGAGAAACTGCTCAA  3300

Qy   3356  ACGGCAGCTGAGTCGACGGAAGCTCCCGGGACGACCGCTGACTCGCCTGGAGGCCCGCAGCCAAC  3415
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Qy   1196  CGCCTGCCCCAGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTG  1255
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Db   1141  AGATTGCCACAAAGATACTGGCAAATGAGACCCATTGTCTTCTTGGGTAACCAC  1200

Qy   1256  GCGCAGTGCCCCTACGGCGTGCTGTCCCCGGGAGAAGCCCAGGCGCTGGGCGGGTCACC  1315
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Db   1201  GCTCAATGTCCATACGGTGTTTTTGTTGCGGGAGACTCACTGGTCATTGCTGGGTTTACT  1260

Qy   1316  CCAGCAGCCGGTGCTGTGCCCGGGAGAAGCCCCAGGCGCCCGAGGCGGCCCCGAGGAG  1375
            ||||| || |  || |||  |||| ||||  |  ||   |  ||||  ||| |||||
Db   1261  CCAGCTGCTGGTTGTGTGTCTGGACGAAAAGCCACCAAGGTTCTGTGCTGTCCAGAAGAA  1320

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            |  ||||| |||   ||   | |  ||| ||  ||||| |  || ||||||||
Db   1321  GAAGACACTGACCCAAGAAGAAGTGGTTCAATTGTTGATGACAACACTCTTCTCCATGGCA  1380

Qy   1436  GTGTACGGCTTCGTGCGCGGCCTGCCTCGGCCGCCGGTGCCCCCAGGGCCTCTGGGCGTCC  1495
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Db   1381  GTTTACGGTTTCGTTAGAGCTTTGGTTCCACCAGGTTGTGTGGGTTCT  1440

Qy   1496  AGGCACACGAACGCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCAT  1555
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Db   1441  AGACACAACGAAAGAAGAATCTTGAGAAACACTAAGAGTTCATTTGTTTGGGTAAGCAC  1500

Qy   1556  GCCAAGCTCCGCTGCTGCAGGAGCTGACGTGAAGATGAGCGTGCCGGCTGCGGTG  1615
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Db   1501  GCTAAGTTGTCTTGCAAGAATTGACTTGGAAGATGTCTGTGTTAGAGACTGTCGCTGGTTG  1560

Qy   1616  CCGAGGAGCCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC  1675
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Db   1561  AGAAGATCTTCCAGTGTTTGTTGTTCAGCTGCTGGCTGCTGCTGAGAGGAGAAATT  1620

Qy   1676  CTGGCCAAGTTCCTGCTACTGCTCGATGAGTGTGCTACGTGTCGTCGAGCTGCTCAGTCTTTC  1735
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Db   1621  TTGGCTAAGTTCTTGTCACTGCTGTCAGTTGCTGTGTTCGTGTTGACTTGACTTGAGATCTTTC  1680

Qy   1736  TTTTATGTCACGGAGACCACAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTC  1795
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Db   1681  TTCTACGTTACTGAAACTACTTTCCAAAAGAACAGATTGTCTTTCTACACGAAGAGTCTGTT  1740

Qy   1796  TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGATC  1855
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Db   1741  TGGTCTAAGTTGCAATCTATTGGTTATTGGTATTAGACAACACTTGAAAGAAGAAATT  1800

Qy   1856  CTGTTCGGAAGCAGAGGTGCAGGCAGCATCGGGAGCCCAGGCCTCGACGTCCCAGA  1915
            || || | |  |  |  || ||  ||||| |||| |||| ||   | ||||  |||
Db   1801  TTGTTCTGAAGTTGAAGTTGCAACACAGTTGACGAGAGCTTTGTTGTTGGACTTCTAGA  1860

Qy   1916  CTCCGCTTCACTCCCCAAGCCTGACGGGCTGCCGCGATTGTGAACATGGACTACGTCGTG  1975
            || | ||||  ||| || ||  ||  | | |    ||| | |||| |  |||| |||
Db   1861  TTGAGATTCATTCAGACGGGTTGAGACCCAATTGTTAACATGGACTACGTTGTT  1920

Qy   1976  GGAGCCAGAACGTTCCGCAGAGAAAAGAGGCCCGAGCGCTCTCACCTTGCGTGAAGGTCAAGGCA  2035
            ||||| | |  |||  |||| | |||| | ||||| | |  || | |||| |||| ||||| |
Db   1921  GGTGCTAGAAGGTTTCGTAGAGAGAAAAGACCAGAGCGTTTTCACTTTACGGGTCAATTGCCA  1980

Qy   2036  CTGTTCAGCGTGCTCAACTACGAGGCCCGGCGGGAGGCGCCCGGGCCTGGGGCGCCTCTGTG  2095
            |||| |||  |||| ||  |  | || | | ||||| | | |   |||| |||  | ||||
Db   1981  TTGTTGTCTGTTTGAACTACGAAGCTAGAGCTAGAGGTGCTCCCCCTGGGTGGGGTCTTCTGT  2040

Qy   2096  CTGGGCCTGGACGAGATATCCAGAGATCACAGGGGCTGTGCGTGCCGTGTGCCGGCGCCCAG  2155
            ||| | ||||| || | | ||  | || || ||  | |||  ||| | |  |  |||||
Db   2041  TTGGGTTTGGACGATATTCAGAGATTCACATTTGGACGTTGTGCTTTACGGACCTGTAAGTC  2100

Qy   2156  GACCCCGGCCGCCGCCCTGAGCGTGACTTTGTCAAGGGCGCGCCGTTACCGCCACCACATC  2215
            |  ||| | || || |||||  |||| |||| |||| |  | |||  ||| || ||
Db   2101  GACCCACCACCACCAGGAATTGTGCTTCGTTGACGTTGACGTTACTGCTTACGGACACATATT  2160

Qy   2216  CCCCAGGACAGGCTCACGGAGGTCATCCGCCAGCAGCCCCAGGAACGCCTACTGC  2275
            ||  || | |  |||  |  |||  || |||   |||   | |  | ||| | ||
Db   2161  CCACAAGACAGATTGACTGAAGTTATTCGTCTATTATTAAGCCACAAAAACACTTACTGT  2220
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Db   3301 ACTCAATTGTCTAGAAAGTTGCCAGTGACTTCAAGACCATCCTGGAC 3360

Qy   3416 CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC 3451
Db   3361 CCAGCTTTGCCATCTGACTTCAAGACTATTTTGGAC 3396

RESULT 13
PCT-US03-19844-5
; Sequence 5, Application PC/TUS0319844
; GENERAL INFORMATION:
;   APPLICANT: Geron Corporation
;   APPLICANT: Majumdar, Anish Sen
;   APPLICANT: Ferber, Iris
;   APPLICANT: Frolkis, Maria
;   APPLICANT: Wang, Zhuo
;   TITLE OF INVENTION: Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase Reve
;   TITLE OF INVENTION: Transcriptase
;   FILE REFERENCE: 086/200
;   CURRENT APPLICATION NUMBER: PCT/US03/19844
;   CURRENT FILING DATE:  2003-06-24
;   PRIOR APPLICATION NUMBER: 60/393,295
;   PRIOR FILING DATE: 2002-06-27
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
;   LENGTH: 4170
;   TYPE: DNA
;   ORGANISM: Mesocricetus auratus
PCT-US03-19844-5

  Query Match            41.6%;  Score 1670.6;  DB 1;  Length 4170;
  Best Local Similarity  69.7%;  Pred. No. 0;
  Matches  2419;  Conservative    0;  Mismatches  964;  Indels  90;  Gaps  8;

Qy     52 CGCGATGCCCGCGGCGTCCCCGCTGCCGAGCCCGTGCGCTCCCTGCTGCGCAGCCACTACCG 111
          ||  |||||||||||||| ||||||||||||||||| |||||||||  || |||||||||||
Db     24 CGCGATGCCCGCGGCGTCCCCGCTGCCGAGCCCGTGCGCTGCGCGCAGTCAATACCG 83

Qy    112 CGAGGTGCTGCCGCTGGCCAGTCTGTGCGGCGGCCTGGGGCGCCCCCCAGGGCGTGGCGGCTGGT 171
          ||||||||||||| |||| ||||||||||||||  |||||||||| |||||||||||||||||
Db     84 TCAGGTGTGGGCCGCTGGCAACCTTCGTGCGCCTCGGGGGCGGGCCTGAGGGCAGCAGTTGT 143

Qy    172 GCAGCCGGGGACCCCGGGCTTCCCGCCGGGGTGGCCCAGTGCGCTGGTGCGTGCGCC 231
          ||  |||||||||||  ||||||||||||||| || |||||||||| |||||||||
Db    144 ACAACCCGGGGACCCCAAAAGGTCTTCCGCACCTCCGCACGCTGCCTGCTAGTCGTGCGCC 203

Qy    232 CTGGGACGCACGGGCCGCCCCGCCGCCCCCTTCCTCCGCCAGGTGTCCTGCCTGAAGGA 291
          |||||||||||| |||||||||||| |||||||| ||||||| |||||||| |||||||
Db    204 CTGGGACTCACAACCTGCCCAACCTCCGACCTTTCCTCCACCAGGTGTCATCACTGAAGGA 263

Qy    292 GCTGGTGGCCCAGTGCTGCAGAGCCTGTGCGAGCGGGGGCCCGGGGGGGCCCCTGCTT 351
          ||  |||||||||||  ||||||||| |||||||||||||||  || ||||||||||||
Db    264 CTGGGTGGCCAGGGTCTGTGCGAGGCCTGCGAGAGGGAACGGCGGCGGCGGCCCTGCTT 323

Qy    352 CGGCTTCGGCGTCGTGCTGACGGGGGGCCCCCAGGGCGGGGGCGTGGGGGCT 411
          ||||||||||| |||  ||||  |||||||| |||||||||||  |||||||
Db    324 TGGCTTCGGCGTCGTTAACGGAGCCCCAAGGCGGTCGGTGTCCCTGCGTGGCT 383

Qy    412 GCGCAGCTACCTGCCCAACACAGTGACCGACTGCGGGGGAGGCGTGGGGGGCT 471
          ||||||||||||||| |||||| |||  ||||||||||||| || |||||||||
Db    384 GCGCAGCTACCTGCCCAACTCGGTAACCACGTCTCGGCGTGCGCGTGCTTGGATGCT 443

Qy    472 GCTGCTGCGCCGGTGGGGACGACGGCCTGTTCACCTGCGCCTGCGCGCTCTT 531
          ||||| | |||||||||||| ||||| |||||||||||| ||||||||||||
Db    444 TCTGCTGAACCGAGTGGGCGACGACTGTTCTACCTGCTGGTCTACCTGCGCTTA 503

Qy    532 TGTGCTGGTGCGCCTCCCAGCTGCGCCTACCAGGTGTGCGGGGCCCCGTGTACCAGCTCGG 591
          |||||||| || |||||||||||||| |||||||||||||| |||||  ||||||||| ||
Db    504 CCTGCTGCGTGCCCCCAGCTGCCCTACCAGGTGTGCGGGGCCTCACCCCTGTACCAAATCTG 563

Qy    592 CGCTGCCACTCAGGC---------------CCGGCCCCCGCCACACGCTAG 627
          |||||||||  | ||                 ||||  |||  ||||||||
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Db    564 TGGCACCGCAGAAACCTGGCCTTCTGTGTCCCGCCATCACAGGCCCACACGACCCGTGGG 623
          |||  ||| |||||||||||||||  ||||||   || |||||||||||| || ||||||

Qy    628 TGGACCCCGAAGGCGTCTGGGATGC---GAACGGGCCTGGACCATAGCGTCAGGGAGGC 684
          |||||   | ||| ||||| |||||     ||| |||||  |||| ||| |||||||||
Db    624 CAGAAATTTACTCATCTGGATCACACACCGGTCAGGAACAGCAGTCACCAGGAGAGC 683

Qy    685 CGGGGTCCCCCTGGGCCTGCAGCCCGCGGGTGCGGTGCCCGGGTGCGGTGGAGGAGGCGGGGGGGCAGTGCCAGCCG 744
          |||||||||   |||| || |||||||  ||||| || |||||||||| |||||||| || || |||||||||||||
Db    684 ATGGAAACCCCGCCCCTGCCATCTCGAGAGCGGCAAGCGGAGTCTAAGCATCACCAATAG 743

Qy    745 AAGTCTGCGTTGCCAAGAGGCCAGGCGGTGGCGCTGCCCCTGAGCCGGCGGACGCC 804
          ||  |||||| ||||||| ||||  ||||| ||||||||||  ||||||| ||||
Db    744 AAGTGTGCCTCCATCTAAGAAAGGCCAGTGCCAGTCGGATCTGGCCCCGAGACTGGAGAAGGGACC 803

Qy    805 CGTTGGGCAGGGTCCTGGCCCACCCGGCAGGACCCGTGACCGACTGACCGTGGTTT 864
          |||||||||||||||  ||||||||||| ||||||||||||||| ||||||| |||
Db    804 CTACAGGCAGGGCAGTTCAACCCCATCAGACAACAAATCGGTGCCAAAATCCTGCCAAGTC 863

Qy    865 CTGTGGTGGTCACCTGCCAGACCCGCCGGGTGCGCTCTC 924
          |||| |||| ||| ||||| |||||  || ||||||||
Db    864 CCATGCAGTGCCTATTAGTAGAACTACCAAGGAAGATTTGTCTTCCGGGTGAAGGCACC 923

Qy    925 TGGCACGCGCCACTCCCACCATCCGTGGGCCCGCAGCACCGCGGCCCCCATCCAC 984
          |||||||||||||||  |||  ||  |||| |||     ||||| ||||||||||
Db    924 TGGCCTGAGTCGCTCTGGGTCA-----GTGTCTATAAACACAAGCCCAGTTCCAACATC 977

Qy    985 ATCGGCGGCCACCACGTCCCTGGACACGCCTTGTCCCCGGTACGCCGAGACCAAGCA 1044
          || || ||||||  | || |||||| ||  ||| ||| |||||||||||||| |||
Db    978 CCTGCAGTCACCACTGTGCCAAAATGCCTTTCAGCTCAGACCATATACTGAGACCAAACG 1037

Qy   1045 CTTCCTCACTC-------CTCAGGCGACAAGGAGCAGCTGCGGCGCTCGTGGAGACCGTCCTCCTACTCAGCTC 1101
          |||||||| |         ||||| |||||| |||||| || |||||| || || ||||| || ||||| ||
Db   1038 CTTCCTCACTCTAGGGAAGTTGGCCGAGAGAGTGGCCGAGGCTGAACCCCTCGTTCCTACTCAACAA 1097

Qy   1102 TCTGAGGCCAGGCCGCTGACTGGCGCTGGAGACCATCTTCTGGGTTCCAG 1161
          ||  ||||||||||||| || |||| || ||||| ||||| ||||| |||
Db   1098 CCTGCAGCCCAGCTTGACTGGGCGCCAGGAGACTGGTAGAGATACTCTTTCTAGGCATGAG 1157

Qy   1162 GCCCTGATGCCAGGGACTCCCGCGCAGGTTGCCCCGGCTACTGGCAAAT 1221
          |||| |||||  || |||||||||||  ||||||||||||||||| |||
Db   1158 ACCTAGGACATCGGACCACTCTGTGGAGACCGCCCTCATCGAAGCCGTACTGGCAGAT 1217

Qy   1222 GCGGCCCCCTGTTTCTGGAGCTGCTGGCCCAGTGCCGGCGCGTTACGGGGTGTCCT 1281
          ||||||||  ||| ||||||| |||||  ||||| |||||| ||||  ||||||||
Db   1218 GCGGCCCCCTATTCCAGCAGTTGCTTGTGAACATGCCGGTGCCCGGTATGTCCGGCGTCCT 1277

Qy   1282 CAAGACGACTGCCGCGCTGCGAGCTGCGTCACCCGAGCAGCCGGGA 1341
          ||  |||||| || | |||| | || |   |||| |||||  |||
Db   1278 CAGGTCCCATTGCAGTTTCGGAGCGTTTCGGACGCAGCCGCCACCAGGTGGCAGGTGCCT 1327

Qy   1342 GAAGCCCCAGGGTCTGTTGCGCGGGCACAGAGACCCCCGTCGCCTGGT 1401
          |||||||| ||||||||  ||| ||||| ||||||||||||| |||||
Db   1328 ----------------------------------------TGAACACCACCAGCCACCCAGCCTCCAGCGCCTCAT 1355

Qy   1402 GCAGCTGCTGCTCCGCCAGCAGCAGCCCCTGGCTTCGTCGGGGCGGCTGCCT 1461
          |||||||| ||||| ||||||||| || ||||| ||||||||||| ||||||
Db   1356 GAATTTGCTCCGTCTACACAGACAGTCCCTGGCAGGTATATGGCTTTTCTTCAGGCGTGT 1415

Qy   1462 GCGCGGCGGTGGTGCCCAACACAGTGGGGGGGCTTCCTCAG 1521
          |||||||||||||||| ||||| ||  || |||||||||||
Db   1416 CGGAAAGTGGTGCCTCCGGGTCTCTGGGGAAGCAGCGACGCGTTCTTTAA 1475

Qy   1522 GAACACCAAGAGAGTTCATCTCCCTGGGGAAGCAATGCCAAGCTCTGCAGAGCTGAC 1581
          |||||| |||||| | || || ||||||||||||  |  ||||| || || || ||
Db   1476 GAACGTGAAGCGGTTCATCTCCTGGGGAGTATGACAAGCGTCGTCGCCAGGAGGTGAC 1535

Qy   1582 GTGGAAGATGAGCGTGCGGGGACTGCCTCGGCGTGCGCCCCGGTTGGCGTGTGT 1641
          ||| ||||||  |||||  ||| ||  ||||||  ||||||||| || |||||||
Db   1536 GTGGAAGATGAAGTTCAAGACTGCAGGTGGCTTCGCAGCAGCCCAGGGAACAACTGTGT 1595

Qy   1642 TCCGGCCCCGCAGCACCACGCTTTGCCTGCGTGAGGAGATCCTGCCTGAGGAGATCCTGCCTGCGAT 1701
          |||||||||| || ||||||||||||| | ||||||||||||| || |||||||||
Db                                                              
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Db        1596 CCCGGCTGCAGAGCACCGCACGAGGGAAAGGATCCTGGCTGTGTTCTTGTTCTGGCTGAT 1655

Qy        1702 GAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCA 1761
               |   | |||||| || ||||||  |||| |||||||| ||||| ||||||||| || ||
Db        1656 GGACGCGTACGTGGTAGAGCTGCTTCGGTCATTCTTTTACGTCACAGAGACCACTTTCCA 1715

Qy        1762 AAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAAT 1821
                |||||| |||||| |||||||| |||||  | |||||| | | |||| |||||||| |
Db        1716 GAAGAACCGGCTCTTCTTCTACCGAAAGAGCATGTGGAGAAGGCTGCAGAGCATTGGAGT 1775

Qy        1822 CAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGGTCAGGCAGCA 1881
               ||| || ||| |  |||| |||| ||| |   | |||||  ||| ||| |||||||||
Db        1776 CAGGCATCACCTTGAGAGAGTGCGGCTACAAGAACTGTCTCAAGAAGAAGTCAGGCAGCG 1835

Qy        1882 TCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACGG 1941
                | ||| ||| |||| ||| |||  |  | |||||| || ||||||||||||||    ||
Db        1836 CCAGGAGGCCTGGCCAGCCATGCCCATCTGCAGACTGCGTTTCATCCCCAAGCCCAGTGG 1895

Qy        1942 GCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAA 2001
                || |||||||||||||||||   ||     ||||  ||||| | ||   || ||  ||
Db        1896 TCTTCGGCCCATTGTGAACATGAGTTA---TATGGGCACCAGAGCCTTTGACAAAGGGAA 1952

Qy        2002 GAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGAGCG 2061
               |  |||  ||| | |||||  | |  | ||| | ||||||||||||||||||| || |
Db        1953 GCAGGCTCAGCATTTCACCCAGTGTCTCAAGACTCTGTTCAGCGTGCTCAACTATGAACT 2012

Qy        2062 GGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGC 2121
               | |    |   |   ||| ||||| || ||||| |||||||||| | |||||| ||||| |
Db        2013 GACAAAACATACTAACCTTCTGGGGGCATCTGTACTGGGCCTGAATGATATCTACAGGAC 2072

Qy        2122 CTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGAGCTGTACTTTGT 2181
               |||||| |||||||| |||||||||||  | | ||||||  | ||  ||  ||||||||||
Db        2073 CTGGCGGACCTTCGTACTGCGTGTGCGCACTCTGGACCCAGCACCCAGGATGTACTTTGT 2132

Qy        2182 CAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGTCAT 2241
                ||||  |||||||| || || || ||  |||||||||||||||| |||    |||||| ||
Db        2133 TAAGGCAGATGTGACAGGGGCATATGATGCCATCCCCCAGGACAAGCTTGTGGAGGTTAT 2192

Qy        2242 CGCCAGCATCATCAAACCCC---AGAACACGTACTGCGTGCGTCGGTATGCCGTGGTCCA 2298
                ||||  || |||| || ||   | ||| ||||||||  | |  |  ||||| ||||||||
Db        2193 TGCCAATATGATCAGACACCCAGACAACTCGTACTGTATCCACCAATATGCAGTGGTCCA 2252

Qy        2299 GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGA 2358
                |  |     || || ||  ||| |||| |||||| ||| || ||||| ||| |  | ||
Db        2253 AAGAGATAGACAAGGCCAAATCCACAAGTCCTTCAGGAGACAGGTCTCCACCCTCTCTGA 2312

Qy        2359 CCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAG------GAGACCAGCCCGCT 2412
               |||||||||  ||||| | ||||||| ||   || || |||      || |||||  ||||
Db        2313 CCTCCAGCCACACATGGGCCAGTTCTTGAAGCATCTTCAGGACTCAGACACCAGTGCGCT 2372

Qy        2413 GAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTT 2472
               |||| |  |||| ||||| ||||||||||  || |||||  |||||||||||  |||| ||
Db        2373 GAGGAACTCCGTTGTCATTGAGCAGAGCTTATCTCTGAACGAGGCCAGCAGCAGCCTGTT 2432

Qy        2473 CGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGT 2532
               |||| ||||||| |||||  |||   ||   | ||||   ||| | |||| || ||| ||
Db        2433 CGACTTCTTCCTGCGCTTTGTGCGTAACAGTGTCGTGAAGATCGGTGGCAGGTGCTATGT 2492

Qy        2533 CCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTA 2592
               |||||||||||| ||||| ||||||||| ||| ||||| ||||||||||| ||||| |
Db        2493 CCAGTGCCAGGGCATCCCCCAGGGCTCCAGCCTGTCCACCCTGCTCTGCAGTCTGTGTTT 2552

Qy        2593 CGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTT 2652
               ||| |||||||||||||||||||||| |   | | || ||| ||||||||  |||||||
Db        2553 CGGGGACATGGAGAACAAGCTGTTTGCTGAAGTGCAGCAGGATGGGCTGCTTTTGCGTTT 2612

Qy        2653 GGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGAC 2712
                || ||||| ||  ||||||||||||||||||||||   ||| ||| || |||||||||| |
Db        2613 TGTTGATGACTTTCTGTTGGTGACACCTCACCTGGTCCAGGCGGAAGCCTTCCTCAGGGC 2672

Qy        2713 CCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAA 2772
               ||| ||||| ||  |||||||||| ||||||| || | ||||||| ||||||||||| ||
Db        2673 CCTCGTCCGTGGCATCCCTGAGTACGGCTGCATGATAAACTTGCAGAAGACAGTGGTAAA 2732

Qy        2773 CTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGG 2832
               ||||||||| || |  |   |||||| |||||| |||      ||| |||| || ||| |
Db        2733 CTTCCCTGTGGACGCTGGTACCCTGGATGGCACAGCTCCACACCAGCTGCCTGCTCACTG 2792

Qy        2833 CCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTA 2892
               ||| || |||||||| ||| | |||||||| || | ||| ||||||||||   | |||||
Db        2793 CCTGTTTCCCTGGTGTGGCTTACTGCTGGACACTCAGACTCTGGAGGTGCTCTGTGACTA 2852

Qy        2893 CTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGC 2952
               | |  | ||||||||||||| || |  ||||| |||||||||| | |||  |||||||||
Db        2853 CACTGGTTATGCCCGGACCTCAATTAAGGCCAGCCTCACCTTCCAGCGCACCTTCAAGGC 2912

Qy        2953 TGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTT 3012
                |||||||||||||| |  || ||||| |  || ||||||  ||||||||||||| |||||
Db        2913 GGGGAGGAACATGCGACAGAAGCTCTTAGCTGTTTTGCGGTTGAAGTGTCACAGTCTGTT 2972

Qy        3013 TCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCT 3072
               ||| || |||||| |||| ||||| ||||| || || | |||  | |||||||||| ||||
Db        2973 TCTAGACTTGCAGATGAATAGCCTTCAGACAGTCTGTATCAATGTGTACAAGATCTTCCT 3032

Qy        3073 GCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTG 3132
               ||| ||||| |||||||| || || |||| ||| ||||| || ||| | || || ||| |
Db        3033 GCTTCAGGCCTACAGGTTCCATGCGTGTGCGCTTCAGCTTCCCTTTGACCAACATGTTAG 3092

Qy        3133 GAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCAT 3192
                ||||||||| |||| || ||| || ||||||||  |||  || |||  ||||||||||||
Db        3093 AAAGAACCCCGCATTCTTTCTGAGCATCATCTCCAACATAGCATCCTGCTGCTACTCCAT 3152

Qy        3193 CCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCCCTCTGCC 3252
               |||||| | ||||| ||||| ||| | ||   ||||||||| || ||| | || |  | ||
Db        3153 CCTGAAGGTCAAGAATGCAGGAATGACACTAAAGGCCAAGGGTGCCTCTGGCTCATTTCC 3212

Qy        3253 CTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCG 3312
                 | || || |  |  ||||| ||| |||| ||| ||||||||||||||| || | ||
Db        3213 TCCTGAAGCTGCACGTTGGCTCTGCTACCAAGCCTTCCTGCTCAAGCTGGCTGGTCATTC 3272

Qy        3313 TGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAA 3372
               ||||||||||  |   ||||||||  | ||||||||||||| || |  |||||| | |||||
Db        3273 TGTCACCTACAAGTGTCTCCTGGGACCTCTCAGGACAGCACAAAAACAGCTGTGCCGGAA 3332

Qy        3373 GCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGCCCTCAGA 3432
               ||||||  || | ||  || |   ||| ||| | || ||  |||| || ||   | ||||
Db        3333 GCTCCCAAGGGCAACAATGGCCATCCTTGAGACTGCCGCTGACCCAGCCCTAAGCACAGA 3392

Qy        3433 CTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGAGAGCA 3485
               |||  |||||||  |||||| |   |  |||  |  | |    |  |  |  |||
Db        3393 CTTTCAGACCATTTTGGACTAACCCCTCCCCTTCAGCTGGATGAACATGGGCA 3445

RESULT 14
PCT-US03-19844-3
; Sequence 3, Application PC/TUS0319844
; GENERAL INFORMATION:
;  APPLICANT: Geron Corporation
;  APPLICANT:  Majumdar, Anish Sen
;  APPLICANT:  Ferber, Iris
;  APPLICANT:  Frolkis, Maria
;  APPLICANT:  Wang, Zhuo
;  TITLE OF INVENTION: Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase R
;  TITLE OF INVENTION:  Transcriptase
;  FILE REFERENCE: 086/200
;  CURRENT APPLICATION NUMBER: PCT/US03/19844
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: 60/393,295
;  PRIOR FILING DATE: 2002-06-27
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 3426
;   TYPE: DNA
;   ORGANISM: Mus musculus
PCT-US03-19844-3
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Query Match   39.9%;   Score 1600.8;   DB 1;   Length 3426;
Best Local Similarity   68.9%;   Pred. No. 0;
Matches 2379;   Conservative 0;   Mismatches 0;   Indels 108;   Gaps 9;

Qy   40 CCCGGCCACCCCGCGATGCGCGCTCCCCGCCTGCGCGCTCCTCCTGCTGCG 99
         |||||| | ||| ||||||||| |||| ||||||||||||||||||
Db   14 CCCGGCCCTTGAGCACAATGACCCGCGCTCCTCGTTGCCCGCGTGCGCTCCTCTGCTGCG 73

Qy   100 CAGCCACTACCGCGAGGTCTGCGCCGCTGGCCACCGGCGGGGACCCGGCGGCGGTTCGGC 159
         | |||| || |||||||||| || |||| ||| | |||||||||||| |||||||||
Db   74 CAGCCGATACCGGGAGGTGTGGCGAACCTTTGTCGGCGCCGGCCCTGGGCCCGGGCCGAGGG 133

Qy   160 CTGGCGGTGGTCAGCGCGGGGACCCGGCGGCGGTTCCGCGGCGGCCTGCCCAGTGCCT 219
         | ||||||| ||||| | |||||||||| ||||| ||| ||||||||| |||||||
Db   134 CAGGCGGGCTTGTGCAACCCGGGAGACCTACCGCACTTTGGTTGCCCAATGCCT 193

Qy   220 GGTGCGTCCCTGGGACGCACGGCGCGCCCCTTCCTTCCGCCAGGCCT 279
         |||||| ||||||||| | | |||||||||| ||||| ||| |||||
Db   194 AGTGTGCAATGCACTGGGGCTCACAGCCTCCACCTGCCTTCCACCAGGTGTC 253

Qy   280 CTGCCTGAAGGAGTGGTGCGCCCAGTGCTGCACGAGGCGGCGGCGCGCGAAGAA 339
         ||||| |||| |||| || |||||| | |||||| || ||||||||
Db   254 ATCCCTGAAAGAGAGTGGTGCCAGGTTGTGCAGAGACTCTGCGAGCGACGAGAAA 313

Qy   340 CGTGCTGGCCTTCGCGTCGCTGCTGAGCGACGGGGGCCCCGGGGGCCTT 399
         ||||||| || | ||| | |||||| ||| |||||| | ||||||||
Db   314 CGTGCTGGCTTTTGAGCTGCTTAAGCAGGCCAGGCGGGGGCCCGGGGGCCTT 373

Qy   400 CACCACCAGGTGCGCAGCTACCTGCCCAACACGGTGACCGACGGCGGGGAGCGG 459
         || || | | | ||||| ||| |||||| | |||||| ||| |||||||| |||
Db   374 CACTAGTAGCGTGGTGCAGCTGTTATTGAGACCCTGCGTGTCAGTGG 433

Qy   460 GGCTTGGGGCTGTCGCTGCGCTGCGGCGACGACGTGCTGGTTCACCTGCTGGCACG 519
         |||| ||||| ||||||| |||| |||||||| || | |||||| | |||| |||
Db   434 TGCATGGGATCTACTGTTGAGCGATGGCGGAGCCTTCGTGGGCGAACTTAAAGAAGT 493

Qy   520 CTGGCGGCTCTTGTGGTCGTGTGCCCGCTGGCCACCAGCTGCGGGGGCCCCGCT 579
         |||||| |||| | |||| ||||| ||||||| ||||| ||| || | |||
Db   494 CTGTGCTTTGTTTATCTTCTGTGCCCCCCAGCTGTCCCTGGGGTCTCCCT 553

Qy   580 GTACCAGCTCGGCGGCTGCCACTCAGGCCCCACACGTGAGTTGGACCCCGAAG 639
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Qy   640 GCGTCTGGGATGC------------GAACCGGACCTGGAACCATAG 672
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Qy   673 CGTCAGGAGGACCGGGGTCCCGGGTCCCAGCCCCGGCTGCGGAGGCGGGGG 732
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Qy   733 CAGTCCCAGCGCCGGAAGTCTGCGCTTGCCCAAGAGGCCAGGCGGCTGCCCTGAGCC 792
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Qy   853 TGACCTGGTTTCTGTGTGCCGCTGTGTCGACCGGCCACTCCCACCATCCGAGGCCACCCTCTTTGGA 912
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Qy   913 GGGTCGCTCTCTGGCACGGCGGCCACCATCCCACCATCCGTGGCGCGCCACGCGGG 972
         || || ||| ||| | ||||| || || |||| |||||||| | | |||||||||
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Qy 1033 CGAGACCAAGCACTTCCTCTACTCCTCAGGCGA---CAAGGAGCAGCTGCGCGCCCCCTT 1089
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Qy 1510 CCGCTTCCTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGAAGCCATGCCAAGCTCTCGCT 1569
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Qy 1570 GCAGGAGCTGACGTGGAAGATGAGCGTGCAGGCTTGGCTGCTGCGGAGCCCAGG 1629
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Db 1514 GCAGGAACTGATGTGGAAGATGAAAGTAGAGGATTGCCACTGCTCCCAGCAGCCCGGG 1573

Qy 1630 GGTTGGCTGCTGTGTTCCGGCCGAGCAGCACCCTGCGTGAGGAGATCCTGGCCAAGTTCCT 1689
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Db 1694 GAGCACATTCCAGAAGAACAGGCTCTCTTCTTTCCTGCCTCGTAAGAGTGTGTGTGAGCAAGCTGCA 1753

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Qy 1990 CCCGAGAAAAAGAGGGCCGCTGGCCCCGCATCCGTGTTCAGGGTGCTGCT 2049
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RESULT 15
US-09-721-456-640
; Sequence 640, Application US/09721456
GENERAL INFORMATION:
  APPLICANT: Cech, Thomas R.
           Lingner, Joachim
           Nakamura, Toru
           Chapman, Karen B.
           Morin, Gregg B.
           Harley, Calvin B.
           Andrews, William H.
  TITLE OF INVENTION: Human Telomerase Catalytic Subunit
  NUMBER OF SEQUENCES: 727
  CORRESPONDENCE ADDRESS:
     ADDRESSEE: Townsend and Townsend and Crew LLP
     STREET: Two Embarcadero Center, Eighth Floor
     CITY: San Francisco
     STATE: California
     COUNTRY: USA
     ZIP: 94111-3834
  COMPUTER READABLE FORM:
     MEDIUM TYPE: Floppy disk
     COMPUTER: IBM PC compatible
     OPERATING SYSTEM: PC-DOS/MS-DOS
     SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/09/721,456
     FILING DATE: 22-Nov-2000
     CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
     APPLICATION NUMBER: US/08/974,549A
     FILING DATE: 19-NOV-1997
     APPLICATION NUMBER: US 08/724,643
     FILING DATE: 01-OCT-1996
     APPLICATION NUMBER: US 08/844,419
     FILING DATE: 18-APR-1997
     APPLICATION NUMBER: US 08/846,017
     FILING DATE: 25-APR-1997
     APPLICATION NUMBER: US 08/851,843
     FILING DATE: 06-MAY-1997
     APPLICATION NUMBER: US 08/854,050
     FILING DATE: 09-MAY-1997
     APPLICATION NUMBER: US 08/911,312
     FILING DATE: 14-AUG-1997
     APPLICATION NUMBER: US 08/912,951
     FILING DATE: 14-AUG-1997
     APPLICATION NUMBER: US 08/915,503
     FILING DATE: 14-AUG-1997
     APPLICATION NUMBER: WO PCT/US97/17618
     FILING DATE: 01-OCT-1997
     APPLICATION NUMBER: WO PCT/US97/17885
     FILING DATE: 01-OCT-1997
  ATTORNEY/AGENT INFORMATION:
     NAME: Apple, Randolph Ted

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Qy 2287 TGCCGTGGTGCCAGAAGGCCGCCCCATGGCCACGTCCGGAAGGCCTTCAAGAGCCACGTCTC 2346
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Qy 2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGACGAGCTCCTCCCTGAATGAGGCCAG 2460
Db 2354 TGCCAGTGCACTGAGGAACTCCGTGTCATCGAGCAGCAGAGCATCTCTATGAATGAGAGCAG 2413

Qy 2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCGTGCGCATCAGGGG 2520
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Db 2474 CAGGTGCTATACGCCAGTGCCAGGGCCATCCCCCAGGGCTCCAGCCTATCCACCCTGCTCTG 2533

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Qy 2641 GCTCCTGCGTTGGTGATGATTTCTTGTTGGTGACACCTCACCTCACCACCGCGAAAAC 2700
Db 2594 GCTTTACGTTTTTGTTGATGACTTTCTGTTTGGTGACGCCCTCACTTGGACCAAGCAAAAAC 2653

Qy 2701 CTTCCTCCAGGACCTGGTTCCCGAGGTGTCCCTGAGTAGTGTCCGTGGTGAACTTGCCGAA 2760
Db 2654 CTTCCTCAGCACCACCCTGGTCCCATGGCGGTTCCATGCATGGATGAAACTTGCAGAA 2713

Qy 2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGTCCTTTGTTCAGAT 2820
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Db 2774 GCCTGCTCACTGCCTGCTCGTGTTCCCGGTGTGGCTTGCTGTCTGCTGGAGACACTCAGACTTGGAGGT 2833

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Db 2834 GTTCTGTGACTACTCAGGTTATGCCCAGACCTTCAATTAAGACGAGCCTCACCTTCCAGAG 2893

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Qy 3061 CAAGATCCTCTTGCTCGTGCTGCATCGGCGCTGCAGCTCCCATTTCA 3120
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;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-002610US
;   TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 576-0200
;      TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 640:
;   SEQUENCE CHARACTERISTICS:
;      LENGTH: 3396 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   FEATURE:
;      NAME/KEY: -
;      LOCATION: 1..3396
;      OTHER INFORMATION:   /note= "hTRT-encoding sequence employing
         alternative codon distributions for
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;   SEQUENCE DESCRIPTION: SEQ ID NO: 640:
US-09-721-456-640
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Qy          776 GGCGCTGCCCCTGAGCCGGAGCGGAGCCCCGTTGGGCAGGGGTCCTGGCCACCCGGGC 835
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Db          721 GGTGTGCTGCTCCAGAAACCAGAGAACTCAGTTGGTCAAGGTTCTTGGGCTCATCCAGGT 780

Qy          836 AGGACGGCGTGGACGAGTGACCGTGGTTCTGTGTGTGTGTGTTCTTCCAGCTAGACCAGCTGAA 895
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Db          781 AGAACTAGAGGTGCCATCTGATAGAGGTTTTGTGTTGTGTTGGATCCATCTGTTGT 840

Qy          896 GAAGCCACCTCTTGGAGGGTGCGCTCTCTGGCACGGCCACCATCCGTGGGC 955
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Db          841 GAAGCTACTTCTTTGGAAGGTGCTTTGCTGTCGTGTACTAGACATTCTCATCCATCTGTTGT 900

Qy          956 CGCCAGCACCACGCGGGGCCCCCATCCACAATGCGGCCACACGTCCCTGGACACGCCT 1015
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Db          901 AGACAACATCATGCTGGTCCACCATCTACTTCTGAGACCATCGCATGGGATACTCCA 960

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Qy         1076 CTGCGGCCCCTCCTCCTACTCCAGCTCTCTGAGGCCCAGCTCGACTCGGGCCGGGAGCTC 1135
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Db         1561 AGAAGATCTCCAGGTCTGTTGGTTGTTCCAGCTGCTGCTGTAACATAGATTGAGAAGAAATT 1620

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Qy         1796 TGGAGCAAGTTGCAAAGCATTGAATCAGCAGTTGCCAGCCGAAGTCTGCGCGGGTGCAGCTGCGGGAG 1855
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Qy   2996 AAGTGTCACAGCCTGTTTCTGGATTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC 3055
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Search completed: October 15, 2003, 08:06:26
Job time : 935 secs

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               GenCore version 5.1.6
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        October 14, 2003, 22:28:01 ; Search time 11414 Seconds
                                  (without alignments)
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Title:         US-10-054-295-224
Perfect score: 4015
Sequence:      1 GCAGCGCTGCGTCCTGCCTGC.........TTTTCAGTTTTGAAAAAAA 4015

Scoring table: IDENTITY_NUC
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Searched:      3336688 seqs, 1658188987 residues

Total number of hits satisfying chosen parameters:       66727376

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4015	100.0	4015	1	PCT-US01-15774-3	Sequence 3, Appl1
2	4015	100.0	4015	1	PCT-US02-14867-1	Sequence 1, Appl1
3	4015	100.0	4015	1	PCT-US02-31635-1	Sequence 1, Appl1
4	4015	100.0	4015	1	PCT-US02-33146-19	Sequence 19, Appl1

Matches 4015;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy  121  GCGCGTGGCCACGTTCGTGCGCGGCCTGCTGGGGCCCCAGGGCTGGCGGCTGGTGTCAGCGCGG  180
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Qy  241  ACGGGCCGCGCCCCCTCCCGCGCGGCGCGCCGAGTGCTGCAGAGGCGTGTGCGCGGCCTTCGC  300
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ALIGNMENTS

RESULT 1
PCT-US01-15774-3
; Sequence 3, Application PC/TUS0115774
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0568
; CURRENT APPLICATION NUMBER: PCT/US01/15774
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
PCT-US01-15774-3

Query Match 100.0%;   Score 4015;   DB 1;   Length 4015;
Best Local Similarity 100.0%;   Pred. No. 0;

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Qy  1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGCCGCTCGGAGGCTCGTGGA  1140
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Db  1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGCCGCTCGGAGGCTCGTGGA  1140

Qy  1141  GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT  1200

Qy  1201  GCCCCAGCGCTACTGGCAAATGCGGCCCCGTTTCTGGAGCTGCTTGGGAACCACGCGCA  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  GCCCCAGCGCTACTGGCAAATGCGGCCCCGTTTCTGGAGCTGCTTGGGAACCACGCGCA  1260

Qy  1261  GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCGGCCGCTGGGTGCGGTCACCCCAGC  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCGGCCGCTGGGTGCGGTCACCCCAGC  1320

Qy  1321  AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGGCTCTGTGGCGGCCCCGAGGAGGAGA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGGCTCTGTGGCGGCCCCGAGGAGGAGA  1380

Qy  1381  CACAGACCCCGTGGCTGCAGTCTGCTCCGCACAGCAGCCCTGCCAGGTGTA  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CACAGACCCCGTGGCTGCAGTCTGCTCCGCACAGCAGCCCTGCCAGGTGTA  1440

Qy  1441  CGGCTTCGTGCGGGCCTGCCTGGCCGGCCTGCCCCCCAGGCCTCTGGGGCTCCAGGCA  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  CGGCTTCGTGCGGGCCTGCCTGGCCGGCCTGCCCCCCAGGCCTCTGGGGCTCCAGGCA  1500

Qy  1501  CAACGAACGCCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  CAACGAACGCCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560

Qy  1561  GCTCTCGCTGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGCCTTGGCTGCGCGCAG  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  GCTCTCGCTGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGCCTTGGCTGCGCGCAG  1620

Qy  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGGCCGCAGAGCACCGTGGTCGTGGAGATCCTGGC  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGGCCGCAGAGCACCGTGGTCGTGGAGATCCTGGC  1680

Qy  1681  CAAGTTCCTGCAACTGGCTGATGAGTGTACGTCGTCGAGCTCGTCAGCTGCGCTCGTCAGGTCTTTTA  1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CAAGTTCCTGCAACTGGCTGATGAGTGTACGTCGTCGAGCTCGTCAGCTGCGCTCGTCAGGTCTTTTA  1740

Qy  1741  TGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  TGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG  1800

Qy  1801  CAAGTTGCAAAGCATTGGAATCAGAGAGGCCCGAGCGGTGCAGCTGCGGGAGCTGTC  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  CAAGTTGCAAAGCATTGGAATCAGAGAGGCCCGAGCGGTGCAGCTGCGGGAGCTGTC  1860

Qy  1861  GGAAGCAGAGGTCAGGCGATCGGGAGCATCGGGAAGCCCGCCCGCTGCTGCTCGTCGTCCG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  GGAAGCAGAGGTCAGGCGATCGGGAGCATCGGGAAGCCCGCCCGCTGCTGCTCGTCGTCCG  1920

Qy  1921  CTTCATCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CTTCATCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980

Qy  1981  CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCCGCTCTCCGAGGGTGAAGGCACTGTT  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCCGCTCTCCGAGGGTGAAGGCACTGTT  2040

Qy  2041  CAGCGTGCTCAACTACGAGCGGGGCCCCGCCTCGTGGCCTCTGTGCTGG  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CAGCGTGCTCAACTACGAGCGGGGCCCCGCCTCGTGGCCTCTGTGCTGG  2100

Qy  2101  CCTGGACGATATCCACAGGGGCTGCGCACCTTCGTGCGTGCTGCGGGCCCCAGGACCC  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTGGACGATATCCACAGGGGCTGCGCACCTTCGTGCGTGCTGCGGGCCCCAGGACCC  2160
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Qy  2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGGTACGACCACCATCCCCCA  2220
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Db  2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGGTACGACACCATCCCCCA  2220

Qy  2221  GGACAGGGCTCACGGAGGTCATCGCCAGCAGCATCATCGGGGACGTCGCGAAGGCCTTCAGAGACCA  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGACAGGGCTCACGGAGGTCATCGCCAGCAGCATCATCGGGGACGTCGCGAAGGCCTTCAGAGCCA  2280

Qy  2281  TCGGTATGCGCTGGTCCAGAGACCGCCGCAAGGCGTCGCGACGTCGCCATCAGGGG  2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCGGTATGCGCTGGTCCAGAGACCGCCGCAAGGCGTCGCGACGTCGCCATCAGGGG  2340

Qy  2341  CGTCTCCACCTTGACAGACCTCCAGCCGTACATGCGACGTACATGCGACAGTTCGTGGCTCACCTGCAGGA  2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGTCTCCACCTTGACAGACCTCCAGCCGTACATGCGACGTACATGCGACAGTTCGTGGCTCACCTGCAGGA  2400

Qy  2401  GACCAGCCCGCTGAGGGGATGCCGTCGTCATCGAGCAGGAGCAGCTCCTCCCTGAATGAGGCCAG  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GACCAGCCCGCTGAGGGGATGCCGTCGTCATCGAGCAGGAGCAGCTCCTCCCTGAATGAGGCCAG  2460

Qy  2461  CAGTGGCCCTTCTCGACGTCTTCATGTGCCACACGCGTGCGCATCAGGGG  2520
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CAGTGGCCGTCTACGTCTTCATGTGCCACACGCGTGCGCATCAGGGG  2520

Qy  2521  CAGGTCCTACGTCCAGTGCCAGTGGGATCCCGCAGGGCGTCCATCCTCTCCACGCTGCTCTG  2580
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Db  2521  CAAGTCCTACGTCCAGTGCCAGTGGGATCCCGCAGGGCGTCCATCCTCTCCACGCGTCTG  2580

Qy  2581  CAGGCCTGTGCTACGGCGACATGAGCACGCAGGGATTCGGCGGGATTCGGCGGGACGGGCT  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CAGGCCTGTGCTACGGCGACATGAGCACGCAGGGATTCGGCGGGATTCGGCGGGACGGGCT  2640

Qy  2641  GCTCCGTGCGTTTGGTGGATGATTTCTTTGTTGGTGACACCCTCACCCTCACCCACCGCGAAAAC  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCTCCGTGTGCGTTTGGTGTGTGATGATTTCTTGTTGGTGACACCCTCACCCTCACCGCGGAAAC  2700

Qy  2701  CTTCCTCAGGACCCGGTTCCGAGTGTCCCTGAGCTATGGCGTGCGGTGAACTTGCGGAA  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CTTCCTCAGGACCCGGTTCCGAGTGTCCCTGAGCTATGGCGTGCGGTGAACTTGCGGAA  2760

Qy  2761  GACAGTGGTGGAACTTCCCTGTAGAAGACGAGGAGCCCGGGTGGCACGCGCTTTTGTTGTTCAGAT  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGAGCCCGGGTGGCACGCGCTTTTGTTGTTCAGAT  2820

Qy  2821  GCCGGCCACGCGCTATTCCCGTGTCCGTGCTGCTGGACCCTGGAGGT  2880
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  GCCGGCCACGCGCTATTCCCGTGTCCGTGCTGCTGGACCCTGGAGGT  2880

Qy  2881  GCAGAGGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCCACCTTCAACCG  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  GCAGAGGGACTACTCCAGCTACTCCAGCCAGTCTCCATCAGAGCCAGTCTCCACCTTCAACCG  2940

Qy  2941  CGGCTTCAAGGCTCGGGAGGAACATGTCGCAAACTCTTTGGGGTCTTGGGGCTGAAGTG  3000
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Db  2941  CGGCTTCAAGGCTCGGGAGGAACATGTCGCAAACTCTTTGGGGTCTTGGGGCTGAAGTG  3000

Qy  3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACATTGCAGGTGTGCCACCAACATCTA  3060
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Db  3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACATTGCAGGTGTGCCACCAACATCTA  3060

Qy  3061  CAAGATCCTCCTGCTGCAGGCGTACGGTTTCACGGCATGTGTGCTGCAGCTCCCATTTCA  3120
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Db  3061  CAAGATCCTCCTGCTGCAGGCGTACGGTTTCACGGCATGTGTGCTGCAGCTCCCATTTCA  3120

Qy  3121  TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT  3180
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Db  3121  TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT  3180

Qy  3181  CTGCTACTCCATCCTGAAAGCCAAGAACCAGAGGGATGTCGCTGCGTGCGTGCCACCAACACTA  3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  CTGCTACTCCATCCTGAAAGCCTGAAACCCAGAGGGATGTCGCTGCGTGCGTGCCACCAACACTA  3240

Qy  3241  CGGCCCCTCTGCCTTCGCCCGAGGCCGTGCAGTGGCTGGCGTGCTGCCACCAAGCATTCCTGCTCAAGCT  3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  CGGCCCCTCTGCCTTCGCCCGAGGCCGTGCAGTGGCTGGCGTGCTGCCACCAAGCATTCCTGCTCAAGCT  3300
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;
;  NAME/KEY: CDS
;  LOCATION: (56)..(3454)
;  OTHER INFORMATION:
PCT-US02-14867-1

Query Match            100.0%;   Score 4015;   DB 1;   Length 4015;
Best Local Similarity  100.0%;   Pred. NO. 0;
Matches 4015;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 GCAGGCGTGCGTCCTGCGCACGTGGAAGCCCTGGCCCCGCCACCCCGCGATGCC 60
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Qy    61 GCGCGTCCCCGCTGCGCCGAGCCGTGCGTCCCTGCTGCGCTGCCTACCACGGTGCT 120
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Qy   121 GCCGCTGGCCACGTTCGTGCGGCCGCGCCTGGGCGTGCGCTCGTGCAGCGCGCG 180
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Db   121 GCCGCTGGCCACGTTCGTGCGGCCGCGCCTGGGCGTGCGCTCGTGCAGCGCGCG 180

Qy   181 GGACCCGGCGCGGCGCTTTCCCGCGCCGCCCCTGGTGCCCTGGCCCTGGGACGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACCCGGCGCGGCGCTTTCCCGCGCCGCCCCTGGTGCCCTGGCCCTGGGACGC 240

Qy   241 ACGGCCGCGCCCCCGCCCCCGCCCCTCTTCCGCGCGCGCGAAGGAGCTTCGGTGGC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACGGCCGCGCCCCCGCCCCCGCCCCTCTTCCGCGCGCGCGAAGGAGCTTCGGTGGC 300

Qy   301 CCGAGTGCTGCAGAGGCTGTGCGACGCGCGGGGGCCCCGCGAGAACGTGCTGGCTTCGC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGAGTGCTGCAGAGGCTGTGCGACGCGCGGGGGCCCCGCGAGAACGTGCTGGCTTCGC 360

Qy   361 GCTGCTGGACGGGCCCGCGGGCGCCTTCACCACCAGCGTGCGCAGCTA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCTGCTGGACGGGCCCGCGGGCGCCTTCACCACCAGCGTGCGCAGCTA 420

Qy   421 CCTGCCCACACGTGACCGACGCTGGTTCACCTGGGCGTGGGGCGCTGCTGCGCG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTGCCCACACGTGACCGACGCTGGTTCACCTGGGCGTGGGGCGCTGCTGCGCG 480

Qy   481 CCGGCTGGGCGGCGACGACGCTGCTGCTGGTTCACCTGGCACGCTCGCGCGCTGTGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCGGCTGGGCGGCGACGACGCTGCTGCTGGTTCACCTGGCACGCTCGCGCGCTGTGT 540

Qy   541 GGCTCCAGCTGCGCCTACCAGGTGCGGGCCGCGCCGCGTACCAGCTCGGCGCTGCCAC 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCTCCAGCTGCGCCTACCAGGTGCGGGCCGCGCCGCGTACCAGCTCGGCGCTGCCAC 600

Qy   601 TCAGGCCCGGCCCCGCCACACGTAGTGCACCTAGTGCGAACGGGC 660
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Db   601 TCAGGCCCGGCCCCGCCACACGTAGTGCACCTAGTGCGAACGGGC 660

Qy   661 CTGGAACCATAGCGTCAGGAGGCCGGGTCCCCGGTGCCAG 720
           ||||||||||||||||||||||||||||||||||||||||
Db   661 CTGGAACCATAGCGTCAGGAGGCCGGGTCCCCGGTGCCAG 720

Qy   721 GAGGGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCGTTGGCGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GAGGGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCGTTGGCGC 780

Qy   781 TGCCCCTGAGCCGGACGACCCGTTGGGCGCCCACCGGGCCAGGAC 840
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Db   781 TGCCCCTGAGCCGGACGACCCGTTGGGCGCCCACCGGGCCAGGAC 840

Qy   841 GCGTGGACCGAGTGACGTGGTTTCTGCGTCTGCACGCGCCACTCCCAGACCCGAAGAGC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCGTGGACCGAGTGACGTGGTTTCTGCGTCTGCACGCGCCACTCCCAGACCCGAAGAGC 900

Qy   901 CACCTCTTTGGAGGTGCGCTCTGCACGCGCCACTCCCACCATCCGTGGGCCGCCA 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Left column (continuation):

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Db  3241 CGGCCCCTGCCCTCCGAGGCCGTGCTGTGCCACCAGCATTCCTGCTCAAGCT 3300
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Qy  3301 GACTGCACACGTGTCACCTAGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GACTGCACACGTGTCACCTAGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360
Qy  3361 GCTGAGTCGGAAGCTCCCGGGACGACCTCGGGACCCTGCCCTGGAGGCCGCAGCCAACCCGGC 3420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 GCTGAGTCGGAAGCTCCCGGGACGACCTCGGGACCCTGCCCTGGAGGCCGCAGCCAACCCGGC 3420
Qy  3421 ACTGCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCCCACAGCCAGGCCGA 3480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 ACTGCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCCCACAGCCAGGCCGA 3480
Qy  3481 GAGCAGACACCAGCAGCCCCTGTCACGCGGGCTCTAGGTCCAGGGAGGGGAGGGGCGGCC 3540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GAGCAGACACCAGCAGCCCCTGTCACGCGGGCTCTAGGTCCAGGGAGGGGAGGGGCGGCC 3540
Qy  3541 CACACCCAGGCCCGCACCCGCACCCGGGCTCTGAGGCCTGAGTGAGTGTTTGGCCTGGCCTG 3600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CACACCCAGGCCCGCACCCGCACCCGGGCTCTGAGGCCTGAGTGAGTGTTTGGCCTGGCCTG 3600
Qy  3601 CATGTCCGCTGAAGGCTGAGTCCGGCTGAGGCCTGAGCCTGAGCGCGTGTCCAGCCAAGGCT 3660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CATGTCCGCTGAAGGCTGAGTCCGGCTGAGGCCTGAGCCTGAGCGCGTGTCCAGCCAAGGCT 3660
Qy  3661 GAGTGTCCAGCAGCACCTGCCGTCTTCACTTCCCCACAGGCTGCCGCTCGGCTCCACCCCA 3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GAGTGTCCAGCAGCACCTGCCGTCTTCACTTCCCCACAGGCTGCCGCTCGGCTCCACCCCA 3720
Qy  3721 GGGCCAGCTGTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GGGCCAGCTGTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
Qy  3781 CCAGATTCGCCATTGTTCACCCCTGCCCTCGCCCTCGCCCTTGCCTTCCACCCCCACCATCC 3840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 CCAGATTCGCCATTGTTCACCCCTGCCCTCGCCCTCGCCCTTGCCTTCCACCCCCACCATCC 3840
Qy  3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGAGCTCTGGGAATTCGGAGTGACCAAAGGTGTG 3900
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Db  3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGAGCTCTGGGAATTCGGAGTGACCAAAGGTGTG 3900
Qy  3901 CCCTGTACACAGGCGGAGGACGCGGAGGACCCTGCACCTGGATGGGGGTCCCGTGTGGGTCAAATTGGGGG 3960
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Db  3901 CCCTGTACACAGGCGGAGGACGCGGAGGACCCTGCACCTGGATGGGGGTCCCGTGTGGGTCAAATTGGGGG 3960
Qy  3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTGAAAAAAA 4015
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Db  3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA 4015
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RESULT 2
PCT-US02-14867-1
; Sequence 1, Application PC/TUS0214867
; GENERAL INFORMATION:
;  APPLICANT: Geron Corporation
;  APPLICANT: Jiang, Xu-Rong
;  APPLICANT: Chiu, Choy-Pik
;  APPLICANT: Harley, Calvin B.
;  TITLE OF INVENTION: Treatment for Wounds
;  FILE REFERENCE: 120/200
;  CURRENT APPLICATION NUMBER: PCT/US02/14867
;  CURRENT FILING DATE: 2002-05-09
;  PRIOR APPLICATION NUMBER: 60/289,903
;  PRIOR FILING DATE: 2001-05-09
;  SOFTWARE: PatentIn version 3.1
;  NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
;  LENGTH: 4015
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
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us-10-054-295-224.rnpm

Left column:

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Qy    961  GCACCACGCGGGGCCCCCCATCCACATCGGCGGCCACCAGTGCCCTGGACACGCCTTGTCC  1020
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Db    961  GCACCACGCGGGGCCCCCCATCCACATCGGCGGCCACCAGTGCCCTGGACACGCCTTGTCC  1020

Qy   1021  CCCGGTGTACGGCCGAGACCAAGCACTTCCTACTCCTACTCCTCAGGCGGACAAGCAGCTGCG  1080
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Db   1021  CCCGGTGTACGCGGAGACCAAGCACTTCCTACTCCTACTCCTCGAGGCCGACAAGCAGCTGCG  1080

Qy   1081  GCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCTCGGAGGCTCGTGGA  1140
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Db   1081  GCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCTCGGAGGCTCGTGGA  1140

Qy   1141  GACCATCTTTCTGGGTTCCAGGCCTGGATGCCAGGGACTTCCCCGCCAGGTTGCCCCGCCT  1200
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Db   1141  GACCATCTTTCTGGGTTCCAGGCCTGGATGCCAGGGACTTCCCCGCCAGGTTGCCCCGCCT  1200

Qy   1201  GCCCCAGCGCTACTGCCAAATGCGCCCCGTGTTGTTGGGAGCCTGCTTGGGAACCACGCGCA  1260
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Db   1201  GCCCCAGCGCTACTGCCAAATGCGCCCCGTGTTGTTGGAGCTGCTTGGGAACCACGCGCA  1260

Qy   1261  GTGCCCCTACGGGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGGCGTCGGGCTCGGA  1320
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Db   1261  GTGCCCCTACGGGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGGCGTCGGGCTCGGA  1320

Qy   1321  AGCCGGTGTCTGTGCCCGGGAGAGCCCAGGGCTCGTGTGGCGGCCCCCGAGGAGGAGGA  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  AGCCGGTGTCTGTGCCCGGGAGAGCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGA  1380

Qy   1381  CACAGACCCCCGTCGCAGCTGGTGACGTGCTGCGCCGGCCAGCACCAGCCCCTGGCAGGTGTA  1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CACAGACCCCCGTCGCAGCTGGTGACGTGCTGCGCCGGCCAGCACCAGCCCCTGGCAGGTGTA  1440

Qy   1441  CGGCTTCGTGTGCGGGGCCTGCGCCTGCGGCCCGGCGGCCTCCGGGGGCTCCCAGGCA  1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  CGGCTTCGTGTGCGGGGCCTGCGCCTGCGGCCCGGCGGCCTCCGGGGGCTCCCAGGCA  1500

Qy   1501  CAAGAACGGCGCGCTTCCTCAGGACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  CAAGAACGGCGCGCTTCCTCAGGACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560

Qy   1561  GCTCCTCGCTGCGAGCTGGACGTGGAAGATGAGCGTGCGGGGACTGCCGGCTGCGGCAG  1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  GCTCCTCGCTGCGAGCTGGACGTGGAAGATGAGCGTGCGGGGACTGCCGGCTGCGGCAG  1620

Qy   1621  GAGCCCAGGGGTTGGCGTGTGTCCGCGCGCAGACCACCGTCCTGCGTCTGAGGAGATCCGGC  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  GAGCCCAGGGGTTGGCGTGTGTCCGCGCGCAGACCACCGTCCTGCGTCTGAGGAGATCCGGC  1680

Qy   1681  CAAGTTGCAAAGCATTGGAATCAGACAGCACTGGCAGGGCCAGGCCCTGTCAGCTGTCGTCTTTCTTTTA  1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  CAAGTTGCAAAGCATTGGAATCAGACAGCACTGGCAGGGCCAGGCCCTGTACGTCGTCTTTCTTTTA  1740

Qy   1741  TGTCACGGAGACCACGTTCAAAAGAAACAGGCTCGGCGTGCGCCGCCGATTGTGAACATGAAGTCGTCGGAG  1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  TGTCACGGAGACCACGTTCAAAAGAAACAGGCTCGGCGTGCGCCGCCGATTGTGAACATGAAGTCGTCGGAG  1800

Qy   1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC  1860

Qy   1861  GGAAGCAGAGGTCAGGCAGCATCGGGAACGCCGGAAGCCAGGCCCGCTGCTTCGACGTCCG  1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  GGAAGCAGAGGTCAGGCAGCATCGGGAACGCCGGAAGCCAGGCCCGCTGCTTCGACGTCCG  1920

Qy   1921  CTTCATCCCCAAGCTGACGGGCTGCGCGCCGATTGTGAACATGTGAACATGAAGTCGTCGTGGGAGC  1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  CTTCATCCCCAAGCTGACGGGCTGCGCGCCGATTGTGAACATGTGAACATGAAGTCGTCGTGGGAGC  1980

Qy   1981  CAGAACGTTCCGCAGAGAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT  2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  CAGAACGTTCCGCAGAGAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT  2040

Qy   2041  CAGCGTGCTCAACTACGACAGCGGCCCCCGGCGGCCCTCGTGGGCGCCCTCTGTGCTGGG  2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  CAGCGTGCTCAACTACGACAGCGGCCCCCGGCGGCCCTCGTGGGCGCCCTCTGTGCTGGG  2100
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Right column:

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Db   2041  CAGCGTGCTCAACTACGACAGCGGGCGGCGGCCTCGTGGGCGCCCTCTGTGCTGGG  2100

Qy   2101  CCTGGACGATATCCACAGACGGGCGGCCTGGCGCCCACCTTCGTGCTGCGGTGTGCGGGACCCC  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  CCTGGACGATATCCACAGACGGGCGGCCTGGCGCCCACCTTCGTGCTGCGGTGTGCGGGACCCC  2160

Qy   2161  GCCGCCTGAGCTGGTACTTGTCAAGTGGATGGATGTGACGGGCGCGCTACGACACCATCCCCCA  2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GCCGCCTGAGCTGGTACTTGTCAAGTGGATGGATGTGACGGGCGCGCTACGACACCATCCCCCA  2220

Qy   2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG  2280

Qy   2281  TCGGTATGCCGTGGTCCAGAAGGCCGCGCACGTGCCCAAGGCCTTCAAGAGACCA  2340
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Db   2281  TCGGTATGCCGTGGTCCAGAAGGCCGCGCACGTGCCCAAGGCCTTCAAGAGACCA  2340

Qy   2341  CGTCTCTACCTTGACAGACCTCCAGCCGTCGCGCCGCGTACACATGGACAGTTCGTGGCTCACCGAGGA  2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  CGTCTCTACCTTGACAGACCTCCAGCCGTCGCGCCGCGTACACATGGACAGTTCGTGGCTCACCGAGGA  2400

Qy   2401  GACCAGCCCGCTGAGGGATGCCGTCGTCGTGTCATCGAGCAGAGCTCCCTGAATGAGGCCAG  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  GACCAGCCCGCTGAGGGATGCCGTCGTCGTGTCATCGAGCAGAGCTCCCTGAATGAGGCCAG  2460

Qy   2461  CAGTGGCCTCTTCGACGTCTTCTTGCACGTCTTCATGTGCCACCGTTCATGTGCCATCAGGGG  2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  CAGTGGCCTCTTCGACGTCTTCTTGCACGTCTTCATGTGCCACCGTTCATGTGCCATCAGGGG  2520

Qy   2521  CAAGTCTACGTCCAGTGCCAGGGGATCCCCGCGGTCATCCTCTCCACGCTGCTCTG  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  CAAGTCTACGTCCAGTGCCAGGGGATCCCCGCGGTCCAGGGGCTCCACGCTGCTCTG  2580

Qy   2581  CAGCCTGTCTACGGCGGCCTTCGTTCGGGATTCGGCGGCGTGTTCGGCGGACGGGCT  2640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  CAGCCTGTCTACGGCGGCCTTCGTTCGGGATTCGGCGGCGTGTTCGGCGGACGGGCT  2640

Qy   2641  GCTCCTGCGTTTGGTGATGATTTCTTGTTGGTGGACACCTCACCTCACCTCACCGCGAAAAC  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  GCTCCTGCGTTTGGTGATGATTTCTTGTTGGTGGACACCTCACCTCACCTCACCGCGAAAAC  2700

Qy   2701  CTTCCCTCAGGACCCTGGTCCCGAGGTGTCCCGAGTATGGCGCGTGGTTGTAATTGCGGAA  2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  CTTCCCTCAGGACCCTGGTCCCGAGGTGTCCCGAGTATGGCGCGTGGTTGTAATTGCGGAA  2760

Qy   2761  GACAGTGTGAACTGTCCCTGTGAGAAGACGAGGCCCTGGGTGGCGGACGGGCT  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  GACAGTGTGAACTGTCCCTGTGAGAAGACGAGGCCCTGGGTGGCGGACGGGCT  2820

Qy   2821  GCCGGCCCACGGCCTATTCCCCGTGCTGCTGGATACCCGGACCCTGGAGGT  2880
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  GCCGGCCCACGGCCTATTCCCCGTGCTGCTGGATACCCGGACCCTGGAGGT  2880

Qy   2881  GCGAGAGGGACTACTCCAGCTATGCGCCGACCTCCATCAGAGCCAGTCTCAACCG  2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  GCGAGAGGGACTACTCCAGCTATGCGCCGACCTCCATCAGAGCCAGTCTCAACCG  2940

Qy   2941  CGGCTTCAAGGCTGTCTTGGGAGGAAACATGCGTCGCAAACTCTTTGGGGTCTTGAAGTG  3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  CGGCTTCAAGGCTGTCTTGGGAGGAAACATGCGTCGCAAACTCTTTGGGGTCTTGAAGTG  3000

Qy   3001  TCACAGCCGTGTTTCTGGATTTCGGAGTTGCAGGTGAACATGCTGCACCAACATCTA  3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  TCACAGCCGTGTTTCTGGATTTCGGAGTTGCAGGTGAACATGCTGCACCAACATCTA  3060

Qy   3061  CAAGATCCTCCTGCTGCTACAGGTTCACGCATGTGTGCTGCAGCAGTCAGCTCCCATTTCA  3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  CAAGATCCTCCTGCTGCTACAGGTTCACGCATGTGTGCTGCAGCAGTCAGCTCCCATTTCA  3120

Qy   3121  TCAGCAAGTTTGGAAGAACCCCACCATTTTTCCTGCGCGTCATCTCTGACACGGGCCTCCCCT  3180
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;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 1
;   LENGTH: 4015
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-31635-1

Query Match              100.0%;  Score 4015;  DB 1;  Length 4015;
Best Local Similarity    100.0%;  Pred. No. 0;
Matches 4015;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 GCAGCGCTGCGTCCTGCTGCGCACGTGGAAGCCCTGGCCCGCCACCCCGCGGATGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAGCGCTGCGTCCTGCTGCGCACGTGGAAGCCCTGGCCCGCCACCCCGCGGATGCC 60

Qy     61 GCGCGCTCCCGCTGCCGAGCCGTGCGTCCCTGCTGCGCGAGCCGTGCGCGAGGTGCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGCGCTCCCGCTGCCGAGCCGTGCGTCCCTGCTGCGCGAGCCGTGCGCGAGGTGCT 120

Qy    121 GCCGCTGGCCACGTTCGTTGCGGCCCCAGGCCGCTGGCCGCTGGTGCAGCGCGGG 180
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Qy    181 GGACCCGGGCGCTTTCCGCGCGCGCCCCCGCCCCGCCCCGCCCCGCCCCGGGACGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGACCCGGGCGCTTTCCGCGCGCGCCCCCGCCCCGCCCCGCCCCGCCCCGGGACGC 240

Qy    241 ACGGCCCGCGCCCGCGCCCCTCCTTCGCCCAGGTGTCCTGCTGAAGGAGCTGGTGGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACGGCCCGCGCCCGCGCCCCTCCTTCGCCCAGGTGTCCTGCTGAAGGAGCTGGTGGC 300

Qy    301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGGCGAAGAACGTGCTGGCCTTCGCCTTCGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGGCGAAGAACGTGCTGGCCTTCGCCTTCGC 360

Qy    361 GCTCTGGACGGGGCCCCCGGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCCAGCTA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTCTGGACGGGGCCCCCGGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCCAGCTA 420

Qy    421 CCTGCCCAACACGTGACCGACGTGCTGTGGTTCACCTGCGGTGTGCTGCGGGGCTGCTGCG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCTGCCCAACACGTGACCGACGTGCTGTGGTTCACCTGCGGTGTGCTGCGGGGCTGCTGCG 480

Qy    481 CCGCGTGGGCGACGACGTGCTGTGGTTCACCTGCGGTTACCAGTGTCGGCGGCTGCCAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCGCGTGGGCGACGACGTGCTGTGGTTCACCTGCGGTTACCAGTGTCGGCGGCTGCCAC 540

Qy    541 GGCTCCCAGCTGGGCCCGTAGGTGGCCCACACGTCTGGGGTCTCACCTGCGGTGATGCGAACGGGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCTCCCAGCTGGGCCCGTAGGTGGCCCACACGTCTGGGGTCTCACCTGCGGTGATGCGAACGGGC 600

Qy    601 TCAGGCCCGGCCCCGCCACACGTCTGGGATGGACCCCACACGTGGATGCGAACGGGC 660
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Db    601 TCAGGCCCGGCCCCGCCACACGTCTGGGATGGACCCCACACGTGGATGCGAACGGGC 660

Qy    661 CTGAACCATAGCGTCAGGGAGGCCCGGGGTCCCCGGGGTCCCAGCCCCGGGTGCGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGAACCATAGCGTCAGGGAGGCCCGGGGTCCCCGGGGTCCCAGCCCCGGGTGCGAG 720

Qy    721 GAGGCGCGGGGCAGTGCCAGCCGGAAGTCTGCCGTTGCCGGGGCTGGGCC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GAGGCGCGGGGCAGTGCCAGCCGGAAGTCTGCCGTTGCCGGGGCTGGGCC 780

Qy    781 TGCCCCTGAGCCGGAGCGGACGCGCCCGTTGGGCCAGGGTCCTGGGCCACCCCGGGCAGGAC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TGCCCCTGAGCCGGAGCGGACGCGCCCGTTGGGCCAGGGTCCTGGGCCACCCCGGGCAGGAC 840

Qy    841 GCGTGGACCGAGTGACGTGGTTTCTGTGGTGTCACCTGCCGAAGAAGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCGTGGACCGAGTGACGTGGTTTCTGTGGTGTCACCTGCCGAAGAAGC 900

Qy    901 CACCTCTTTGGAGGTGGCTCTCTGGCACGCCCACTCCACCCATCCCTGGCCCGCCA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3121 TCAGCAAGTTTGGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCCT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCAAGGGCGCCGC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCAAGGGCGCCGC 3240

Qy   3241 CGGCCCTCTGCCCTCCGAGCCGTGCAGTGGCTGGCGTGCCACCAAGCATTCCTGCTCAAGCT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CGGCCCTCTGCCCTCCGAGCCGTGCAGTGGCTGGCGTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy   3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGTCACTCAGGACAGCAGCCAGACGCA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGTCACTCAGGACAGCAGCCAGACGCA 3360

Qy   3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACGCTCCTGGAGGCCCGAGGCCCAACCCGGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACGCTCCTGGAGGCCCGAGGCCCAACCCGGC 3420

Qy   3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGCCACCCGCCACCAGCCAGGCCGA 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGCCACCCGCCACCAGCCAGGCCGA 3480

Qy   3481 GAGCAGACACCAGCAGCCCGTGTCACGCCGGGCTCTACGTCCCAGGAGGGAGGGGGGCC 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GAGCAGACACCAGCAGCCCGTGTCACGCCGGGCTCTACGTCCCAGGAGGGAGGGGGGCC 3540

Qy   3541 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGGCTGGTTGGCCGAGGCCTG 3600
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Db   3541 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGGCTGGTTGGCCGAGGCCTG 3600

Qy   3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCGAGTGTCCAGCCAAGGGCT 3660
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Db   3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCGAGTGTCCAGCCAAGGGCT 3660

Qy   3661 GAGTGTCAGCACACCTGCCGTCTTCACTTCCCACAGGCTGCGCGGTCGGCTCCACCCCA 3720
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Db   3661 GAGTGTCAGCACACCTGCCGTCTTCACTTCCCACAGGCTGCGCGGTCGGCTCCACCCCA 3720

Qy   3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCCACTCCCACATAGGAATAGTCCATCC 3780
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Db   3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCCACTCCCACATAGGAATAGTCCATCC 3780

Qy   3781 CCAGATTCGCCATTGTTCACCCGGAGCCCTGGCCCTGCCTTTCACCCCCACCATCC 3840
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Qy   3841 AGGTGGAGACCCTGAGAAGGCTGGAGAATTGGAGTGACCAAAGGTGTG 3900
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Db   3841 AGGTGGAGACCCTGAGAAGGCTGGAGAATTGGAGTGACCAAAGGTGTG 3900

Qy   3901 CCCTGTACACAGGCGAGGAGGACCCTGCACCTGGTGGGGGTCCCTGGGTCAAATTGGGGG 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CCCTGTACACAGGCGAGGAGGACCCTGCACCTGGTGGGGGTCCCTGGGTCAAATTGGGGG 3960

Qy   3961 GAGGTGCTGTGGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA 4015
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Db   3961 GAGGTGCTGTGGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA 4015
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Db    901 CACCTCTTTGGAGGGTGCGCTCTCTGCACGCGCCACTCCCACCCATCCGTGGCCGCCA  960
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Qy    961 GCACCACGCGGGCGCCCCATCCAACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GCACCACGCGGGCGCCCCATCCAACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 1020

Qy   1021 CCCGGTGTACGGCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080
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Db   1021 CCCGGTGTACGGCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080

Qy   1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGGCCCAGCCTGACTGGCTGCGCTCGGAGGCTCGTGGA 1140
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Db   1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGGCCCAGCCTGACTGGCTGCGCTCGGAGGCTCGTGGA 1140

Qy   1141 GACCATCTTTCGGGTTCCAGGCCCTGAATGCCAGGGACTCCCCGCAGGTTGCCCCCCT 1200
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Qy   1201 GCCCCAGCGCTACTGGCAAATGCGGCCCGTGTTTCTGGAGCTGCTTGGGAACCACCACGCGCA 1260
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Db   1201 GCCCCAGCGCTACTGGCAAATGCGGCCCGTGTTTCTGGAGCTGCTTGGGAACCACCACGCGCA 1260

Qy   1261 GTGCCCCTACGGGGTGCTCTTCAAGACGCACTGCCCGCTGGTGCGGTGCGGTCACCCTGCAGGA 1320
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Db   1261 GTGCCCCTACGGGGTGCTCTTCAAGACGCACTGCCCGCTGGTGCGGTGCGGTCACCCTGCAGC 1320

Qy   1321 AGCCGGTGTCTGTGCCCGGGAGAAGCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGA 1380
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Qy   1381 CACAGAACCCCCGTGGCTGCGCTGCTCCGCCAGCACAGCAGCCCCTGCCAGTGTA 1440
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Db   1381 CACAGAACCCCCGTGGCTGCGCTGCTCCGCCAGCACCACAGCAGCCCCTGCCAGTGTA 1440

Qy   1441 CGGCTTCGTGCGGGGCCTGCCGGCTGTGCCGGCTGGTGCTGCCGCTGCTGGGGGCTCCAGGCA 1500
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Qy   1501 CAACGAACGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
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Db   1501 CAACGAACGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

Qy   1561 GCTCTCGCTGCTCAGGAGGCTGACGTGGAAGATGAGCGTGCGGCTGCCGGCTGCGTCGAGCG 1620
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Db   1561 GCTCTCGCTGCTCAGGAGGCTGACGTGGAAGATGAGCGTGCGGCTGCCGGCTGCGTCGAGCG 1620

Qy   1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680
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Db   1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680

Qy   1681 CAAGTTCCTGCACTGGCTGCGTACGTCGTCAGCTGCTCAGCTCTTTCTTTA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CAAGTTCCTGCACTGGCTGCGTACGTCGTCAGCTGCTCAGCTCTTTTCTTTA 1740

Qy   1741 TGTCACGGAGACCACGTTGGCTGTGTTCAAAAGAACAGGCTCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800
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Db   1741 TGTCACGGAGACCACGTTGGCTGTGTTCAAAAGAACAGGCTCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800

Qy   1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCGTGTC 1860
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Db   1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCGTGTC 1860

Qy   1861 GGAAGCAGAGGTCAGGCAGCATCGGGGAAGCCAGGCCAGGCCCGCCGGTCGACGACTCCG 1920
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Db   1861 GGAAGCAGAGGTCAGGCAGCATCGGGGAAGCCAGGCCAGGCCCGCCGGTCGACGACTCCG 1920

Qy   1921 CTTCATCCCCAAGCCTGTCACGCGGCTGCGGCCCGATTGTGAACATGGTACGTCGTGGGGAGC 1980
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Db   1921 CTTCATCCCCAAGCCTGTCACGCGGCTGCGGCCCGATTGTGAACATGGTACGTCGTGGGGAGC 1980

Qy   1981 CAGAACGTTCCGCAGAGAAAGAGGAGAGAGGGGCCGAGCCGTGCTCCACCTTCACCGAGGGTGAAGGCACTGTT 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAGAACGTTCCGCAGAGAAAGAGGAGAGAGGGGCCGAGCCGTGCTCCACCTTCACCGAGGGTGAAGGCACTGTT 2040
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Db   2041 CAGCGTGCTCAACTACGACGAGGCGGGGGCGGGGCCCCGGCCTCCTGGGCGCCTCGTGCTGGG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2041 CAGCGTGCTCAACTACGACGAGGCGGGGGCGGGGGCCCGGCCTCCTGGCGCCTCGTGCTGGG 2100

Qy   2101 CCTGGACGATATCCACAGGCCTGCTTGTGCTGCTGCCGACACCTTCGTGCTGCGGGCCCGACACCCCCA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTGGACGATATCCACAGGCCTGCTTGTGCTGCTGCCGACACCTTCGTGCTGCGGGCCCGACACCCCCA 2160

Qy   2161 GCGCCTGAGCTGTACTTTGTCAAGGTGGATGATGTGACGGGCGCGTACGGCGACCACCATCCCCCA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCCCCTGAGCTGTACTTTGTCAAGGTGGATGATGTGACGGGCGCGTACGGCGACCACCATCCCCCA 2220

Qy   2221 GGACAGGCTCACGGAGGTCATCGCCAGCAGTCATCATCAAACCCAGAAGGCCTTCAAGAGCCA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGACAGGCTCACGGAGGTCATCGCCAGCAGTCATCATCAAACCCAGAAGGCCTTCAAGAGCCA 2280

Qy   2281 TCGGTATGCCGTGGTCAGAGGCCGCCCCATGGGCAAGGGCGACGTCGCGCAAGTTCGTGGCTCACCTGCAGGA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TCGGTATGCCGTGGTCAGAGGCCGCCCCATGGGCAAGGGCGACGTCGCGCAAGTTCGTGGCTCACCTGCAGGA 2340

Qy   2341 CGTCTCTACCTTGACAGACCTCCAGCCGTCGTCGTCATCGAGCAGAGCTCCTGAATGAGGCCAG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CGTCTCTACCTTGACAGACCTCCAGCCGTCGTCGTCATCGAGCAGAGCTCCTGAATGAGGCCAG 2400

Qy   2401 GACCAGCCCGCTGAGGGATGCGTCGTCGTCATCGAGCAGCAGCTCCCGTGAATGAGGCCAG 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GACCAGCCCGCTGAGGGATGCGTCGTCGTCATCGAGCAGCAGCTCCCGTGAATGAGGCCAG 2460

Qy   2461 CAGTGGCCTTCTCGACGTCTTCTCATGTGCCACACGCGTGCGCATCAGGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CAGTGGCCTTCTCGACGTCTTCTCATGTGCCACACGCGTGCGCATCAGGGG 2520

Qy   2521 CAAGTCCTACGTCCAGTGCCAGTCCGCAGGGATCCCCATCCTCTCCCACGCTGCTCTG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 CAAGTCCTACGTCCAGTGCCAGTCCGCAGGGATCCCCATCCTCTCCCACGCTGCTCTG 2580

Qy   2581 CAGCCTGTCGTGCTACAGGCGACATGGAGAACAAAGCTCGTTGGTGACACCCACGGGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 CAGCCGTGTCGTGCTACAGGCGACATGGAGAACAAAGCTGTTTGGTGACACCCACGGGCT 2640

Qy   2641 GCTCTGCGTTGGTGGATGATTCTTGTTGGTGACACCCACCGCGGGCGGAAAAC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCTCTGCGTTGGTTTGTGGATGATTCTTGTTGGTGACACCCACCTCACCGCGGCGGAAAAC 2700

Qy   2701 CTTCCTCAGGACCCTGGTCTCCGAGTATGGCTGCGGGTGAACTTGCGGAA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTTCCTCAGGACCCTGGTCTCCGAGTATGGCTGCGGGTGAACTTGCGGAA 2760

Qy   2761 GACAGTGGTGAACTTCCCTGTAGAAGAGGAGGCCCTGGGTGGCACGGCCTTTGTTGTTCAGAT 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GACAGTGGTGAACTTCCCTGTAGAAGAGGAGGCCCTGGGTGGCACGGCCTTTGTTGTTCAGAT 2820

Qy   2821 GCCGGCCACGCCGCTATTCCCGTGTCCCGTGCTGCTGGATACCGGACCCCTGGAGGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GCCGGCCCACGCCGCTATTCCCGTGTCCCGTGCTGCTGGATACCGGACCCCTGGAGGT 2880

Qy   2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940

Qy   2941 CGGCTTCAAGGTGGAGGAACATGGGGTGCAAACTCTTGGCGGCTTGGCTCGGCGGTGAAGTG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CGGCTTCAAGGTGGAGGAACATGCGGTGCAAACTCTTTGGGCGGCTTGGCTCGGCGGTGAAGTG 3000

Qy   3001 TCACAGCCTGTTTCTGGATTTGAACATGTGAACAGGCTCCAGGTGAACACGCGTGTCGACCAACATCTA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TCACAGCCTGTTTCTGGATTTGAACATGTGAACAGGCTCCAGGTGAACACGCGTGTCGACCAACATCTA 3060

Qy   3061 CAAGATCCTCCTGCTCAGGCGTACAGGTTTCACGCAGTTCACGCATGTGTCGCAGCTCCCATTTCA 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CAAGATCCTCCTGCTCAGGCGTACAGGTTTCACGCAGTTCACGCATGTGTCGCAGCTCCCATTTCA 3120
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;  SEQ ID NO 19
;;  LENGTH: 4015
;  TYPE: DNA
;  ORGANISM: Homo sapiens
PCT-US02-33146-19

Query Match             100.0%;  Score 4015;  DB 1;  Length 4015;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 4015;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1  GCAGCGCTGCGTCCTGCTGCGCACGTGGAAGCCCTGGCCCGGCCACCCCGCGATGCC   60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GCAGCGCTGCGTCCTGCTGCGCACGTGGAAGCCCTGGCCCGGCCACCCCGCGATGCC   60

Qy     61  GCGCGCCTCCCGCGTCGCCGAGCGCTGCGCGGCCGCGCCCTGGGCGTGCCAGCCGGTGCT  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GCGCGCCTCCCGCGTCGCCGAGCGCTGCGCGGCCGCGCCCTGGGCGTGCCAGCCGGTGCT  120

Qy    121  GCCGCTGGCCACGTTCGTGCGCGCCTGGGCGCCCACCAGCCAGGTGCAGCGCGCG  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCCGCTGGCCACGTTCGTGCGCGCCTGGGCGCCCACCAGCCAGGTGCAGCGCGCG  180

Qy    181  GGACCCGGCGGCTTTCCGCGCGCTGGTGCTGGTGCTGCCTGGGACGC  240
           ||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GGACCCGGCGGCTTTCCGCGCGCTGGTGCTGGTGCTGCCTGGGACGC  240

Qy    241  ACGGCGCGCCCCCGCGCCCCTCCTTCGCGGAGCGCGGCGGCGCCGAAGGAGCTGGTGGC  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ACGGCGCGCCCCCGCGCCCCTCCTTCGCGGAGCGCGGCGGCGCCGAAGGAGCTGGTGGC  300

Qy    301  CCGAGTGCTGCAGAGGCTGTGCGAGCGCTGTTCGGCCTTCGCGC  360
           |||||||||||||||||||||||||||||||||||||||||||
Db    301  CCGAGTGCTGCAGAGGCTGTGCGAGCGCTGTTCGGCCTTCGCGC  360

Qy    361  GCTGGTGGACGGGCCCGGGGGCCCCCGAGGCCTTCACCACCAGGTGCCAGCTA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GCTGGTGGACGGGCCCGGGGGCCCCCGAGGCCTTCACCACCAGGTGCCAGCTA  420

Qy    421  CCTGCCCAACGGTGACCGACGCGCTGGTTCACCTGCTGGGCGGCGTGCTGCG  480
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CCTGCCCAACGGTGACCGACGCGCTGGTTCACCTGCTGGGCGGCGTGCTGCG  480

Qy    481  CCGGCGTGGGGACGGGCCCCGCGCTGCTGGGCCGCGCCGCTGTACCAGCTC  540
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CCGGCGTGGGGACGGGCCCCGCGCTGCTGGGCCGCGCCGCTGTACCAGCTC  540

Qy    541  GGCTCCCAGCTGCCGCCTACCAGGTGTGCGGCCGCGCTGCCCAC  600
           |||||||||||||||||||||||||||||||||||||||||||
Db    541  GGCTCCCAGCTGCCGCCTACCAGGTGTGCGGCCGCGCTGCCCAC  600

Qy    601  TCAGGCCCGCCGCCCCGCCACGCGTAGTGGACCCCGAAGGGC  660
           ||||||||||||||||||||||||||||||||||||||||||
Db    601  TCAGGCCCGCCGCCCCGCCACGCGTAGTGGACCCCGAAGGGC  660

Qy    661  CTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCGCCAGCCCCGGGTGCGAG  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCGCCAGCCCCGGGTGCGAG  720

Qy    721  GAGGCGGGGGCAGTGCCAGCGAAGTCTGCCGGTGCCGGTGCCGGTGGCGC  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GAGGCGGGGGCAGTGCCAGCGAAGTCTGCCGGTGCCGGTGCCGGTGGCGC  780

Qy    781  TGCCCCTGAGCCGGACGGACGGGTCCTGGGCGCCCACCCGGCCCAGGAC  840
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TGCCCCTGAGCCGGACGGACGGGTCCTGGGCGCCCACCCGGCCCAGGAC  840

Qy    841  GCGTGGACCGAGTGACCGTGGTTTCGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GCGTGGACCGAGTGACCGTGGTTTCGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC  900

Qy    901  CACCTTTTGAGGTGCGCGTCTCTGGCACGCCGCCACTCCCACCCATCCGTGGGCCGCCA  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CACCTTTTGAGGTGCGCGTCTCTGGCACGCCGCCACTCCCACCCATCCGTGGGCCGCCA  960
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Qy   3121  TCAGCAAGTTTGGAAGAACCCCACATTTTCCTGCGCGGTCATCTCTGACACGGCCTCCCT  3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  TCAGCAAGTTTGGAAGAACCCCACATTTTCCTGCGCGGTCATCTCTGACACGGCCTCCCT  3180

Qy   3181  CTGCTACTCCATCCTGAAAGCCAGAACGCAGGATGTCGCTGGGGCGCCAAGGGCGCCGC  3240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  CTGCTACTCCATCCTGAAAGCCAGAACGCAGGATGTCGCTGGGGCGCCAAGGGCGCCGC  3240

Qy   3241  CGGCCCCTGCCCTCCGAGGCCGTGCAGTGGCGTGTGCCACCAAGCATTCCTGCTCAAGCT  3300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241  CGGCCCCTGCCCTCCGAGGCCGTGCAGTGGCGTGTGCCACCAAGCATTCCTGCTCAAGCT  3300

Qy   3301  GACTCGCACCGTGTCACCTACGTGCCACTCCTCGGGGTCACTCAGGACAGCCCAGACGCA  3360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301  GACTCGCACCGTGTCACCTACGTGCCACTCCTCGGGGTCACTCAGGACAGCCCAGACGCA  3360

Qy   3361  GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACCTGCCTGGAGGCCTGACTCAGCGCCGGC  3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361  GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACCTGCCTGGAGGCCTGACTCAGCGCCGGC  3420

Qy   3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCCACAGCCAGGCCGA  3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCCACAGCCAGGCCGA  3480

Qy   3481  GAGCAGACACCACCAGCAGCCCGTCTCACGTCCCAGGAGGGGGAGGGGCGGCC  3540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  GAGCAGACACCACCAGCAGCCCGTCTCACGTCCCAGGAGGGGGAGGGGCGGCC  3540

Qy   3541  CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGTTGGCCGAGGCCTG  3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGTTGGCCGAGGCCTG  3600

Qy   3601  CATGTCCGGCTGAGGGCTGAGTGTCCGGCTGAGGCCTGAGTGTCCAGCCAAGGGCT  3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  CATGTCCGGCTGAGGGCTGAGTGTCCGGCTGAGGCCTGAGTGTCCAGCCAAGGGCT  3660

Qy   3661  GAGTGTCCACCAGCCACCGTGTCTTCACTTCACTCGGCGCTGGCGCTGCTGGGCTCCACCCCA  3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  GAGTGTCCACCAGCCACCGTGTCTTCACTTCACTCGGCGCTGGCGCTGCTGGGCTCCACCCCA  3720

Qy   3721  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCCACTCCCACCATAGGAATAGTCCATCC  3780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCCACTCCCACCATAGGAATAGTCCATCC  3780

Qy   3781  CCAGATTCGCCATTGTTCACCCCTGCCCTGCGCCCCCTCGCCCCTTGCCTTCCACCCCCACCATCC  3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781  CCAGATTCGCCATTGTTCACCCCTGCCCTGCGCCCCCTCGCCCCTTGCCTTCCACCCCCACCATCC  3840

Qy   3841  AGTGGGAGCCCTGAGAAGGACCCTGGGGAGTGGAGTTGGACCAAAGGTGTG  3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841  AGTGGGAGCCCTGAGAAGGACCCTGGGGAGTGGAGTTGGACCAAAGGTGTG  3900

Qy   3901  CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG  3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901  CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG  3960

Qy   3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTCAGAAAAAAAA  4015
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTCAGAAAAAAAA  4015
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RESULT 4
PCT-US02-33146-19
; Sequence 19, Application PC/TUS0233146
; GENERAL INFORMATION:
; APPLICANT: University of Rochester Medical Center
; APPLICANT: Rowley, Peter
; TITLE OF INVENTION: Telomerase Interference
; FILE REFERENCE: FP-71506-2/RFT/SRN
; CURRENT APPLICATION NUMBER: PCT/US02/33146
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1

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Qy   961  GCACCACGGCGGCCCCATCCACACTCGCGGCCACCACGTCCCTGGACACGCCTTGTCC  1020
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   961  GCACCACGGCGGCCCCATCCACATCGCGGCCACCACGTCCCTGGACACGCCTTGTCC  1020

Qy  1021  CCGGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  CCGGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1080

Qy  1081  GCCCTCCTTCTACTCCAGCTCTCTGAGGCCCAGCCTGACTGGCTGCGCTCGGAGGCTCGTGGA  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  GCCCTCCTTCTACTCCAGCTCTCTGAGGCCCAGCCTGACTGGCTGCGCTCGGAGGCTCGTGGA  1140

Qy  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGGCCTTGCCCCGCCT  1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGGCCTTGCCCCGCCT  1200

Qy  1201  GCCCCAGCGCTACTGGCAAATGCGGGCCCTGTTCTGGAGCTGCTTGGGAACCACGCGCA  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  GCCCCAGCGCTACTGGCAAATGCGGGCCCTGTTCTGGAGCTGCTTGGGAACCACGCGCA  1260

Qy  1261  GTGCCCCTACGGGTGCTCTCAAGACGCACTGCCCGCTGCGGTGCGGTCACCCCAGC  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  GTGCCCCTACGGGTGCTCTCAAGACGCACTGCCCGCTGCGGTGCGGTCACCCCAGC  1320

Qy  1321  AGCCGGTGTCTGTGCCCCGGGAGAAGCCCCAGGGGTCTGTGGCGCCCCCGAGGAGGAGGA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  AGCCGGTGTCTGTGCCCCGGGAGAAGCCCCAGGGGTCTGTGGCGCCCCCGAGGAGGAGGA  1380

Qy  1381  CACAGACCCCCGTCGGTCAGCTGCTGCGCCAGCACAGCAGCCCCTGGCAGGTGTA  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CACAGACCCCCGTCGGTCAGCTGCTGCGCCAGCACAGCAGCCCCTGGCAGGTGTA  1440

Qy  1441  CGGCTTCGTGCGGGGCTGCCTGCCGGCGTGTGCCCCAGGCCTCTGGGGCTCTCCAGGCA  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  CGGCTTCGTGCGGGGCTGCCTGCCGGCGTGTGCCCCAGGCCTCTGGGGCTCTCCAGGCA  1500

Qy  1501  CAACGAACGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  CAACGAACGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560

Qy  1561  GCTCCTGCCTGCAGGAGCTGACGTGGAAGATGAGCCGTCGGGGACTGCGCCTTGGCGCCAG  1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  GCTCCTGCCTGCAGGAGCTGACGTGGAAGATGAGCCGTCGGGGACTGCGCCTTGGCGCCAG  1620

Qy  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC  1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC  1680

Qy  1681  CAAGTTCCTGCACTGCAGCTGATGAGTGTGTACGTCGTCGAGCTCAGGTCTCTTCTTTA  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CAAGTTCCTGCACTGCAGCTGATGAGTGTGTACGTCGTCGAGCTCAGGTCTCTTCTTTA  1740

Qy  1741  TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG  1800

Qy  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTC  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC  1860

Qy  1861  GGAAGCAGAGGTCAGGCGAGCATCGGGAAGCCAGGAAGCCCGCCCTGGCGTCGACACTCCG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  GGAAGCAGAGGTCAGGCGAGCATCGGGAAGCCAGGAAGCCCGCCCTGGCGTCGACACTCCG  1920

Qy  1921  CTTCATCCCGGAGCGGCTGCGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CTTCATCCCGGAGCGGCTGCGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980

Qy  1981  CAGAACGTTCCCGCAGAGAAAAGAGGGCCGAGCCTGAAGGGTGAAGGCACTGTT  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAGAACGTTCCCGCAGAGAAAAGAGGGCCGAGCCTGAAGGGTGAAGGCACTGTT  2040
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Qy  2041  CAGCGTGCTCAACTACGAGCGGCGGCGGCGGGCCCCTCCTGGCGGCCTCTGTGCTGTGGG  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CAGCGTGCTCAACTACGAGCGGCGGCGGCGGGCCCCTCCTGGCGGCCTGCTGTGCTGTGGG  2100

Qy  2101  CCTGGACGATATCCACAGGCCTTGGCGCGTGCTCGTGCTGCGCGTGTGGGGCCCAGGACCC  2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTGGACGATATCCACAGGCCTTGGCGCGTGCTCGTGCTGCGCGTGTGGGGCCCAGGACCC  2160

Qy  2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGGCGGCGGCCGTACGCACCATCCCCCA  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGGCGGCGGCCGTACGCACCATCCCCCA  2220

Qy  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG  2280

Qy  2281  TCGGTATGCGCTGGTCGTGTTCGTGGAGCTGCTTGGAGCCCGCACGTCCGCAAGGCCTTCAAGAGCCA  2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCGGTATGCCGTGGTCGTGTTCGTGGAGCTGCTTGGAGCACGTCCGCAAGGCCTTCAAGAGCCA  2340

Qy  2341  CGTCTCTACCTTGACAGACCTCCAGCGTCGTACATCGCAGAGTTCGTGGCTCACCTGCAGGA  2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGTCTCTACCTTGACAGACCTCCAGCGTCGTACATCGCAGAGTTCGTGGCTCACCTGCAGGA  2400

Qy  2401  GACCAGCCCGCTGAGGGATTGCCGTCGTCATCGAGCAGCAGAGCTCTCCCGTGAATGAGGCCAG  2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GACCAGCCCGCTGAGGGATTGCCGTCGTCATCGAGCAGCAGAGCTCTCCCGTGAATGAGGCCAG  2460

Qy  2461  CAGTGGCCTCTTCGCGTCTTCATGTGCGCATCAGGGG  2520
          |||||||||||||||||||||||||||||||||||||
Db  2461  CAGTGGCCTCTTCGCGTCTTCATGTGCGCATCAGGGG  2520

Qy  2521  CAAGTCCTACGTCCAGTGCGCAGGGATCCCGCAGGGCTCATCCTCTCCACGCGTCTCTG  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CAAGTCCTACGTCCAGTGCGCAGGGATCCCGCAGGGCTCATCCTCTCCACGCGTCTCTG  2580

Qy  2581  CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT  2640

Qy  2641  GCTCCTGCGTTGGTGGATGATTCTTGTGGTGACACCTCACCTCACCCCGGGG  2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCTCCTGCGTTTGGTGGATGATTCTTGTGGTGACACCTCACCTCACCCCGGGG  2700

Qy  2701  CTTCCTCAGGACCCTGGTCCGAGTGTCCCGAGGTATGGCGTGGTGAACTTGCGGAA  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CTTCCTCAGGACCCTGGTCCGAGTGTCCCGAGGTATGGCGTGGTGAACTTGCGGAA  2760

Qy  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCGCAGCGGCTTTTGTTGTTCAGAT  2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCGCAGCGGCTTTTGTTGTTCAGAT  2820

Qy  2821  GCCGGCCACGCCACCGTCTATTCCCCTGCTGCTGGAACTGGAGGT  2880
          |||||||||||||||||||||||||||||||||||||||||||||
Db  2821  GCCGGCCACGCCACCGTCTATTCCCCTGCTGCTGGAACCCGGAGGT  2880

Qy  2881  GCGAGCGGACTACTCCAGCTATGCCCGGACCTGCCATGAGCCCAGTCTCAACCTTCAACCG  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  GCAAGCGGACTACTCCAGCTATGCCCGGACCTGCCATCAGAGCCCAGTCTCAACCTTCAACCG  2940

Qy  2941  CGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGGGCGTCTTTGTTGTGAAGTG  3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGGGCGTCTTTGTTGTGAAGTG  3000

Qy  3001  TCACAGCCTGTTTCTGCAGGCGTACGGTTCAGCTGTGCAACCAACATCTCA  3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  TCACAGCCTGTTTTCTGCAGGCGTACGGTTCAGCTGTGCAACCAACATCTCA  3060

Qy  3061  CAAGATCCTCCGTCTGCAGGCGTACAGGTTTCAGCTGTGCTGCAGTCCCCATTTCA  3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  CAAGATCCTCCGTCTGCAGGCGTACAGGTTTCAGCTGTGCTGCAGTCCCCATTTCA  3120

Qy  3121  TCAGCAAGTTTGGAAGAACCCCACCATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT  3180
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Db    3121  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            TCAGCAAGTTTGGAGAACCCCACCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT  3180

Qy    3181  CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCGCCAAGGGCGCCGC  3240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3181  CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCCGGGGCGCCAAGGGCGCCGC  3240

Qy    3241  CGGGCCCTCGCCCTCCGAGGCCGTGCAGTGGCGTGCCACCAAGCATTCCTGCTCAAGCT  3300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241  CGGGCCCTCGCCCTCCGAGGCCGTGCAGTGGCGTGCCACCAAGCATTCCTGCTCAAGCT  3300

Qy    3301  GACTCGACACCGTGCACCTAGCTGCCACTCCTCGGGTCACTCAGGACAGCCCAGACGCA  3360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301  GACTCGACACCGTGCACCTAGCTGCCACTCCTCGGGTCACTCAGGACAGCCCAGACGCA  3360

Qy    3361  GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGC  3420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361  GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGC  3420

Qy    3421  ACTCCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGACCCCAGGCCAGGCCA  3480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3421  ACTGCCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGACCCCAGGCCAGGCCA  3480

Qy    3481  GAGCAGACACCAGCAGCCCGTCTGCACGGCCCGGCTCTACGTCCCAGGAGGAGGGCGGCC  3540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3481  GAGCAGACACCAGCAGCCCGTCTGCACGGCCCGGCTCTACGTCCCAGGAGGAGGGCGGCC  3540

Qy    3541  CACACCCAGGCCCCGCCACCCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTGGCCGGAGGCCTG  3600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541  CACACCCAGGCCCCGCCACCCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTGGCCGGAGGCCTG  3600

Qy    3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT  3660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT  3660

Qy    3661  GAGTGTCCAGCACACCTGCCCGTCTCACTTCCCCACAGGCTGCGCGGTCGGCTCCACCCCA  3720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661  GAGTGTCCAGCACACCTGCCCGTCTTCACTTCACTTCCCCACAGGCTGCGCGGTCGGCTCCACCCCA  3720

Qy    3721  GGGCCAGCTTTTCCTCACCAGGAGACCCGGCTTCCAACTCCCCACCACATAGGAATAGTTCCATCC  3780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721  GGGCCAGCTTTTCCTCACCAGGAGACCCGGCTTCCAACTCCCCACCACATAGGAATAGTTCCATCC  3780

Qy    3781  CCAGATTCGCCATTGTTCACCCCTCGCCCTCCTTGCCTTCCACCCCCACCATCC  3840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781  CCAGATTCGCCATTGTTCACCCCTCGCCCTCCTTGCCTTCCACCCCCACCATCC  3840

Qy    3841  AGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTTGACCAAAGGTGTG  3900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841  AGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG  3900

Qy    3901  CCCTGTACACAGGCGAGGCGGAGACCCTGCACCTGATGGGGGTCCCTGTGGGTCAAATTGGGGG  3960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901  CCCTGTACACAGGCGAGGCGGAGACCCTGCACCTGATGGGGGTCCCTGTGGGTCAAATTGGGGG  3960

Qy    3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA  4015
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA  4015
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RESULT 5
PCT-US99-06898-1
; Sequence 1, Application PC/TUS9906898
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: PCT/US99/06898
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14

; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
PCT-US99-06898-1

Query Match   100.0%;   Score 4015;   DB 1;   Length 4015;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 4015;   Mismatches 0;   Conservative 0;   Indels 0;   Gaps 0;

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Qy      1  GCAGGCCTGGCTCCTGCTGCCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCC   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GCAGGCCTGGCTCCTGCTGCCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCC   60

Qy     61  GCGGGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GCGGGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  120

Qy    121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG  180

Qy    181  GGACCCGGCGGCTTTCCGCGCCCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GGACCCGGCGGCTTTCCGCGCCCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC  240

Qy    241  ACGGCCTGGCACGTTCGTGCGGCGCCCTCCTCCGCCAGTGTCTGCCTGCAGTGTCTGGCGGC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ACGGCCTGGCACGTTCGTGCGGCGCCCTCCTCCGCCAGTGTCTGCCTGCAGTGTCTGGCGGC  300

Qy    301  CCGAGTGCTGCAGAGGCGTGCGGAGAGCGGCGGCGCGGAAGAACGTGCTGGCTTCGC  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CCGAGTGCTGCAGAGGCGTGCGGAGAGCGGCGGCGCGGAAGAACGTGCTGGCTTCGC  360

Qy    361  GCTGCTGGACGGGGCCCCCGGGGCGCCCCCCGAGGGCCTTCACCACCAGCGTGCCAGCTA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GCTGCTGGACGGGGCCCCCGGGGCGCCCCCCGAGGGCCTTCACCACCAGCGTGCCAGCTA  420

Qy    421  CCTGCCCAACACGGTGACCGACGCGCTGCGGGGGAGCGGCGCTGCGCCTGCGCTGCTGCG  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CCTGCCCAACACGGTGACCGACGCGCTGCGGGGGAGCGGCGCTGCGCCTGCGCTGCTGCG  480

Qy    481  CCCGTGGCCGACGACGTTGCTGGTTCACGCTGCTGGCACGCTGCTGCCTGCTTCTTTGCTGCTGT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CCCGTGGCCGACGACGTTGCTGGTTCACGCTGCTGGCACGCTGCTGCCTGCTTCTTTGCTGCTGT  540

Qy    541  GGCTCCCAGCTGCCGCTACCAGGTGTGCGGGGCCGCCGCCTGGTGGGGCTGCGCCCAC  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GGCTCCCAGCTGCCGCTACCAGGTGTGCGGGGCCGCCGCCTGGTGGGGCTGCGCCCAC  600

Qy    601  TCAGGCCCGGCCCACGCCACAGCCGTCTGGGATGGAACGGGC  660
           ||||||||||||||||||||||||||||||||||||||||||
Db    601  TCAGGCCCGGCCCACGCCACAGCCGTCTGGGATGGAACGGGC  660

Qy    661  CTGGAACCATAGCTCAGGAGGACCGGGTCCCCTGGGCTCCTGGGATCAGGAGGTGCCGAG  720
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Db   661  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          CTGGAACCATAGCGTCAGGAGGCAGTGCCACCGGTCCCCTGGCGTTGCCCAGAGGCCCAGGCCCGGGTGGCGGAG  720

Qy   721  GAGGCGCCGGGGGCCAGTGCCAGCCGGGTGCTCCGGAGAGTCCAGACGGCACCGGGCCACCCGGGCAGGAC       780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  GAGGCGCCGGGGGCCAGTGCCAGCCGGGTGCTCCGGAGAGTCCAGACGGCACCGGGCCACCCGGGCAGGAC       780

Qy   781  TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCGTTGGTGTTCGTGTGTGCCGGCACGGGCAGGAC      840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCGTTGGTGTTCGTGTGTGCCGGCACGGGCAGGAC      840

Qy   841  GGCGTGGACCGAGTGACCGTGGTTCTCTGGTGTCACCTGCCAGACCGCGCCGAAGAAGC                     900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GGCGTGGACCGAGTGACCGTGGTTCTCTGGTGTCACCTGCCAGACCGCGCCGAAGAAGC                     900

Qy   901  CACCTCTTTGGAGGGTGCGCTCTCTGCACGCGCCACCGCGCCACCCACCTCCGTGGGCCGCCA                 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CACCTCTTTGGAGGGTGCGCTCTCTGCACGCGCCACCGCGCCACCCACCTCCGTGGGCCGCCA                 960

Qy   961  GCACCACGCGGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCCTTGTCC                   1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  GCACCACGCGGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCCTTGTCC                   1020

Qy  1021  CCCGGTGTACGGCCGAGACCAAGCACTTCCTACTCCTCAGGCCGACAAGGAGCAGCTGCG                    1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  CCCGGTGTACGGCCGAGACCAAGCACTTCCTACTCCTCAGGCCGACAAGGAGCAGCTGCG                    1080

Qy  1081  GCCCTCCTTCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCCGTCGGAGGCTCGTGGA                     1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  GCCCTCCTTCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCCGTCGGAGGCTCGTGGA                     1140

Qy  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTGCCCCCGCCAGGTTGCCCCGCCT                  1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTGCCCCCGCCAGGTTGCCCCGCCT                  1200

Qy  1201  GCCCCAGCGCTACTGGCGGGGTGTCTGTTCTGGAGCTGCTGGGGCGCACCACGCGCA                       1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  GCCCCAGCGCTACTGGCGGGGTGTCTGTTCTGGAGCTGCTGGGGCGCACCACGCGCA                       1260

Qy  1261  GTGCCCCTACGGGCGTGCTCCTCAAGACGCACTGCCCGGTGCGGCTGCGGTCACCCCAGC                    1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  GTGCCCCTACGGGCGTGCTCCTCAAGACGCACTGCCCGGTGCGGCTGCGGTCACCCCAGC                    1320

Qy  1321  AGCCGGTGTGTCGTGCCCCGGAGAAGCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGA                    1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  AGCCGGTGTGTCGTGCCCCGGAGAAGCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGA                    1380

Qy  1381  CACAGAGACCCCCGTCGCCGTGGTGCAGCTGCTCCGCAGCACAGCAGCCCTGCAGTGTA                     1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CACAGAGACCCCCGTCGCCGTGGTGCAGCTGCTCCGCAGCACAGCAGCCCTGCAGTGTA                     1440

Qy  1441  CGGCTTCGTGCGGCCTGCCCTGCGTGCCTGGGGCTCTGAGGAGATCCTGGGGCTCCAGGCA                   1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  CGGCTTCGTGCGGCCTGCCCTGCGTGCCTGGGGCTCTGAGGAGATCCTGGGGCTCCAGGCA                   1500

Qy  1501  CAACGAACGCGCGGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA                  1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  CAACGAACGCGCGGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA                  1560

Qy  1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGCCTGCTTGGCTGCTGCCAG                     1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGCCTGCTTGGCTGCTGCCAG                     1620

Qy  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGCACCGTCTGCGTGGAGGAGATCCTGGC                     1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGCACCGTCTGCGTGGAGGAGATCCTGGC                     1680

Qy  1681  CAAGTTCCTGCACTGGCTGTCTACGGCTGTGTACCGTCGTCGAGCTGCTCGTCTCTTTTTA                   1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CAAGTTCCTGCACTGGCTGTCTACGGCTGTGTACCGTCGTCGAGCTGCTCGTCTCTTTTTA                   1740

Qy  1741  TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG                      1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG                      1800

Qy  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCCAGCTGTC                      1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCCAGCTGTC                      1860

Qy  1861  GGAGCAGAGGTCAGGCAGCATGGGAGGCCCGCCCTGCTGGACGTCCAGACTCCG                          1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  GGAGCAGAGGTCAGGCAGCATGGGAGGCCCGCCCTGCTGGACGTCCAGACTCCG                          1920

Qy  1921  CTTCATCCCAAAGCCTTGACGGGCTGCGCCGCGATTGTGAACATGTGGGGAGC                           1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CTTCATCCCAAAGCCTTGACGGGCTGCGCCGCGATTGTGAACATGTGGGGAGC                           1980

Qy  1981  CAGAACGTTCCGCAGAGAAAAGAGGGCCCAGCGTGTCTCTCACCTCGAGGGTGAAGGCACTGTT                2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAGAACGTTCCGCAGAGAAAAGAGGGCCCAGCGTGTCTCTCACCTCGAGGGTGAAGGCACTGTT                2040

Qy  2041  CAGCGTGCTCAACTACGAGCGGGCGGGCCTGCTGCCACCTTCGTGCTGCGGGCCCAGGACCC                  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CAGCGTGCTCAACTACGAGCGGGCGGGCCTGCTGCCACCTTCGTGCTGCGGGCCCAGGACCC                  2100

Qy  2101  CCTGGACGATATCCACAGGGCCCTGCTCAGGCCGACAAGTGATGTGACGGGGCGGCGTACGACCACCATCCCCCCA    2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTGGACGATATCCACAGGGCCCTGCTCAGGCCGACAAGTGATGTGACGGGGCGGCGTACGACCACCATCCCCCCA    2160

Qy  2161  GCCCCCTGAGCTGTACTTTGTCAAGGTGATGTGACGTGGATGTGACGTGGCGGCGTACGACCACCATCCCCCCA     2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCCCCCTGAGCTGTACTTTGTCAAGGTGATGTGACGTGGATGTGACGTGGCGGCGTACGACCACCATCCCCCCA     2220

Qy  2221  GGACAGGGTCACGGAGGTCATCGCCAGGTCATCCCAGCAGCATCAAAACCCAGAACACTACTGCGTGCG           2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGACAGGGTCACGGAGGTCATCGCCAGGTCATCCCAGCAGCATCAAAACCCAGAACACTACTGCGTGCG           2280

Qy  2281  TCGGTATGCCGTGTGTCCGAGGGATGCCGTCGTCATCGAGCAGCACGTCCGAAGGCCTTCAAGGCCA            2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCGGTATGCCGTGTGTCCGAGGGATGCCGTCGTCATCGAGCAGCACGTCCGAAGGCCTTCAAGGCCA            2340

Qy  2341  CGTCTCTACTTGACAGACCTCCGTACATGGCGACAGTTCGTGGCTCCACCTGCAGGA                       2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGTCTCTACTTGACAGACCTCCGTACATGGCGACAGTTCGTGGCTCCACCTGCAGGA                       2400

Qy  2401  GACCAGCCCGCTGAGGGGATGCCGTCGTCATCGAGGCAGAGCTCCTCCCTGAATAGAGGCCAG                 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GACCAGCCCGCTGAGGGGATGCCGTCGTCATCGAGGCAGAGCTCCTCCCTGAATGAGGCCAG                 2460

Qy  2461  CAGTGGCCCTTCCTCTTCGACGTCTTCATGCTGCCGTCCACCACCGTGGTGTCATCAGGGG                   2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CAGTGGCCCTTCCTCTTCGACGTCTTCATGCTGCCGTCCACCACCGTGGTGTCATCAGGGG                   2520

Qy  2521  CAAGTCCTACGTCCAGTGCAGTCCCGGGATCCCCAGGGCTCCAGGGCTGCTCTG                          2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CAAGTCCTACGTCCAGTGCAGTCCCGGGATCCCCAGGGCTCCAGGGCTGCTCTG                          2580

Qy  2581  CAGCCTGTGCTACGGCGACATGGGAAGCAGCTGTTTCGGGGGGATTCGGGGGGACGGGGCT                   2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CAGCCTGTGCTACGGCGACATGGGAAGCAGCTGTTTCGGGGGGATTCGGGGGGACGGGGCT                   2640

Qy  2641  GCTCCTGCGTTGGTGGTGACATCTCTTGTTGGTGACACCTCACCTCACCACCGCGAAAAC                    2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCTCCTGCGTTGGTGGTGACATGATTCTTGTTGGTGACACCTCACCTCACCACCGCGAAAAC                  2700

Qy  2701  CTTCCTCAGGACCCTGGTCCTGAGCCCGTCGTGTGGTGTCCTGAGTATGCGGTGAACTTGCGGAA              2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CTTCCTCAGGACCCTGGTCCTGAGCCCGTCGTGTGGTGTCCTGAGTATGCGGTGAACTTGCGGAA              2760

Qy  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGAGCCCTGGGTGGCACGGCGTTTTGTTCAGAT               2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGAGCCCTGGGTGGCACGGCGTTTTGTTCAGAT               2820

Qy  2821  GCCGGCCCACCGACGCCTATTCCCCTGTGTGCGGCCTGCTGCTGCGGCGACCCCGGACCCTGGAGGT           2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  GCCGGCCCACCGACGCCTATTCCCCTGTGTGCGGCCTGCTGCTGCGGCGACCCCGGACCCTGGAGGT           2880
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Qy   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA 4015
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA 4015
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RESULT 6
PCT-US99-07097-1
; Sequence 1, Application PC/TUS9907097
; GENERAL INFORMATION:
;   APPLICANT: Morin, Gregg B.
;   APPLICANT: Geron Corporation
;   TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
;   FILE REFERENCE: 015389-003310PC
;   CURRENT APPLICATION NUMBER: PCT/US99/07097
;   CURRENT FILING DATE: 1999-03-31
;   EARLIER APPLICATION NUMBER: US 09/052,864
;   EARLIER FILING DATE: 1998-03-31
;   EARLIER APPLICATION NUMBER: US 09/128,354
;   EARLIER FILING DATE: 1998-08-03
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 4015
;   TYPE: DNA
;   ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (56)..(3454)
;   OTHER INFORMATION: human telomerase reverse transcriptase (hTRT) cDNA
PCT-US99-07097-1

Query Match   100.0%; Score 4015; DB 1; Length 4015;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCAGCGCTGCGTCCTGCTGCGCACGTGGAAGCCCTGGCCCGGCCACCCCGGCGATGCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAGCGCTGCGTCCTGCTGCGCACGTGGAAGCCCTGGCCCGGCCACCCCGGCGATGCC 60

Qy     61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120

Qy    121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG 180

Qy    181 GGACCCGGCGGCGTTTCCGGAGCGCGCCTGAGTGCGGCCCTGGACCGC 240
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGACCCGGCGGCGTTTCCGGAGCGCGCCTGAGTGCGGCCCTGGACGC 240

Qy    241 ACGGGCCGCGCCCCCGCGCCCCCGCCCCTCCTTCCGCGGCGGCGGCGGAAGAGCTGCTGGC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACGGGCCGCGCCCCCGCGCCCCCGCCCCTCCTTCCGCGGCGGCGGCGGAAGAGCTGGTGGC 300

Qy    301 CCGAGTGCTGCAGAGGCTGTGCGAGGCGCGGCGGCGGCGGGAAGAAGACGTGCTGGCCTCGC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGAGTGCTGCAGAGGCTGTGCGAGGCGCGGCGGCGGCGGGAAGAAGACGTGCTGGCCTTCGC 360

Qy    361 GCTGCTGGACGGGGCCCCGCCGGGGGGCCCCGAGGCCTTCACCACGCGTGCCAGCTA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTGCTGGACGGGGCCCCGCCGGGGGGCCCCGAGGCCTTCACCACGCGTGCCAGCTA 420

Qy    421 CCTGCCAACACGGTGACCACGCGACCAAAGGTGTG 480
          |||||||||||||||||||||||||||||||||||
Db    421 CCTGCCAACACGGTGACCACGCGACCAAAGGTGTG 480

Qy    481 CCGCGTGGGGCGACGACGTGCTGGTTCACCTGCTCGGTGTGTCTGGT 540
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCGCGTGGGGCGACGACGTGCTGGTTCACCTGCTCGGTGTGTCTGGT 540

Qy    541 GGCTCCCAGCTGCGGCCTACCAGGTGCGGGCGCGCCGCTGCTACCAGTGCTGCCAC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2881 GCAGAGGCGACTACTCCAGCTATGCCGGCGACCTTCCATCAGAGGCCAGTCTTCACCTTCAACCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCAGAGGCGACTACTCCAGCTATGCCGGCGACCTTCCATCAGAGGCCAGTCTTCACCTTCAACCG 2940

Qy   2941 CGGCTTCAAGGCTGGGAGGAGAACATGCGTCGCAAACTCTTTGGGGCTGTTGCGGCTGAGTG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CGGCTTCAAGGCTGGGAGGAGAACATGCGTCGCAAACTCTTTGGGGCTGTTGCGGCTGAGTG 3000

Qy   3001 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060

Qy   3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTCTGCAGCTCCCATTTCA 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTCTGCAGCTCCCATTTCA 3120

Qy   3121 TCAGCAAGTTTGGAAGAACCCCACCATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 TCAGCAAGTTTGGAAGAACCCCACCATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180

Qy   3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGAGGATGTCGCTGGGGGCCAAGGGCGCCGC 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGAGGATGTCGCTGGGGGCCAAGGGCGCCGC 3240

Qy   3241 CGGCCCCTCCTGCCCTCCGAGGCCGTGCAGTGGCGTGCGCAGTGGCGTGCGCCACCAAGCATTCCTGCTCAAGCT 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CGGCCCCTCCTGCCCTCCGAGGCCGTGCAGTGGCGTGCGCAGTGGCGTGCGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy   3301 GACTCGACACCGTCACTCACCTACGTGCCACTCCTGGGGTCACTCAGGAGACGCCAGACGCA 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GACTCGACACCGTCACTCACCTACGTGCCACTCCTGGGGTCACTCAGGAGACGCCAGACGCA 3360

Qy   3361 GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTCGCCCTGGAGGCCGCCGAGCCAACCCGGC 3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTCGCCCTGGAGGCCGCCGAGCCAACCCGGC 3420

Qy   3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGAGCCACCCGAGGCCGCCGCCGCCGA 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGAGCCACCCGAGGCCGCCGCCGCCGA 3480

Qy   3481 GAGCAGACCACCAGCCCCGCCACCCTTCACGCGCTCTACGTCCCAGGAGGAGGGCGGCGGCC 3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GAGCAGACCACCAGCCCCGCCACCCTTCACGCGCTCTACGTCCCAGGAGGAGGGCGGCGGCC 3540

Qy   3541 CACACCCAGGCCCGCCACCCGCACCCCCTGGGAGTCTGAGGCCTGAGTGTTTGGCCGAGGCCTG 3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CACACCCAGGCCCGCCACCCGCACCCCCTGGGAGTCTGAGGCCTGAGTGTTTGGCCGAGGCCTG 3600

Qy   3601 CATGTCCGGCTGAGGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGCCAAGGGCT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CATGTCCGGCTGAGGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGCCAAGGGCT 3660

Qy   3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACGAGCTGGCGCTGGCGCTCCACCCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACGAGCTGGCGCTGGCGCTCCACCCCA 3720

Qy   3721 GGGCCAGGTTTTCCTCACCAGGAGCCGCTTCCACTCCCCATAGGAATAGTCCATCC 3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GGGCCAGGTTTTCCTCACCAGGAGCCGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780

Qy   3781 CCAGATTCGGCCATTGTTCACCCCTCCTTCCTTCACCACCCACCATCC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CCAGATTCGGCCATTGTTCACCCCTCCTTCCTTCACCCACCACCATCC 3840

Qy   3841 AGGTGGAGACCCTGAGAAGGGAGCTCTGGGAGTTGGAGTGAGATGTG 3900
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 AGGTGGAGACCCTGAGAAGGGAGCTCTGGGAGTTGGAGTGAGATGTG 3900

Qy   3901 CCCTGTACACAGGGCAGGAGACCCTGCACCTGGATGGGGGTCCCTGGGTCAATTGGGGG 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CCCTGTACACAGGGCAGGAGACCCTGCACCTGGATGGGGGTCCCTGGGTCAATTGGGGG 3960
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Qy  1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTCGAGCTGCTCAGTCTCTTTCTTTTA 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTCGAGCTGCTCAGTCTCTTTCTTTTA 1740

Qy  1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGCTGGAG 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGCTGGAG 1800

Qy  1801 CAAGTTGCAAAGCATTGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 CAAGTTGCAAAGCATTGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860

Qy  1861 GGAAGCAGAGGTCAGGCAGCAGCATCGGAAGCCCGGCTGCGGCCTGACGTCCAGACTCCG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GGAAGCAGAGGTCAGGCAGCAGCATCGGAAGCCCGGCTGCGGCCTGACGTCCAGACTCCG 1920

Qy  1921 CTTCATCCCAAGCTGACGGCGCTGCGGCCGATTGTGAACATGACTACGTCGTGGGAGC 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CTTCATCCCAAGCTGACGGCGCTGCGGCCGATTGTGAACATGACTACGTCGTGGGAGC 1980

Qy  1981 CAGAAACGTTCCGCAGAGAAAAGAGGGCGGCGGGCGCGCCCAGCCGTCTCACCTGTGCTGG 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CAGAAACGTTCCGCAGAGAAAAGAGGGCGGCGGGCGCGCCCAGCCGTCTCACCTGTGCTGG 2040

Qy  2041 CAGCGTGCTCAACTACGAGCGCCTGGCGACACTTCGTGCGTGTGGGCCCAGGACCC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 CAGCGTGCTCAACTACGAGCGCCTGGCGACACTTCGTGCGTGTGGGCCCAGGACCC 2100

Qy  2101 CCTGGACGATATCGCCAGAGGTCGTCAGGCGACAAGAGCAGCTGCGACCATCGTGCTGCGG 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCTGGACGATATCGCCAGAGGTCGTCAGGCGACAAGAGCAGCTGCGACCATCGTGCTGCGG 2160

Qy  2161 GCCGCCTGAGCGTGACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCCA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCGCCTGAGCGTGACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCCA 2220

Qy  2221 GGACAGGCTCACGGAGGTCATCATCGAGCATCATCGGGCGCCCCAAGGCCTTCAAGAGCA 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GGACAGGCTCACGGAGGTCATCATCGAGCATCATCGGGCGCCCCAAGGCCTTCAAGAGCA 2280

Qy  2281 TCGGTATGCGTGGTCCAGAAGGCCGCACGTCCGCAAGGCCACGTCCGGGCTTCACCTGCAGGA 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TCGGTATGCGTGGTCCAGAAGGCCGCACGTCCGCAAGGCCACGTCCGGGCTTCACCTGCAGGA 2340

Qy  2341 CGTCTCACCTTGACAGACCTCCAGCCGTACATGCAGCAGCAGTCGAGCTGCTCCTGAATGAGGCCAG 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CGTCTCACCTTGACAGACCTCCAGCCGTACATGCAGCAGCAGTCGAGCTGCTCCTGAATGAGGCCAG 2400

Qy  2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGCAGCTCCTCCCGAATGAGGCCAG 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGCAGCTCCTCCCGAATGAGGCCAG 2460

Qy  2461 CAGTGGCCTCTACGGTCCGACGTCTTCATGTGCCACCACGCGTGCATCAGGGG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGTGGCCTCTACGGTCCGACGTCTTCATGTGCCACCACGCGTGCATCAGGGG 2520

Qy  2521 CAAGTTCCTACGTCCAGTGCCAGGGATCCCCAGGGCTCCATCCTCTCCACGTGCTCTG 2580
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Db  2521 CAAGTTCCTACGTCCAGTGCCAGGGATCCCCAGGGCTCCATCCTCTCCACGTGCTCTG 2580

Qy  2581 CAGCCTGTGTCTACGGCGACGACATGAGAACAAGCTGTTTCGGCGGGATTCGGCGGGACGGGCT 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CAGCCTGTGTCTACGGCGACGACATGAGAACAAGCTGTTTCGGCGGGATTCGGCGGGACGGGCT 2640

Qy  2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCGCGAAAAC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCGCGAAAAC 2700

Qy  2701 CTTCCTCAGGACCCTGGTCCCGAGTGTCCCGAGTATGCGCTGGTAACTTGCGAA 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CTTCCTCAGGACCCTGGTCCCGAGTGTCCCGAGTATGCGCTGGTAACTTGCGGAA 2760
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Db   541 GGCTCCAGCTGCGCCTACCAGGTGTGCGGGCCGCGCCTGTACCAGCTGCGGCGCTGCCAC 600

Qy   601 TCAGGCCGGCCGGCCCCCGCCACACGCTAGTGACCCGAAGGCGTCTGGGATGCGAACGGGC 660
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Db   601 TCAGGCCGGCCGGCCCCCGCCACACGCTAGTGACCCGAAGGCGTCTGGGATGCGAACGGGC 660

Qy   661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGGCTGCCAGCCCCGGGGTGCGAG 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGGCTGCCAGCCCCGGGGTGCCGAG 720

Qy   721 GAGGCGGCGGGGACGGGCAGTGCCAGCGAAGTCTGCGGTGCCCAAGAGGCCCAGGCGGTGGCGC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GAGGCGGCGGGGACGGGCAGTGCCAGCGAAGTCTGCGGTGCCCAAGAGGCCCAGGCGGTGGCGC 780

Qy   781 TGCCCCTGAGCCGGACCGGACGCGCCCCCTTGGGCGGAGGGGTCCTGGGCCCCACCCGGGCAGGAC 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGCCCCTGAGCCGGACCGGACGCGCCCCCTTGGGCGGAGGGGTCCTGGGCCCCACCCGGGCAGGAC 840

Qy   841 GCGTGGACCGAGTGACCGTGTTTCTGTGTGTGTGGCACGCGCCACTCCCACCCGTGGGCGCCCCA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCGTGGACCGAGTGACCGTGTTTCTGTGTGTGTGGCACGCGCCACTCCCACCCGTGGGCGCCCCA 900

Qy   901 CACCTTCTTTGGAGGGTGCGCTCTGGCACGCGCCACTCCCACCCGTGGGCGCGCCA 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CACCTTCTTTGGAGGGTGCGCTCTGGCACGCGCCACTCCCACCCGTGGGCGCGCCA 960

Qy   961 GCCACACGCGGGCCCCCATCCACATCGCGGCCAAGCACTTCCTCTACTCCTCAGGCGACAGGAGCAGCTGCG 1020
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Db   961 GCCACACGCGGGCCCCCATCCACATCGCGGCCAAGCACTTCCTCTACTCCTCAGGCGACAGGAGCAGCTGCG 1020

Qy  1021 CCGGTGTACGCGGAGACCAAGGACACTTCCTCTACTCCTCAGGGCGACGCAAGAGCAGCTGCG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 CCGGTGTACGCGGAGACCAAGGACACTTCCTCTACTCCTCAGGGCGACGCAAGAGCAGCTGCG 1080

Qy  1081 GCCCTCCTCCTACTCAGCTTCCCGGCCCAGCGTCTCGAGGCCCTGGCGCTTCGGGGCTCGTGGA 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 GCCCTCCTCCTACTCAGCTTCCCGGCCCAGCGTCTCGAGGCCCTGGCGCTTCGGGGCTCGTGA 1140

Qy  1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATCGCCCAGGTTGCCCCCCCT 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATCGCCCAGGTTGCCCCCCCT 1200

Qy  1201 GCCCCAGCGCTACTGCGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GCCCCAGCGCTACTGCGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260

Qy  1261 GTGCCCCTACGGGGTGTCTCCTCAAGACGCACTGCCGGCTGCGAGCTGCGGTGCTCACTGCGCAGC 1320
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Db  1261 GTGCCCCTACGGGGTGTCTCCTCAAGACGCACTGCCGGCTGCGAGCTGCGGTGCTCACTGCGCAGC 1320

Qy  1321 AGCCGGTGTCTGTGCCCGGGAGAAGCCTCGTGTGTGCCGGGAGGATGAGCGTGCGGGAGGAGGA 1380
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Db  1321 AGCCGGTGTCTGTGCCCGGGAGAAGCCTCGTGTGTGCCGGGAGGATGAGCGTGCGGGAGGAGGA 1380

Qy  1381 CACAGACCCCGTCGGGTTGCAGCTGCTCCGCCGGCCTGGTGCAGCAGCAGCCCTTGGCAGTGTA 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CACAGACCCCGTCGGGTTGCAGCTGCTCCGCCGGCCTGGTGCAGCAGCAGCCCTTGGCAGTGTA 1440

Qy  1441 CGGCTTCGTGGTGCCGGCCTGCTGCGGCCGGCTGCTGTGCCCGCCCTGGGGGCTCCAGGCA 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CGGCTTCGTGGTGCCGGCCTGCTGCGGCCGGCTGCTGTGCCCGCCCTGGGGGCTCCAGGCA 1500

Qy  1501 CAACGAACGCGCCGCCCGCTTCCTCAGGGAACACCAAGAGTTCATCTCCCTGGGAAGCATGCCAA 1560
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Db  1501 CAACGAACGCGCCGCCCGCTTCCTCAGGGAACACCAAGAGTTCATCTCCCTGGGAAGCATGCCAA 1560

Qy  1561 GCTCCTCGCTGCTGCAGGAGCTGACGTGGAAGATGAGCGTGGCTTGGCGACTTGCTGCTGCGCAG 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 GCTCTCGCTGCTGCAGGAGCTGACGTGGAAGATGAGCGTGGCCTTGGCGACTTGCTGCTGCGCAG 1620

Qy  1621 GAGCCCAGGGGGTTGGCTGTGTTCGGCGGCGGTGTTCGCGGCGCCGAGCAGAGAGATCCTGGC 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT  2820

Qy   2821  GCCGGCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGAGACCCTGGAGGT        2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  GCCGGCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGAGACCCTGGAGGT        2880

Qy   2881  GCAGAGGGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTTCACCTTCAACCG    2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  GCAGAGGGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTTCACCTTCAACCG    2940

Qy   2941  CGGCTTCAAGGCTGGGAGGAACATGCTCGCCGCAAACTCTTTGGGGCTCTTGCGGCTGAAGTG    3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  CGGCTTCAAGGCTGGGAGGAACATGCTCGCCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG    3000

Qy   3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA    3060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  CTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA    3060

Qy   3061  CAAGATCTCCTGCTGCAGGCGGTACAGGTTCACGCATGTGTGCTGCAGCTCCCATTTCA    3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  CAAGATCCTCCTGCTGCAGGCGGTACAGGTTCACGCATGTGTGCTGCAGCTCCCATTTCA    3120

Qy   3121  TCAGCCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGGTCATCTCTGACACGGCCTCCCT    3180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  TCAGCCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGGTCATCTCTGACACGGCCTCCCT    3180

Qy   3181  CTGCTACTTCCATCCTGAAAGCCAAGAACGCAGGAGGATGTCGCTCGGGGGCCAAGGGCGCCGC    3240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  CTGCTACTTCCATCCTGAAAGCCAAGAACGCAGGAGGATGTCGCTCGGGGGCCAAGGGCGCCGC    3240

Qy   3241  CGGCCCTCGCCCCTCCGAGGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT    3300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241  CGGCCCTCGCCCCTCCGAGGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT    3300

Qy   3301  GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA    3360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301  GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA    3360

Qy   3361  GCTGTAGTCGGAAGCTCCCGGGACGACCTCCCGGGGACCGCTGACCTGCCCTGGAGGCCGCAACCCGGC    3420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361  GCTGTAGTCGGAAGCTCCCGGGACGACCTCCCGGGGACCGCTGACCTGCCCTGGAGGCCGCAACCCGGC    3420

Qy   3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGGAGGCCGA    3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGGAGGCCGA    3480

Qy   3481  GAGCAGACACCAGCAGCCCTGTCACGCTCACGTCCCAGGGAGGGGGCGGCC    3540
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  GAGCAGACACCAGCAGCCCTGTCACGCTCACGTCCCAGGGAGGGGGCGGCC    3540

Qy   3541  CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGTTTGGCCGAGGCCTG    3600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGTTTGGCCGAGGCCTG    3600

Qy   3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGTGCCAAGGGCT    3660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGTGCCAAGGGCT    3660

Qy   3661  GAGTGTCCAGCACACCTGGCTCCTCACTTCACTTCACGTCGGCCGCTCGGCTCCACCCCA    3720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  GAGTGTCCAGCACACCTGGCTCCTCACTTCACTTCACGTCGGCCGCTCGGCTCCACCCCA    3720

Qy   3721  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCACATAGGAATAGTCCATCC    3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCACATAGGAATAGTCCATCC    3780

Qy   3781  CCAGATTCGCCATTGTTCACCCCGTTCCACCCCCACCATCC    3840
           |||||||||| ||||||||||||||| |||||||||||||||
Db   3781  CCAGATTCGGCCATTGTTCACCCCGTTCCACCCCCACCATCC    3840

Qy   3841  AGTCGGAGACCTGGAAGGACCCTGGGAGTCTGGAATTTGGAGTGACCAAGGTGTG    3900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841  AGGTGCTGGAGACCCTGGAGGAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG    3900

Qy   3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG    3960
           |||| ||||||||||||||||||||| ||||||||||||||||| ||||||||||||||
Db   3901  CCCTGTACACAGGCGAGGACCCCTGCGCCACTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG    3960

Qy   3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAA    4015
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Db   3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAA    4015
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RESULT 7
PCT-US99-07160-1
; Sequence 1, Application PC/TUS9907160
; GENERAL INFORMATION:
;   APPLICANT: Cech, Thomas R.
;   APPLICANT: Lingner, Joachim
;   APPLICANT: Nakamura, Toru
;   APPLICANT: Chapman, Karen B.
;   APPLICANT: Morin, Gregg B.
;   APPLICANT: Harley, Calvin B.
;   APPLICANT: Andrews, William H.
;   APPLICANT: Geron Corporation
;   APPLICANT: University Technology Corporation
;   TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting
;   TITLE OF INVENTION: Telomerase Reverse Transcriptase
;   FILE REFERENCE: 015389-003610PC
;   CURRENT APPLICATION NUMBER: PCT/US99/07160
;   CURRENT FILING DATE: 1999-03-31
;   EARLIER APPLICATION NUMBER: US 08/724,643
;   EARLIER FILING DATE: 1996-10-01
;   EARLIER APPLICATION NUMBER: US 08/844,419
;   EARLIER FILING DATE: 1997-04-18
;   EARLIER APPLICATION NUMBER: US 08/846,017
;   EARLIER FILING DATE: 1997-04-25
;   EARLIER APPLICATION NUMBER: US 08/851,843
;   EARLIER FILING DATE: 1997-05-06
;   EARLIER APPLICATION NUMBER: US 08/854,050
;   EARLIER FILING DATE: 1997-05-09
;   EARLIER APPLICATION NUMBER: US 08/911,312
;   EARLIER FILING DATE: 1997-08-14
;   EARLIER APPLICATION NUMBER: US 08/912,951
;   EARLIER FILING DATE: 1997-08-14
;   EARLIER APPLICATION NUMBER: US 08/915,503
;   EARLIER FILING DATE: 1997-08-14
;   EARLIER APPLICATION NUMBER: WO PCT/US97/17618
;   EARLIER FILING DATE: 1997-10-01
;   EARLIER APPLICATION NUMBER: WO PCT/US97/17885
;   EARLIER FILING DATE: 1997-10-01
;   EARLIER APPLICATION NUMBER: US 08/974,549
;   EARLIER FILING DATE: 1997-11-19
;   EARLIER APPLICATION NUMBER: US 08/974,584
;   EARLIER FILING DATE: 1997-11-19
;   EARLIER APPLICATION NUMBER: US 09/052,919
;   EARLIER FILING DATE: 1998-03-31
;   NUMBER OF SEQ ID NOS: 72
;   SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
;   LENGTH: 4015
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (56)..(3454)
;   OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
PCT-US99-07160-1

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Query Match         100.0%;  Score 4015;  DB 1;  Length 4015;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 4015;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1  GCACGGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCACCCCCGGCGATGCC    60
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Db  1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCTGACTGGCGCTCGGAGGCTCGTGGA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1141 GACCATCTTTCTGGGTTCCAGGCGCTGGCGCTCCCGCAGGTGCCCGCCT 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GACCATCTTTCTGGGTTCCAGGCGCTGGCGCTCCCGCAGGTGCCCGCCT 1200

Qy  1201 GCCCCAGCGCTACTGGCAAATGGGCGCCCCTGTTTCTGGAGCTCTTGGGAACCACGCGCA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GCCCCAGCGCTACTGGCAAATGGGCGCCCCTGTTTCTGGAGCTCTTGGGAACCACGCGCA 1260

Qy  1261 GTGCCCCTACGGGTGTCCTCAAGACGCACTGCGGTGCGGTCACCCAGC 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GTGCCCCTACGGGTGTCCTCAAGACGCACTGCGGTGCGGTCACCCAGC 1320

Qy  1321 AGCCGGTGTCGTGCCCGGAGAGCCCAGGGCTCGTGGGCGGCCCCGAGGAGGAGGA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 AGCCGGTGTCGTGCCCGGAGAGCCCAGGGCTCGTGGGCGGCCCCGAGGAGGAGGA 1380

Qy  1381 CACAGACCCCCGTCGCCTGGTGCAGCTCTCCGCCACAGCAGCACCCCTGGCAGGTGTA 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CACAGACCCCCGTCGCCTGGTGCAGCTCTCCGCCACAGCAGCACCCCTGGCAGGTGTA 1440

Qy  1441 CGGCTTCGTGCCGGCCGCTGGTGCCGCCGCCCCCCAGGCCTCTCCCTGGGGCTCCAGGCA 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CGGCTTCGTGCCGGCCGCTGGTGCCGCCGCCCCCCAGGCCTCTCCCTGGGGCTCCAGGCA 1500

Qy  1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

Qy  1561 GCTCTCGTGCCAGGAGCTGACGTGCGGACTGCCGTTGGCTGCCGCCAG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 GCTCTCGTGCCAGGAGCTGACGTGCGGACTGCCGTTGGCTGCCGCCAG 1620

Qy  1621 GAGCCCAGGGGTTGGCTTGGCTGGTGTTCCGGCGAGAGATCCTGGC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 GAGCCCAGGGGTTGGCTTGGCTGGTGTTCCGGCGAGAGATCCTGGC 1680

Qy  1681 CAAGTTCCTGCACTGGCTGGTGTGTGTACGTCGTCTTTTTA 1740
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Db  1681 CAAGTTCCTGCACTGGCTGGTGTGTGTACGTCGTCTTTTTA 1740

Qy  1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1800

Qy  1801 CAAGTTGCAAAGCATTGAAATCAGACGAGCATCCGGAAGCCCAGCTGTC 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 CAAGTTGCAAAGCATTGAAATCAGACGAGCATCCGGAAGCCCAGCTGTC 1860

Qy  1861 GGAAGCAGAGGTCAGGCAGCAGCATCCGGGAAGCCCGGCCGCCCACCCG 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GGAAGCAGAGGTCAGGCAGCAGCATCCGGGAAGCCCGGCCGCCCACCCG 1920

Qy  1921 CTTCATCCCCAAGCCTGACGGGTGCGGCGGCCGATTGTGAACATGTGGGGAGC 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CTTCATCCCCAAGCCTGACGGGTGCGGCGGCCGATTGTGAACATGTGGGGAGC 1980

Qy  1981 CAGAACGTTCCGACGAATATCCACAGGGCTCACCTGGAGGGTGAAGGCACTGTT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CAGAACGTTCCGACGAATATCCACAGGGCTCACCTGGAGGGTGAAGGCACTGTT 2040

Qy  2041 CAGCGTGCTCAACTAGCGACAGGGCGCCCTGTCTGGGGAGC 2100
         |||||||||||||||||||||||||||||||||||||||||
Db  2041 CAGCGTGCTCAACTAGCGACAGGGCGCCCTGTCTGGGGAGC 2100

Qy  2101 CCTGGACGATATCCACAGGGCTGCGCAGGGCCCAGGACCC 2160
         ||||||||||||||||||||||||||||||||||||||||
Db  2101 CCTGGACGATATCCACAGGGCTGCGCAGGGCCCAGGACCC 2160

Qy  2161 GCCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACCATCCCCA 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACCATCCCCA 2220
```

```
Db     1 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 60
         GCAGGCGGCTGCCTCCTGCCACGTGGGAAGCCCTGGCTGGCCCCGGCCACCCCCGGATGCC

Qy    61 GCGGCGTCCCCGCTGCCGAGCCGTCCTCCTTCGCTGCCGCCCCAGGCGCGGTGCTGCAGCT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GCGGCGTCCCCGCTGCCGAGCCGTCCTCCTTCGCTGCCGCCCCAGGCGCGGTGCTGCAGCT 120

Qy   121 GCCGCTGGCCACGTTCGTGGCGCCGGCCTGGGCGCCCCTGGTGCGTGTCAGCGGCG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCCGCTGGCCACGTTCGTGGCGCCGGCCTGGGCGCCCCTGGTGCGTGTCAGCGGCG 180

Qy   181 GGACCCGGCGGCTTTCCGGCGGCCAGTGGTGGCCCTGGCCCTGGGACGC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACCCGGCGGCTTTCCGGCGGCCAGTGGTGGCCCTGGCCCTGGGACGC 240

Qy   241 ACGGCGCCGCCCCCGCCCCCCGCGCCCCGCGCCCCCGAGTGTCCTGCCTCCGCCAGGAGTGTCCTGCCTCCGCCAGGAGTGCTGGGCTGGTGGC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACGGCGCCGCCCCCGCCCCCCGCGCCCCGCGCCCCCGAGTGTCCTGCCTCCGCCAGGAGTGCTGGGCTGGTGGC 300

Qy   301 CCGAGTGCTGCGAGAGCGTGTCGCGACGCGGCGCGGCCTGGGCGCCTGGTGCGCCTTCGC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGAGTGCTGCGAGAGCGTGTCGCGACGCGGCGCGGCCTGGGCGCCTGGTGCGCCTTCGC 360

Qy   361 GCTGCTGGACGGGGCGCCCCGGGGCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCTGCTGGACGGGGCGCCCCGGGGCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA 420

Qy   421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCCGTGGGGCGTGGGGCGTGCTGCTGCCGCG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCCGTGGGGCGTGCTGCTGCCGCG 480

Qy   481 CCGGTGGGCCACGACGACTGCTGGTTCACCTGTGCCTGCGCCGCCTGCGCCTCTTGTGCTGGT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCGGTGGGCCACGACGACTGCTGGTTCACCTGTGCCTGCGCCGCCTGCGCCTCTTGTGCTGGT 540

Qy   541 GGCTCCCAGCTGCGCCTACCAGTGTCGCGGGCGGCCACCAGCTCGGCGCTGCCAC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCTCCCAGCTGCGCCTACCAGTGTCGCGGGCGGCCACCAGCTCGGCGCTGCCAC 600

Qy   601 TCAGGCCGGCCCCGCCACACGCTAGTGACCCCGAAGGGCGTGGGATGCGAACGGGC 660
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Db   601 TCAGGCCGGCCCCGCCACACGCTAGTGACCCCGAAGGGCGTGGGATGCGAACGGGC 660

Qy   661 CTGGAACCATAGCGTCAGGAGGCCGGGCGGGTCCCCGGGTCCCCAGCGCCCAGGAGGCCCAGAGGCGCGCAG 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGGAACCATAGCGTCAGGAGGCCGGGCGGGTCCCCGGGTCCCCAGCGCCCAGGAGGCCCAGAGGCGCGCAG 720

Qy   721 GAGGGCCGGGGCGGCCGGGGCAGTCGCAGGAGCTGCCAGAAGAGGCCGCCCACCCGTGGGCCCCCA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GAGGGCCGGGGCGGCCGGGGCAGTCGCAGGAGCTGCCAGAAGAGGCCGCCCACCCGTGGGCCCCCA 780

Qy   781 TGCCCCTGAGCCGGAGCCGGACGCCCGTTGGGCAGGGTCCTGGGCCCCACCCGTGGGCCCCCA 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGCCCCTGAGCCGGAGCCGGACGCCCGTTGGGCAGGGTCCTGGGCCCCACCCGTGGGCCCCCA 840

Qy   841 GCGTGGACCGAGTGACCGTTTCTGTGGTGTCGCCCTCACCTGCGCCCCGGCCACCGACCCGAAGAAGC 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCGTGGACCGAGTGACCGTTTCTGTGGTGTCGCCCTCACCTGCGCCCCGGCCACCGACCCGAAGAAGC 900

Qy   901 CACCTTCTTTGGAGGTGCGCTCTCTGCACCACGCGGCCACCATCCCCACCTGGCCCCCCA 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CACCTTCTTTGGAGGTGCGCTCTCTGCACCACGCGGCCACCATCCCCACCTGGCCCCCCA 960

Qy   961 GCACCACGCGGCCCCCCATCCACATCGCGGCCCCTTGTCCCCCGGTGTACGGCCGCAGCGCAGCTGCGCG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GCACCACGCGGCCCCCCATCCACATCGCGGCCCCTTGTCCCCCGGTGTACGGCCGCAGCGCAGCTGCGCG 1020

Qy  1021 CACCTTCTCTACTGTCCTGCACCACTTCCTCTACTCCTCAGGCGACCAAGAGAGCAGCTGCG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 CACCTTCTCTACTGTCCTGCACCACTTCCTCTACTCCTCAGGCGACCAAGAGAGCAGCTGCG 1080

Qy  1081 GCCCCTCCTTCCTACTCAGCTCTCTGAGGCCTGACTGGCGCTCGGAGGCTCGTGGA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 2221 GGACAGGGTCACCGAGGTCATCGCCAGCAGCATCATCAAACCCAGAACACGTACTCGTCGCG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2221 GGACAGGGTCACCGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTCGTCGCG 2280

Qy 2281 TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340
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Db 2281 TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340

Qy 2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGGTCACCTGCAGGA 2400
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Db 2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGGTCACCTGCAGGA 2400

Qy 2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG 2460
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Db 2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG 2460

Qy 2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG 2520
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Db 2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG 2520

Qy 2521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG 2580
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Db 2521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG 2580

Qy 2581 CAGCCTGTGTACGGCGACATGAGAACAAGCTGTTTCGCGGGATTCGCGGGACGGGGCT 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2581 CAGCCTGTGTACGGCGACATGAGAACAAGCTGTTTCGCGGGATTCGCGGGACGGGGCT 2640

Qy 2641 GCTCCTGCGTTTGGTGGTGATGATTTCTTGTTGTGACACCTCACCTCCCACCGCGAAAAC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2641 GCTCCTGCGTTTGGTGGTGATGATTTCTTGTTGTGACACCTCACCTCCCACCGCGAAAAC 2700

Qy 2701 CTTCCTCAGGAGACCCTGGTCCCGAGGTGTCCCTGAGTATGGCGTGGCGTGGTGAACTTGCGGAA 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2701 CTTCCTCAGGAGACCCTGGTCCCGAGGTGTCCCTGAGTATGGCGTGGCGTGGTGAACTTGCGGAA 2760

Qy 2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCCACGCTTTTGTTCAGAT 2820
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Db 2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCCACGCTTTTGTTCAGAT 2820

Qy 2821 GCCGGCCACGCGCTATTCCCCTGGTGCGGCCTGCTGCTGCGGGACCCTGGAGGT 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2821 GCCGGCCACGCGCTATTCCCCTGGTGCGGCCTGCTGCTGCGGGACCCTGGAGGT 2880

Qy 2881 GCAGAGGCGACTACTCCAGCTACCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2881 GCAGAGGCGACTACTCCAGCTACCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940

Qy 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTGGGGTCTTGCGGCTGAAGTG 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTGGGGTCTTGCGGCTGAAGTG 3000

Qy 3001 TCACAGCCGTGTTCTGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3001 TCACAGCCGTGTTCTGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060

Qy 3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGTCTCCCATTTCA 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGTCTCCCATTTCA 3120

Qy 3121 TCAGCAAGTTTGGAAGAACGCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCT 3180
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Db 3121 TCAGCAAGTTTGGAAGAACGCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCT 3180

Qy 3181 CTGCTACTCCATCCTGAAAGCGCAGAACGCAGGGATGTCGCTGGCGTGCTCCCGCGC 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3181 CTGCTACTCCATCCTGAAAGCGCAGAACGCAGGGATGTCGCTGGCGTGCTCCCGCGC 3240

Qy 3241 CGGCCCCTCTGCCCCTCCGAGGCCTCGCAGTGCCGTCGTGCCACCAAGCATTCCTGCTCAAGCT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3241 CGGCCCCTCTGCCCCTCCGAGGCCTCGCAGTGCCGTCGTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy 3301 GACTCGACACCGTGTCACCTACGTCGCCACTCCTGGGTCACTCAGGACAGCCCAGACGCA 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGTCACTCAGGACAGCCCAGACGCA 3360

Qy 3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCCTGGAGGCCGCCGCCAACCGGC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCCTGGAGGCCGCCGCCAACCCGGC 3420

Qy 3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGCCCACCCGGTCGATGGCCAGGCCGA 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGCCCACCCGGTCGATGGCCAGGCCGA 3480

Qy 3481 GAGCAGACACCAGCAGCACCCTGTCACGCCGGCTCTACGTCCCAGGCGTCTCACGCTCCGCCGCC 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3481 GAGCAGACACCAGCAGCACCCTGTCACGCCGGCTCTACGTCCCAGGCGGGGGCGGCGCC 3540

Qy 3541 CACACCCAGGCCCGACCCGGGAGTCTGGGAGTCGGAGTTGGCCGAGGCCTG 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3541 CACACCCAGGCCCGACCCGGGAGTCTGGGAGTCGGAGTGTTTGGCCGAGGCCTG 3600

Qy 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCCTGAGCGAGGGCTGAGCCCAAGGGCT 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCCTGAGCGAGGGCTGAGCCCAAGGGCT 3660

Qy 3661 GAGTGTCCAGCACACTGCCGTCTTCACTTCCCCACAGGCTCGGCCGCTCGGCTCCACCCCA 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3661 GAGTGTCCAGCACACTGCCGTCTTCACTTCCCCACAGGCTGGCCGCTCGGCTCCCACCCCA 3720

Qy 3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3721 GGGCCAGCTTTTCCTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780

Qy 3781 CCAGATTCGCCATTGTTCACCCTCGCCCTCCGCCCCTGCCCCTTTGCCTTCCACCCCACCATCC 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3781 CCAGATTCGCCATTGTTCACCCTCGCCCTCCGCCCCTGCCCCTTTGCCTTCCACCCCACCATCC 3840

Qy 3841 AGGTGGAGACCCTGAGAAGGACCTCTGGGAGCTCTGGGAATTTGACCAAAGGTGTG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3841 AGGTGGAGACCCTGAGAAGGACCTCTGGGAGCTCTGGGAATTTGACCAAAGGTGTG 3900

Qy 3901 CCCTGTACACAGGGGAGGAGACCCTGCACCTGGATGGGGGTCCCTGGGGTCAAATTGGGGG 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3901 CCCTGTACACAGGGGAGGAGACCCTGCACCTGGATGGGGGTCCCTGGGGTCAAATTGGGGG 3960

Qy 3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015

RESULT 8
PCT-US01-15774-3
; Sequence 3, Application PC/TUS0115774
; GENERAL INFORMATION:
;   APPLICANT: Isis Pharmaceuticals, Inc.
;   APPLICANT: Brett P. Monia
;   APPLICANT: William Gaarde
;   APPLICANT: Susan M. Freier
;   APPLICANT: Edward V. Wancewicz
;   TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
;   FILE REFERENCE: ISPH-0568
;   CURRENT APPLICATION NUMBER: PCT/US01/15774
;   CURRENT FILING DATE: 2001-05-15
;   PRIOR APPLICATION NUMBER: 09/572,423
;   PRIOR FILING DATE: 2000-05-16
;   NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
;   LENGTH: 4015
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (56)...(3454)
PCT-US01-15774-3

Query Match   100.0%;   Score 4015;   DB 2;   Length 4015;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 4015;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy      1 GCAGCGCTGCGTCCTGCGCCACGTGGGAAGCCCTGGCCCCGGCCACCCCGGCCGATGCC     60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAGCGCTGCGTCCTGCGCCACGTGGGAAGCCCTGGCCCCGGCCACCCCGGCCGATGCC     60

Qy     61 GCGGCGCTCCCCGCTGCCGAGCCGTGCGGCTCCCCGTGCTGCCGCAGCCACTACCGGAGCTGCT    120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGGCGCTCCCCGCTGCCGAGCCGTGCGGCTCCCCGTGCTGCCGCAGCCACTACCGGAGCTGCT    120

Qy    121 GCCGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGGCTGGCGGCTGGTGCAGCGCGG    180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGGCTGGCGGCTGGTGCAGCGCGG    180

Qy    181 GGACCCGGCGGCTTTCCGCGCGTGGTGCGCGGCGGCGGAAGAACGTGCCTGGTGTGCCCTGGGACGC    240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGACCCGGCGGCTTTCCGCGCGTGGTGCGCGGCGGCGGAAGAACGTGCCTGGTGTGCCCTGGGACGC    240

Qy    241 ACGGCGCCCCCCGCGCCCCTCTTCCCGCGCGCCCCCCCCCGCGCGCCCCCCCGCGC    300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACGGCGCCCCCCGCGCCCCTCTTCCCGCGCGCCCCCCCCCGCGCGCCCCCCCGCGC    300

Qy    301 CCGAGTGCTGCAGAGGCTGTGCGACGACGCTGCTGGTTCACCTGGCCTTCGCCTTCGC    360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGAGTGCTGCAGAGGCTGTGCGACGACGCTGCTGGTTCACCTGGCCTTCGCCTTCGC    360

Qy    361 GCTGCTGGACGGGGCCCCGGGGGGCCCTTCACCACCAGCGTGCCGCAGCTA    420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTGCTGGACGGGGCCCCGGGGGGCCCTTCACCACCAGCGTGCCGCAGCTA    420

Qy    421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGCGTGCTGCTGCG    480
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Db    421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGCGTGCTGCTGCG    480

Qy    481 CCGGCGTGGGGCGACGACGTGCTGGTTCACCTGCTGGTTCACCTGCTGGTTTGTGCTGGT    540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCGGCGTGGGGCGACGACGTGCTGGTTCACCTGCTGGTTCACCTGCTGGTTTGTGCTGGT    540

Qy    541 GGCTCCCAGCTGCCGCCTACCAGGTGTGCGGCGCCGCGTACCAGCTCGGCGGCCTGCCAC    600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCTCCCAGCTGCCGCCTACCAGGTGTGCGGCGCCGCGTACCAGCTCGGCGGCCTGCCAC    600

Qy    601 TCAGGCCCGGCCCCCGCCCACACGTCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGGC    660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TCAGGCCCGGCCCCCGCCCACACGTCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGGC    660

Qy    661 CTGGAACCATAGCGCGGGGCCAGTCGGTGTTTCTGTGTGTCACCGGTGCCAGCTCTCCGGGTGCGAG    720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGGAACCATAGCGCGGGGCCAGTCGGTGTTTCTGTGTGTCACCGGTGCCAGCTCTCCGGGTGCGAG    720

Qy    721 GAGGCGCGGGGCCAGTCGGTGCCAGCCGGAAGTCTCCGTTGCCCAAGAGGCCCAGGCGTGGCGC    780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GAGGCGCGGGGCCAGTCGGTGCCAGCCGGAAGTCTCCGTTGCCCAAGAGGCCCAGGCGTGGCGC    780

Qy    781 TGCCCTGACCCGAGCGGACGCGGAACGGGCCCGGCCCGTTGGGCAGGGTCCTGGGCAGGAGGAC    840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TGCCCTGACCCGAGCGGACGCGGAACGGGCCCGGCCCGTTGGGCAGGGTCCTGGGCAGGAGGAC    840

Qy    841 GCGTGGACCGAGTGACCGTGGTTTCTGTTGTGTCACCGCCTGTGTGTTCCGCCCAAGACCCCGAAGAAGC    900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCGTGGACCGAGTGACCGTGGTTTCTGTTGTGTCACCGCCTGTGTGTTCCGCCCAAGACCCCGAAGAAGC    900

Qy    901 CACTTCTTTGGAGGGTGCGCTCTGCACGCGCCACTCCCACCCCATCCGCTGGGCCGCCA    960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACTTCTTTGGAGGGTGCGCTCTGCACGCGCCACTCCCACCCCATCCGCTGGGCCGCCA    960

Qy    961 GCACCACGCGGGGCCCCCATCCACATCGCGCCGCCACCACGCGTCCCTGGGACACGCCCTTGTCC   1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GCACCACGCGGGGCCCCCATCCACATCGCGCCGCCACCACGCGTCCCTGGGACACGCCCTTGTCC   1020
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Qy   1021 CCCGGTGTACGGCCGAGACCAAGCACTTCCTCTACTCCTCAGCGGACAAGGAGGACAGCTGCG   1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCCGGTGTACGGCCGAGACCAAGCACTTCCTCTACTCCTCAGCGGACAAGGAGGACAGCTGCG   1080

Qy   1081 GCCCTCCTTCCTACTCAGCTCTGAGCCCGACTGGCCCTGGCCCTGGCCTGGGCGCTGGGAGCCTCGTGA   1140
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Db   1081 GCCCTCCTTCCTACTCAGCTCTGAGCCCGACTGGCCCTGGCCCTGGCCTGGGCGCTGGGAGCCTCGTGA   1140

Qy   1141 GACCATCTTTCTGGTTCCAGGCCCTGATGCCGGGGACTCCCGCAGTTGCCCGGCCT   1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GACCATCTTTCTGGTTCCAGGCCCTGATGCCGGGGACTCCCGCAGTTGCCCGGCCT   1200

Qy   1201 GCCCAGGCTACTGGCAAATGCGGCCCCGTGTTTCTGGAGCTGTTCTGGAGCTGGTGCAGCGCGCA   1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GCCCAGGCTACTGGCAAATGCGGCCCCGTGTTTCTGGAGCTGTTCTGGAGCTGGTGCAGCGCGCA   1260

Qy   1261 GTGCCCTACGGGGTGCTCCTCAAGAGCACACTGCTCCCGCTGCCGAGCTGCGGCTGCCACCCCAGC   1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGCCCTACGGGGTGCTCCTCAAGAGCACACTGCTCCCGCTGCCGAGCTGCGGCTGCCACCCCAGC   1320

Qy   1321 AGCCGGTGCTGTGCCCGGAGAGCCCCCAGGGCTCTGTGCGGCCGCCCCCAGGAGGAGA   1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGCCGGTGCTGTGCCCGGAGAGCCCCCAGGGCTCTGTGCGGCCGCCCCCAGGAGGAGA   1380

Qy   1381 CACAGACCCCGTCGCGTGGTGCGACGCTGCTCCGCGCGGTGCTGCTGGCGGTGCGGCTTCGC   1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CACAGACCCCGTCGCGTGGTGCGACGCTGCTCCGCGCGGTGCTGCTGGCGGTGCGGCTTCGC   1440

Qy   1441 CGGCTTCGTGTGGGGCCTGGTCGTGGGCCGCCGGTGCCTCTGGGCTCGGGCTCCCAGGCA   1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CGGCTTCGTGTGGGGCCTGGTCGTGGGCCGCCGGTGCCTCTGGGCTCGGGCTCCCAGGCA   1500

Qy   1501 CAACGAACGCCGTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAA   1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CAACGAACGCCGTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAA   1560

Qy   1561 GCTCTCGCTGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGTTGGCTGCGCGCAG   1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GCTCTCGCTGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGTTGGCTGCGCGCAG   1620

Qy   1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCCAGAGCACCGTGCTGCGTGCGGCGCTGCTGCGGCGC    1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCCAGAGCACCGTGCTGCGTGCGGCGCTGCTGCGGCGC    1680

Qy   1681 CAAGTTCCTGCACTGGCTGATGAGTGTGACGTGTCGCGAGCTCGTCAGTCTTCTTTTA    1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CAAGTTCCTGCACTGGCTGATGAGTGTGACGTGTCGCGAGCTCGTCAGTCTTCTTTTA    1740

Qy   1741 TGTCACGGAGCACCGTTTCAAAGAGAACAGCAGGCTCTTTTTCTACCGGAAGAGTCTGGAG   1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 TGTCACGGAGCACCGTTTCAAAGAGAACAGCAGGCTCTTTTTCTACCGGAAGAGTCTGGAG   1800

Qy   1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACACTTGAAGAGGTCGCAGCTGTGGCGC   1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACACTTGAAGAGGTCGCAGCTGTGGCGC   1860

Qy   1861 GGAAGCAGGATCAGGCAGCATCGGGAAGCCCAGGCCCCGCCCTTCCGACGTCCAGACTCCG   1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 GGAAGCAGGATCAGGCAGCATCGGGAAGCCCAGGCCCCGCCCTTCCGACGTCCAGACTCCG   1920

Qy   1921 CTTCATCCCAAGCCCGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGGAGC   1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTTCATCCCAAGCCCGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGGAGC   1980

Qy   1981 CAGAACGTTCCGCAGAGAAAAGAGGGCGGGCGGCGGGGTGAAGGCACTGTT   2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAGAACGTTCCGCAGAGAAAAGAGGGCGGGCGGCGGGGTGAAGGCACTGTT   2040

Qy   2041 CAGCGTGCTCAACTACGAGCGGGCGCCCTGGGACACGCCCTTGTCGGG   2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGCGTGCTCAACTACGAGCGGGCGCCCTGGGACACGCCCTTGTCGGG   2100

Qy   2101 CCTGGACGGATATCCACAGGCCTGGCGCACCTTCGTGCTGTGCGGTGGGGCAGGACCC   2160
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Qy   2101  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  2160
Db   2101  CCTGGACGATATCCACAGGGCCTGGCCGTGCTGCCGTGTGCGGGCCCAGGACCCC  2160

Qy   2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGACGGGCGCCGTACGACACCATCCCCA   2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGACGGGCGCCGTACGACACCATCCCCA   2220

Qy   2221  GGACAGGCTCACGGAGGCTCATCGGCACATCATCAAACCCCAGAACACCCAGAACCCCAGAAC  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  GGACAGGCTCACGGAGGCTCATCGGCACATCATCAAACCCCAGAACACCCAGAACCCCAGAAC  2280

Qy   2281  TCGGTATGCCGTGGTCCAGAAGGCCGCGCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA   2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  TCGGTATGCCGTGGTCCAGAAGGCCGCGCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA   2340

Qy   2341  CGTCTCTTACCTTGACAGACCTCCAGCCGCTACATGCGACAGTTCGTGGCTCACCTGCAGGA  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  CGTCTCTTACCTTGACAGACCTCCAGCCGCTACATGCGACAGTTCGTGGCTCACCTGCAGGA  2400

Qy   2401  GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAG     2460
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Db   2401  GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAG     2460

Qy   2461  CAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCCACTCAGGGG     2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  CAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCCACTCAGGGG     2520

Qy   2521  CAAGTCCTACGTCCAGTGCCAGTGGGATCCCGCAGGGCTCCATCCTCTCGCACGTGCTCTG   2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  CAAGTCCTACGTCCAGTGCCAGTGGGATCCCGCAGGGCTCCATCCTCTCGCACGTGCTCTG   2580

Qy   2581  CAGCCTGTGTACGGCTACGGACCGGACACAAGCTGTTTGGTGACACTTCACCCACCACGGGGCT  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  CAGCCTGTGTACGGCTACGGACCGGACACAAGCTGTTTGGTGACACTTCACCCACCACGGGGCT  2640

Qy   2641  GCTCCTGCGTTTGGTGGATGAGTTCTTGTTCTTGGTGACACCTCACCTCACCCACGCGAAAAC  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  GCTCCTGCGTTTGGTGGATGAGTTCTTGTTCTTGGTGACACCTCACCTCACCCACGCGAAAAC  2700

Qy   2701  CTTCCTCAGGACCCTGGTCCGAGTGTCCGAGTATGGCTGCCTGAGTGGTGAACTTGCGGAA    2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  CTTCCTCAGGACCCTGGTCCGAGTGTCCGAGTATGGCTGCCTGAGTGGTGAACTTGCGGAA    2760

Qy   2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGGCCCTGGGTGGCCACGCGTTTTGTTCAGAT   2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGGCCCTGGGTGGCCACGCGTTTTGTTCAGAT   2820

Qy   2821  GCCGGCCACGCGCCGCTATTCCCCTGGTGCGCGCCTGCTGCGATACCCGGACCCTGGAGGT   2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  GCCGGCCACGCGCCGCTATTCCCCTGGTGCGCGCCTGCTGCGATACCCGGACCCTGGAGGT   2880

Qy   2881  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCCACCTTCAACCG   2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCCACCTTCAACCG   2940

Qy   2941  CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGGCTGAAGTG   3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGGCTGAAGTG   3000

Qy   3001  TCACAGCCTGTTTCTGGATTGCGAGTTGAACAGCCTCCAGACAGGTGCCACCAAACATCTA   3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  TCACAGCCTGTTTCTGGATTGCGAGTTGAACAGCCTCCAGACAGGTGCCACCAAACATCTA   3060

Qy   3061  CAAGATCCTCCTGCTCAGGCGTACAGGTTTCACGCATCGTGCTGCCAGCTCCCATTTCA    3120
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Db   3061  CAAGATCCTCCTGCTCAGGCGTACAGGTTTCACGCATCGTGCTGCCAGCTCCCATTTCA    3120

Qy   3121  TCAGCAAGTTTGGAAGAACCCACCATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT   3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  TCAGCAAGTTTGGAAGAACCCACCATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT   3180

Qy   3181  CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCCGC     3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCCGC     3240

Qy   3241  CGGCCCCTCTGCCCTCCGAGGCCGTGCAGTGGGTCAGTTGCCACCAAGCATTCCTGCTCAAGCT  3300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241  CGGCCCCTTCTGCCCTCTGCCCTCCGAGGCCGTGCAGTGGGTCAGTGCCACCAAGCATTCCTGCTCAAGCT  3300

Qy   3301  GACTCGACACCGTGTCACTCGACTGCCACTCCTGGGTCACTCGGACAGCCCAGACGCA      3360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301  GACTCGACACCGTGTCACTCGACTGCCACTCCTGGGTCACTCGGACAGCCCAGACGCCA     3360

Qy   3361  GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGAGGAGCCCGCAGCCAACCCGGC    3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361  GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGAGGCCGCAGCCAACCCGGC      3420

Qy   3421  ACTGCCCTCAAGACTTCAAGACCATCTGGACTGATGGCCACCCGCCCACCAGCCAGGCCGA   3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  ACTGCCCTCAAGACTTCAAGACCATCTGGACTGATGGCCACCCGCCCACCAGCCAGGCCGA   3480

Qy   3481  GAGCAGACCACCAGCAGCCCTGTCACGCGCGGCTCTCACGGAGGAGGAGGGGCCGGCC     3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  GAGCAGACCACCAGCAGCCCTGTCACGCGCGGCTCTCACGGAGGAGGAGGGGCCGGCC     3540

Qy   3541  CACACCCAGGCCCGCACCGCCGCTGGGAGTCGAGCGCTGAGTGAGTGTTTGGCCGAGGCCTG     3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  CACACCCAGGCCCGCACCGCCGCTGGGAGTCGAGCGCTGAGTGAGTGTTTGGCCGAGGCCTG     3600

Qy   3601  CATGTCCGCTGAAGGCTGAGTCTCCGGCTGCTGAGGCCTGAGGCCTCGGCTCGGCTCCACCCA   3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  CATGTCCGCTGAAGGCTGAGTCTCCGGCTGCTGAGGCCTGAGGCCTCGGCTCGGCTCCACCCCA   3660

Qy   3661  GAGTGTCCAGCACACTGCCGTCTTCACTTCCCACAGGCTCGGCGCTGGGCTCGGCTCCACCCCA  3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  GAGTGTCCAGCACACTGCCGTCTTCACTTCCCACAGGCTCGGCGCTGGGCTCGGCTCCACCCCA  3720

Qy   3721  GGGCCAGCTTTTCCTCACCGAGAGCCCGGCTTCCACTCCCCACTAGGAATAGTCCATCC      3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  GGGCCAGCTTTTCCTCACCGAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC     3780

Qy   3781  CCAGATTCGCCATTGTTCACCCGTCGCTTGGCTGTGAAGTTTGCCTTCCCACCCCCACCATCC   3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781  CCAGATTCGCCATTGTTCACCCGTCGCTTCACCCCGCTGCCTTGCCTTCCCACCCCCACCATCC   3840

Qy   3841  AGTGGAGACCCTGAGAAGGACCTGGGAGAGCTGGGAGCTCGGGAATTTGGACCAAAGGTGTG    3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841  AGTGGAGACCCTGAGAAGGACCTGGGAGAGCTGGGAGCTCGGGAATTTGGACCAAAGGTGTG    3900

Qy   3901  CCCTGTACACAGGCGAGGACCCTGCCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG     3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901  CCCTGTACACAGGCGAGGACCCTGCCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG     3960

Qy   3961  GAGGTGTGTGGGAGTAAAATATCTGAATATATGAGTTTTCAGTTTTCAGTTTTTGAAAAAA   4015
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961  GAGGTGTGTGGGAGTAAAATATCTGAATATATGAGTTTTCAGTTTTCAGTTTTTGAAAAAA   4015
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RESULT 9
PCT-US99-06898-1

; Sequence 1, Application PC/TUS9906898
; GENERAL INFORMATION:
APPLICANT: Gaeta, Federico C.A.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
TITLE OF INVENTION: Response to a Telomerase Antigen
FILE REFERENCE: 015389-003500PC
CURRENT APPLICATION NUMBER: PCT/US99/06898
CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: US 08/911,312
EARLIER FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: US 08/912,951
EARLIER FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: US 08/915,503
EARLIER FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: WO PCT/US97/17618

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; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
PCT-US99-06898-1
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Query Match         100.0%;  Score 4015;  DB 2;  Length 4015;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 4015;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy      1  GCAGGCGCTGCGTCCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC         60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GCAGGCGCTGCGTCCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC         60

Qy     61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT        120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT        120

Qy    121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCGCCCGGGCTGGCGCTGGTGCAGCGCGG        180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCGCCCGGGCTGGCGCTGGTGCAGCGCGG        180

Qy    181  GGACCCGGCGGCTTTCCGCGCGCCCCTCCTTCCGCGCCAGGTGTCCTGCCTGAAGGAAGT        240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GGACCCGGCGGCTTTCCGCGCGCCCCTCCTTCCGCGCCAGGTGTCCTGCCTGAAGGAAGT        240

Qy    241  ACGGCTGTCGCAGAGGCTGTGTCGAGCGCGGGCCCCGGGGGCCGCTGCCGGCGTCGGTGGC        300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ACGGCTGTCGCAGAGGCTGTGTCGAGCGCGGGCCCCGGGGGCCGCTGCCGGCGTCGGTGGC        300

Qy    301  CCGAGTGCTGCGACGGCTGTGGCCCGGGCGCCCCCCGGGGGGCCGCTGCCAGCTGGCTTCGC        360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CCGAGTGCTGCGACGGCTGTGGCCCGGGCGCCCCCCGGGGGGCCGCTGCCAGCTGGCTTCGC        360

Qy    361  GCTGCTGGACGGGGCCCGGCCTACCAGTGTGCGGGCCGCTGCCAGCTGCGCAGCTGCTCGGCGC        420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GCTGCTGGACGGGGCCCGGCCTACCAGTGTGCGGGCCGCTGCCAGCTGCGCAGCTGCTCGGCGC        420

Qy    421  CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCCGCGGCGTGGGGCGTGCTGCTGCCG        480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCCGCGGCGTGGGGCGTGCTGCTGCCG        480

Qy    481  CCGCGGTGGGGGACGACGCTGTGGTTCACCGTGGTTCACCTGCACGCTGCGGCCTGCGCCAG        540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CCGCGGTGGGGGACGACGCTGTGGTTCACCGTGGTTCACCTGCACGCTGCGGCCTGCGCCAG        540

Qy    541  GGCTCCCAGTCGCCTACCAGTGTGCGGGCCCGCGCCTACCAGTGTGCGGGCCCGCTGCCAC        600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GGCTCCCAGTCGCCTACCAGTGTGCGGGCCCGCGCCTACCAGTGTGCGGGCCCGCTGCCAC        600

Qy    601  TCAGGCCCGGCCCCGCCCACACGCTAGTGGACCTGGGATGCGAACGGGC        660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TCAGGCCCGGCCCCGCCCACACGCTAGTGGACCTGGGATGCGAACGGGC        660

Qy    661  CTGGAACCATAGCGTCAGGAGGTGGCGGGGTCCCCTGGGGCCCGCCGAGCCGCGGGTGCGAG        720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTGGAACCATAGCGTCAGGAGGTGGCGGGGTCCCCTGGGGCCCGCCGAGCCGCGGGTGCGAG        720

Qy    721  GAGGGCCGGGGGCAGTGCCAGCCGAAGTCTGCCGTGTGCCCAAGAGGGCCCAGGCGTGCGC        780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    721  GAGGGCCGGGGGCAGTGCCAGCCGAAGTCTGCCGTGTGCCCAAGAGGGCCCAGGCGTGCGC        780

Qy    781  TGCCCCTGAGCCCGGACGGCGAGCCCGTTGGGCAGGGGTCCTGGCAGGGGTCCTGGCAGGAC        840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TGCCCCTGAGCCCGGACGGCGAGCCCGTTGGGCAGGGGTCCTGGCAGGGGTCCTGGCAGGAC        840

Qy    841  GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTGTGGTGTCACCTGCACCGCGCGAAGAGC        900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTGTGGTGTCACCTGCACCGCGCGAAGAGC        900

Qy    901  CACCTCTTTGGAGGTGCGCTCTGCGGCACGCGCCACTCCACCATCCGTGTGGGCCGCCA        960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CACCTCTTTGGAGGTGCGCTCTGCGGCACGCGCCACTCCACCATCCGTGTGGGCCGCCA        960

Qy    961  GCACCAGCGCGGGCCCCATCCACACACGCTCCCTGGGACACCGCCCTTGTCC        1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  GCACCAGCGCGGGCCCCATCCACACACGCTCCCTGGGACACCGCCCTTGTCC        1020

Qy   1021  CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG        1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG        1080

Qy   1081  GCCCTCCTTCCTACTCAGCTCTCTGAGCGCTGGCGCTGGCGCTGGGAGCGCTCGTCGGTGGA        1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  GCCCTCCTTCCTACTCAGCTCTCTGAGCGCTGGCGCTGGCGCTGGGAGCGCTCGTCGGTGGA        1140

Qy   1141  GACCATCTTTCTGGGTTCCAGGCCCTGATGCGCAGCCACTACCGCGAGGTGCTGCCCCGCT        1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GACCATCTTTCTGGGTTCCAGGCCCTGATGCGCAGCCACTACCGCGAGGTGCTGCCCCGCT        1200

Qy   1201  GCCCCAGCGCTACTGGCAAATGCGGCGCCGGTGGCCGGTTCTGGAACCGCAGCGCGGCCA        1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  GCCCCAGCGCTACTGGCAAATGCGGCGCCGGTGGCCGGTTCTGGAACCGCAGCGCGGCCA        1260

Qy   1261  GTGCCCCTACGCGGTGCTCTCCGGGGAGGCCACTGCCCGCGCCAGGTCTCGTGGGCGGCGCCCAGC        1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  GTGCCCCTACGCGGTGCTCTCCGGGGAGGCCACTGCCCGCGCCAGGTCTCGTGGGCGGCGCCCAGC        1320

Qy   1321  AGCCGGTGCTGTGTGCCCGGGAGGCGGCGGCGAAGAACCGTGCCTGCCTGAAGGAGAGAGA        1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  AGCCGGTGCTGTGTGCCCGGGAGGCGGCGGCGAAGAACCGTGCCTGCCTGAAGGAGAGAGA        1380

Qy   1381  CACAGACCCCGTCGCCTTGGTCGGGCGCCTGCTGCGCCGGCGTGCGCCTGCTGCCTCGGCTTCGC        1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CACAGACCCCGTCGCCTTGGTCGGGCGCCTGCTGCGCCGGCGTGCGCCTGCTGCCTCGGCTTCGC        1440

Qy   1441  CGGCTTCGTGTCGGCGCCTGCTCGCCGGCTGCCCCCAGCAGCGCCTCTCGGGCGTCCCCTGGGGCTCCCAGGCA        1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  CGGCTTCGTGTCGGCGCCTGCTCGCCGGCTGCCCCCAGCAGCGCCTCTCGGGCGTCCCCTGGGGCTCCCAGGCA        1500

Qy   1501  CAACGAACGCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGAAGCATGCCAA        1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  CAACGAACGCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGAAGCATGCCAA        1560

Qy   1561  GCTCTCGCTGCACGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCCGCAG        1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  GCTCTCGCTGCACGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCCGCAG        1620

Qy   1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTGTCTGCCTGCTGCGGAGATCCTGGC        1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTGTCTGCCTGCTGCGGAGATCCTGGC        1680

Qy   1681  CAAGTTCCTCACTGGCTGATGAGTGTACGGTCGTCGTCGCTCTTTTCTACGGACTCGTCTTTTA        1740
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Db   1681  CAAGTTCCTCACTGGCTGATGAGTGTACGGTCGTCGTCGCTCTTTTCTACGGACTCGTCTTTTA        1740

Qy   1741  TGTCACGGAGGACCACGTTTCAAAGAACAGCAGCAGCAGCACACTTGAAGAGGTGCTCTGGAG        1800
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Db   1741  TGTCACGGAGGACCACGTTTCAAAGAACAGCAGCAGCAGCACACTTGAAGAGGTGCTCTGGAG        1800

Qy   1801  CAAGTTGCAAAGCATTGAATCAGACACAGCAGCACTTGAAGAGGTGCGGGAGCTGTC        1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  CAAGTTGCAAAGCATTGAATCAGACACAGCAGCACTTGAAGAGGTGCGGGAGCTGTC        1860
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Qy  2941 CGGCTTCAAGGCTGGGAGGAACATGTCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000
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Db  2941 CGGCTTCAAGGCTGGGAGGAACATGTCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000

Qy  3001 TCACAGCCTGTTCTGGATTGCAGTGAACAGCCTCCAGACGGTGTCACCAACATCTA 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 TCACAGCCTGTTCTGGATTGCAGTGAACAGCCTCCAGACGGTGTCACCAACATCTA 3060

Qy  3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCAGTTGTGCTGCAGCTCCATTTCA 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCAGTTGTGCTGCAGCTCCATTTCA 3120

Qy  3121 TCAGCAAGTTTGAAGAACCCCACCATTTTCCTGCGGCGTCATCTCTGACACGGCCTCCCT 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 TCAGCAAGTTTGAAGAACCCCACCATTTTCCTGCGGCGTCATCTCTGACACGGCCTCCCT 3180

Qy  3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGAGGATGTCGCTGGGGGCCAAGGGCCGC 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGAGGATGTCGCTGGGGGCCAAGGGCCGC 3240

Qy  3241 CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCGTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCGTGTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy  3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCCA 3360
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Db  3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCCA 3360

Qy  3361 GCTGAGTCGGAAGCTCCCGGGACGACCTGACGTGCCCGGAGGCCGCCAACCCGGC 3420
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Qy  3421 ACTGCCCTCAGACTTCAAGACCATCCTGACTGGCCACCCCGCCCAGAGCCAGGCCGA 3480
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Db  3421 ACTGCCCTCAGACTTCAAGACCATCCTGACTGGCCACCCCGCCCAGAGCCAGGCCGA 3480

Qy  3481 GAGGCAGACACCAGCAGCCCTGTCACGCCCGGCCTCACGGAGGGGGCGGCC 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GAGGCAGACACCAGCAGCCCTGTCACGCCCGGCCTCACGGAGGGGGCGGCC 3540

Qy  3541 CACACCCAGGCCCGCTGAGGAGTCGAGGGCCTGAGTGGTGTTTGGCCGAGGGCCTG 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CACACCCAGGCCCGCTGAGGAGTCGAGGGCCTGAGTGGTGTTTGGCCGAGGGCCTG 3600

Qy  3601 CATGTCCGGCTGAAGGCTGAGTGTCCCGCCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT 3660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CATGTCCGGCTGAAGGCTGAGTGTCCCGCCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT 3660

Qy  3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACCAGAGCCCGGCTCGCGCTCCCACCCA 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACCAGAGCCCGGCTCGCGCTCCCACCCA 3720

Qy  3721 GGGCCAGCTTTTCCTCCACTCCCACTAGGATAGTCCATCC 3780
         ||||||||||||||||||||||||||||||||||||||||
Db  3721 GGGCCAGCTTTTCCTCCACTCCCACTAGGAATAGTCCATCC 3780

Qy  3781 CCAGATTCGCCATTGTTCACCCCTTGCCTTCCTTGCCTTCCTGCGCCCCACCATCC 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 CCAGATTCGCCATTGTTCACCCCTTGCCTTCCTTGCCTTCCTGCGCCCCACCATCC 3840

Qy  3841 AGGTGGAGACCCTGGGAGTAAATATACTGAATATATGAGTTTTTCAGTTTTGACCAAGGTGTG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 AGGTGGAGACCCTGGGAGTAAATATACTGAATATATGAGTTTTTCAGTTTTGACCAAGGTGTG 3900

Qy  3901 CCCTGTACACAGGCGGAGGACCCTGCGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 CCCTGTACACAGGCGGAGGACCCTGCGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960

Qy  3961 GAGGTGCTGCTGGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAA 4015
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 GAGGTGCTGCTGGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAA 4015
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Qy  1861 GGAAGCAGAGGTCAGGCAGCATCGGGAGAGCCAGGCCCGCCCGCCCTGCTGCTCCAGACTCCG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GGAAGCAGAGGTCAGGCAGCATCGGGAGAGCCAGGCCCGCCCGCCCTGCTGCTCCAGACTCCG 1920

Qy  1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980

Qy  1981 CAGAACGTTCCCAGAGAAAAGAGGGCCGAGCGTCTCACCTGCGAAGGCACTGTT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTGCGAAGGCACTGTT 2040

Qy  2041 CAGCCGTGCTCAACTACGAGCGCGGCGGCGCGCCCGGCCTCCTGTGCCTCGTGCTGG 2100
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Db  2041 CAGCCGTGCTCAACTACGAGCGCGGCGGCGCGCCCGGCCTCCTGTGCCTCGTGCTGG 2100

Qy  2101 CCTGACGATATCCACAGGCCCTGGCGCACCTTCGTGCGTGCGGCCCAGGACCC 2160
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Db  2101 CCTGACGATATCCACAGGCCCTGGCGCACCTTCGTGCGTGCGGCCCAGGACCC 2160

Qy  2161 GCCGCCTGAGCGTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCCA 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCGCCTGAGCGTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCCA 2220

Qy  2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCAAACCCCAGAACACGTACTGCGTGCG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCAAACCCCAGAACACGTACTGCGTGCG 2280

Qy  2281 TCGGTATGCCGTGTCCAGAAGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TCGGTATGCCGTGTCCAGAAGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340

Qy  2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCACAGTTCGTGGCTCACCTGCAGGA 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCACAGTTCGTGGCTCACCTGCAGGA 2400

Qy  2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460

Qy  2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG 2520

Qy  2521 CAAGAACGTTCCTACGTCCAGTGCCAGGGGATCCCGATCCTCCATCTCTCCACGCTGCTCTG 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CAAGAACGTTCCTACGTCCAGTGCCAGGGGATCCCGATCCTCCATCTCTCCACGCTGCTCTG 2580

Qy  2581 CAGCCGTGTCTACGGCGACATGAGAACAAGCTGTTTCGGGGATTCGGCGGGGACGGGGCT 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CAGCCGTGTCTACGGCGACATGAGAACAAGCTGTTTCGGGGATTCGGCGGGGACGGGGCT 2640

Qy  2641 GCTCCTGGCGTTTGGTGTGGATGATTCTTGTTGGTGACACCTCACCTGACCGGCGAAAAC 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 GCTCCTGCGTTTGGTGTGGATGATTTCTTGTTGGTGACACCTCACCTGACCGGCGAAAAC 2700

Qy  2701 CTTCCTCAGGACCCTGGTCCCGAGTGTGCTGGTGAACTTGCCGAA 2760
         |||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CTTCCTCAGGACCCTGGTCCCGAGTGTGCTGGTGAACTTGCCGAA 2760

Qy  2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTCTCACCTTGTCAGAT 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTCTCACCTTGTTCAGAT 2820

Qy  2821 GCCGGCCCACGCGCTATTCCCCTGCTGCCGCGGCCTGCTGCGGCCGACCCCGACCCTGGAGGT 2880
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Db  2821 GCCGGCCCACGCGCTATTCCCCTGCTGCCGCGGCCTGCTGCGGCCGACCCCGACCCTGGAGGT 2880

Qy  2881 GCAGAGCGACTACTCCAGCTACTCCAGCGACCTCCATCAGAGCCCAGTCTCAACCTTCAACCG 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 GCAGAGCGACTACTCCAGCTACTCCAGCGACCTCCATCAGAGCCCAGTCTCAACCTTCAACCG 2940
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RESULT 10
PCT-US99-07097-1
; Sequence 1, Application PC/TUS9907097
; GENERAL INFORMATION:
;  APPLICANT: Morin, Gregg B.
;  APPLICANT: Geron Corporation
;  TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
;  FILE REFERENCE: 015389-003310PC
;  CURRENT APPLICATION NUMBER: PCT/US99/07097
;  CURRENT FILING DATE: 1999-03-31
;  EARLIER APPLICATION NUMBER: US 09/052,864
;  EARLIER FILING DATE: 1998-03-31
;  EARLIER APPLICATION NUMBER: US 09/128,354
;  EARLIER FILING DATE: 1998-08-03
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
;  LENGTH: 4015
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (56)..(3454)
;  OTHER INFORMATION: human telomerase reverse transcriptase (hTRT) cDNA
PCT-US99-07097-1

Query Match       100.0%;    Score 4015;   DB 2;   Length 4015;
Best Local Similarity  100.0%;    Pred. No. 0;
Matches 4015;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;
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Qy        1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAGCCCTGGCCCCCGGCCACCCCCGCGATGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAGCCCTGGCCCCCGGCCACCCCCGCGATGCC 60

Qy       61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCCGCGAGTGCT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCCGCGAGTGCT 120

Qy      121 GCGCCTGGCCACGTTCGTGCGGCGCCCCAGGGCTGGCCGGCTGGCAGCCCGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCGCCTGGCCACGTTCGTGCGGCGCCCCAGGGCTGGCCGGCTGGCAGCCCGG 180

Qy      181 GGACCCGGCCGGCTTTCCGCGCGCCGTGTGGCCCAGTGCCTGGTGTGCCTGGGACGC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGACCCGGCCGGCTTTCCGCGCGCCGTGTGGCCCAGTGCCTGGTGTGCCTGGGACGC 240

Qy      241 ACGGGTGTCTGTGCCCGCGCCCCGCGCCCTCCTTCCGCCTGTCCGCCTGAAGGAGCTGGTGGC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACGGGTGTCTGTGCCCGCGCCCCGCGCCCTCCTTCCGCCTGTCCGCCTGAAGGAGCTGGTGGC 300

Qy      301 CCGAGTGCTGCAGAGGCGTGCGGGGCCCCGCGGGGGCCCCCCGAGGGCGCGGCCTTCACCGTGCTGGCTTCGC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGAGTGCTGCAGAGGCGTGCGGGGCCCCGCGGGGGCCCCCCGAGGGCGCGGCCTTCACCGTGCTGGCTTCGC 360

Qy      361 GCTGTGCTGGACGGGGCCCCGGGGGGCCCCCCGAGGCCCTTCACCACCAGCGTGCCGCAGCTA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCTGTGCTGGACGGGGCCCCGGGGGGCCCCCCGAGGCCCTTCACCACCAGCGTGCCGCACTA 420

Qy      421 CCTGCCCAACACGGTGACCGACGCACCGTGGTGGGTTCGGGGACGGGCGGGCCCTGCGTGCTGCG 480
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Db      421 CCTGCCCAACACGGTGACCGACGCACCGTGGTGGGTTCGGGGACGGGCGGGCCCTGCGTGCTGCG 480

Qy      481 CGGCGTGGCGACGACTGCTTGGTTCACCTGGGGCACGCGCTCGCGCGCTCTTTGTCTGGT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CGGCGTGGCGACGACTGCTTGGTTCACCTGGGGCACGCGCTCGCGCGCTCTTTGTCTGGT 540

Qy      541 GGCTCCCAGTGCGCCTACCAGGTGTGCGGGGCCGCCACACGCTAGTGGACACCCCGAACCGGGC 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GGCTCCCAGTGCGCCTACCAGGTGTGCGGGGCCGCCACACGCTAGTGGACACCCCGAACCGGGC 600

Qy      601 TCAGGGCCCGGCCCCGCCGCCCCCCACCACGTAGTGGACACCCGAAGGGCGTCGGGATGCGAACGGGGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TCAGGGCCCGGCCCCGCCGCCCCCCACCACGTAGTGGACACCCGAAGGGCGTCGGGATGCGAACGGGGC 660
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Qy      661 CTGGAACCATAGCGTCAGGAGGCCGGGGTCCCCTGGGGCCTGCCCAGCCCCGGGTGGGTGCGAG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CTGGAACCATAGCGTCAGGAGGCCGGGGTCCCCTGGGGCCTGCCCAGCCCCGGGTGGGTGCGAG 720

Qy      721 GAGGCGCGGGGACGAGTGCCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCGTGGGGCC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GAGGCGCGGGGACGAGTGCCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCGTGGGGCC 780

Qy      781 TGCCCCTGAGCCGGAGCGGAGCACCCCGTTGGGCAGGGGTCCTGGGCAGGGGTCCTGGGCCACCCGGGCAGGAC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 TGCCCCTGAGCCGGAGCGGAGCACCCCGTTGGGCAGGGGTCCTGGGCAGGGGTCCTGGGCCACCCGGGCAGGAC 840

Qy      841 GGCTGGACCGAGTGACCGTGGTTTCTGTGGTGTGCACGCGCCACTCGCACCTGCCCAGACCCGCCGAAGAAGC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GGGTGGACCGAGTGACCGTGGTTTCTGTGGTGTGCACGCGCCACTCGCACCTGCCCAGACCCGCCGAAGAAGC 900

Qy      901 CACCTCTTTGGAGGGTGCGCTCTTGCAGCGCCACTCCACCATCCGTGGGCCGCCA 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 CACCTCTTTGGAGGGTGCGCTCTTGCAGCGCCACTCCACCATCCGTGGGCCGCCA 960

Qy      961 GGACCACGCGGGGCCCCATCACAATCGCGGCCACCACAGTCCCTGGGACACGGCCTTGTCC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 GCACCACGCGGGGCCCCCATCACAATCCACCATCCACCACAGTCCCTGGGACACGGCCTTGTCC 1020

Qy     1021 CCCGGTGTACGCGCGAGACCAAGCACTTCCTCACTCCTCAGGCGGCGACAAGGAGCAGCTGCG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 CCCGGTGTACGCGCGAGACCAAGCACTTCCTCTCTCCTCAGGCGGCGACAAGGAGCAGCTGCG 1080

Qy     1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCAGCCCTGACTGCGCTCGAGGCTCGTGA 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCAGCCCTGACTGCGCTCGAGGCTCGTGA 1140

Qy     1141 GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGTGCCAGCCACTACCGCTGCCCCGGCCT 1200
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Db     1141 GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGTGCCAGCCACTACCGCTGCCCCGCCT 1200

Qy     1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGCAGGCGTGGTTGCAGCCCGCA 1260
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Db     1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGCAGGCGTGGTTGCAGCCCGCA 1260

Qy     1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCGCTGCGCGAGCTGCGCTCACCCAGC 1320
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Db     1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCGCTGCGCGAGCTGCGCTCACCCAGC 1320

Qy     1321 AGCCGGTGTCTGTGCCCCGGAGAAGCCCTGGCCAGCAGCCCTGGCAGGTGTA 1380
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Qy     1381 CACAGACCCCGGCTCGCCGTCGCCAGCAGCACACAGCCCCCTGGGGTGCCCCGCCA 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 CACAGACCCCGGCTCGCCGTCGCCAGCAGCACACAGCCCCCTGGGGTGCCCCGGCA 1440

Qy     1441 CGGCTTCGTGCGGACGGGCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA 1500
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Qy     1561 GCTCTCGCTTGCTGCAGGAGCTGACGTGAGATGAGCGTGCCCGGGACTGCGTGCTGCAG 1620
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Qy     1621 GAGCCAGGGGTTGCCACTGCGTGCCGGCCGCGTACCAGCTCCGGTGCCAC 1680
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Db     1621 GAGCCAGGGGTTGGCTGTCGTGTTCCGGCCCCGCAGACACCCGTCGCGGATCCTGGCC 1680

Qy     1681 CAAGTTCCTGCACTGGCTGATGAGTGTACGTCGTCAGGTCTTTCTTTTA 1740
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Db     1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCAGGTCTTTCTTTTA 1740
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Qy  1741  TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTTCTACGGAAGAGTGTCTGGAG  1800
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Db  1741  TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTTCTACGGAAGAGTGTCTGGAG  1800

Qy  1801  CAAGTTGCAAAAGCATTGGAATCAGATCAGACGCACTTGAAGAGGTGCAGCTGCGTGTC  1860
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Db  1801  CAAGTTGCAAAAGCATTGGAATCAGATCAGACGCACTTGAAGAGGTGCAGCTGCGTGTC  1860

Qy  1861  GGAAGCAGGAGGTCAGGCAGCATCGGGAAGCAGGCCAGCCAGGCCCCGCCCAGACTCCG  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  GGAAGCAGGAGGTCAGGCAGCATCGGGAAGCAGGCCAGCCAGGCCCCGCCCAGACTCCG  1920

Qy  1921  CTTCATCCCAAGCCTGACGGCTGCCGCGATTGTGAACATGGACTACGTCGTGGGAGC    1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CTTCATCCCAAGCCTGACGGCTGCCGCGATTGTGAACATGGACTACGTCGTGGGAGC    1980

Qy  1981  CAGAAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTTCACCTCACCTGTGAAGGCACTGTT  2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAGAAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTTCACCTCACCTGTGAAGGCACTGTT  2040

Qy  2041  CAGCGTGCTCAACTACGAGCGGCGGCGGCCCCGGCCCTCCTGCGCCGCTCTGTCTGCTGG  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CAGCGTGCTCAACTACGAGCGGCGGCGGCCCCGGCCCTCCTGCGCCGCTCTGTCTGCTGG  2100

Qy  2101  CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGCGGGCCCCAGGACCC  2160
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Db  2101  CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGCGGGCCCCAGGACCC  2160

Qy  2161  GCGCCCTGAGCTGTACTTGTCAAGGTGGATGTGACGGCGGCGTACGACACCATCCCCCA   2220
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Db  2161  GCGCCCTGAGCTGTACTTGTCAAGGTGGATGTGACGGCGGCGTACGACACCATCCCCCA   2220

Qy  2221  GGACAGGGCCACGGAGGTCATCGCCAGCATCAAAACCCAGAACCCAGAACACGTACTGCG  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGACAGGGCCACGGAGGTCATCGCCAGCATCAAAACCCAGAACCCAGAACACGTACTGCG  2280

Qy  2281  TCGGTATGCCGTGCTGTCCAGAAGGCACGTCCGACAAGGCCTTCAAGAGCCA          2340
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Db  2281  TCGGTATGCCGTGCTGTCCAGAAGGCACGTCCGACAAGGCCTTCAAGAGCCA          2340

Qy  2341  CGTCTCTACCTTGACAGACCTCCAGAGTTCGACAGTTCGTGGCTCACCTGCAGGA       2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGTCTCTACCTTGACAGACCTCCAGAGTTCGACAGTTCGTGGCTCACCTGCAGGA       2400

Qy  2401  GACCAGCCCGCTGAGGGATGCCGTCGTCGTCGTCCTGAATGAGGCCAG             2460
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Db  2401  GACCAGCCCGCTGAGGGATGCCGTCGTCGTCGTCCTGAATGAGGCCAG             2460

Qy  2461  CAGTGGCCTCTTCGACGTCTTCGCAGGGGATCCGCAGAGTTCGGCGGGATCAGGGG      2520
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Db  2461  CAGTGGCCTCTTCGACGTCTTCGCAGGGGATCCGCAGAGTTCGGCGGGATCAGGGG      2520

Qy  2521  CAAGTCCTACGTGGTTGGCGTTCTTGTTGGTGACAACTGGCGGTGCTCCCACCGTGCTCTG  2580
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Db  2521  CAAGTCCTACGTGGTTGGCGTTCTTGTTGGTGACAACTGGCGGTGCTCCCACCGTGCTCTG  2580

Qy  2581  CAGCCAGCTTTCGGTTTGGTTGGTGACACCTCACCTCACCCACCCGCGAAAAC          2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CAGCCAGCTTTCGGTTTGGTTGGTGACACCTCACCTCACCCACCCGCGAAAAC          2640

Qy  2641  GCTCCTCGCGTTCTTGTTGGTGATGATTCTTGTTCTTGGTGACACCTCACCCGGAA       2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCTCCTCGCGTTCTTGTTGGTGATGATTCTTGTTCTTGGTGACACCTCACCCGGAA       2700

Qy  2701  CTTCCTCAGGACTTCGGTTCCTGTGGTTGGTGTCCTGAGTATGCGTGCGGTGACTTGCGGAA  2760
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Db  2701  CTTCCTCAGGACTTCGGTTCCTGTGGTTGGTGTCCTGAGTATGCGTGCGGTGACTTGCGGAA  2760

Qy  2761  GACAGTGGTGAACTTCCCCTGTAGAAGACCAGGACCCTGGCCACGGCCTTTTGTTCAGAT   2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  GACAGTGGTGAACTTCCCCTGTAGAAGACCAGGACCCTGGCCACGGCCTTTTGTTCAGAT   2820

Qy  2821  GCCGGCCCCACGGCCTATTCCCGTGGTGCGGGCCTATTCCCTGGTGCTGCTGGTGGTGGCGACCTGGATGGT  2880
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Db  2821  GCCGGCCCCACGGCCTATTCCCGTGGTGCGGGCCTATTCCCTGGTGCTGCTGGTGGTGGCGACCTGGATGGT  2880
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Qy  2821  GCGAGCGACTACTCCAGCTATGCCCGGACCTGCTGCCTGGTGGATCAGCGACCTCTCACCTTCAACCG  2940
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Db  2881  GCAGCGGCGACTACTCCAGCTATGCCCGGACCTGCTGCCTGGTGGATCAGCGACCTCTCACCTTCAACCG  2940

Qy  2941  CGGCTTCAAGGCTGGGAGGAACATGGTCGCAAACTCTTGGGGTCTTGCGGGTCTGGGAGTG  3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  CGGCTTCAAGGCTGGGAGGAACATGGTCGCAAACTCTTTGGGGTCTTGCGGGTCTGGGAGTG  3000

Qy  3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGGCCTCAGACGGTGTGCACCAACATCTA  3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGGCCTCAGACGGTGTGCACCAACATCTA  3060

Qy  3061  CAAGATCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCATTTCA  3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  CAAGATCCTCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCATTTCA  3120

Qy  3121  TCAGCAAGTTGAAGAAGCCCCACCATTTTCCTTGCCGCGTCATCCTGCTGACGACGTG  3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  TCAGCAAGTTGAAGAAGCCCCACCATTTTCCTTGCCGCGTCATCCTGCTGACGACGTG  3180

Qy  3181  CTGGTACTCCATCCTGAAAGCCAGGATGTCGCTGGGGGGGCCAAGGGCGGCCGGC      3240
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Db  3181  CTGCTACTCCATCCTGAAAGCCAGGATGTCGCTGGGGGGGCCAAGGGCGGCCGGC      3240

Qy  3241  CGGCCCTCTGCCCTGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT        3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  CGGCCCTCTGCCCCTGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT        3300

Qy  3301  GACTCGACACCGTGTCACCTAGCTGCCACTCCTGGGTCACGGGACCGCCAGCCAGACGCA  3360
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Db  3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGTCACGGGACAGCCCAGACGCA      3360

Qy  3361  GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCCTGAGGCCGAGTCGTGAGGCCGGC  3420
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Db  3361  GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCCTGAGGCCGAGTCGTGAGGCCGGC  3420

Qy  3421  ACTGCCCTCAGACTTCAAGACCATCCAGGACACGCCGGCGATGGCCAGGCCAGGCCAGGCA  3480
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Db  3421  ACTGCCCTCAGACTTCAAGACCATCCAGGACACGCCGGCGATGGCCAGGCCAGGCCAGGCA  3480

Qy  3481  GAGCAGACACCAGCAGCCCTGTCACGCCCGGCGTCCAGGAGGGCGGCC             3540
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Db  3481  GAGCAGACACCAGCAGCCCTGTCACGCCCGGCGTCCAGGAGGGCGGCC             3540

Qy  3541  CACACCCAGGCCCCGCACCCGTGGGAGTCTGAGGTCTGAGAGTGTTTGCCGAGGCCTG    3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  CACACCCAGGCCCCGCACCCGTGGGAGTCTGAGGTCTGAGAGTGTTTGCCGAGGCCTG    3600

Qy  3601  CATGTCCGGCTGGCTCCGGCTCGAGTGTCGTCCGGCCTGAGCGAGTGTCGAGCCAGGGCT  3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  CATGTCCGGCTGGCTCCGGCTCGAGTGTCGTCCGGCCTGAGCGAGTGTCGAGCCAGGGCT  3660

Qy  3661  GAGTGTCCAGCTTTCACTTCACCGCGCTTCACTTCCCCACCAGGCTGGCGCCTCCACCCCA  3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  GAGTGTCCAGCTTTTCCTTCACCGCGCTTCACTTCCCCACCAGGCTGGCGCCTCCACCCCA  3720

Qy  3721  GGGCCAGCGTTTCCTCACCAGGAGCCCGGCTTCCGCCCTGCCTCTGGACTCTGGAATAGTCCATCC  3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  GGGCCAGCGTTTTCCTCACCAGGAGCCCGGCTTCCGCCCTGCCTCCTGGACTCTGGAATAGTCCATCC  3780

Qy  3781  CCAGATTCGCCATTGTTCACCCCGCCCTGGGAGCTTCCTTCCGCCTTGCCTTCCCCCACCACCATCC  3840
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Db  3781  CCAGATTCGCCATTGTTCACCCCGCCCTGGGAGCTTCCTTCCGCCTTGCCTTCCCCCACCACCATCC  3840

Qy  3841  AGGTGGAGACCCTGGCTCCTGTAGAAGACCGAGAAGGCGTTCGGGAATTGGAGTGACCAAAGGTGTG  3900
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Db  3841  AGGTGGAGACCCTGGCTCCTGTAGAAGACCGAGAAGGCGTTCGGGAATTTGGAGTGACCAAAGGTGTG  3900

Qy  3901  CCCTGTACACAGGTGGAGGACCCTGGCCTGTGCGGGCCACCTGGATGGGGTCCCTGTGGGCAAATTGGGGG  3960
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Db  3901  CCCTGTACACAGGTGGAGGACCCTGGCCTGTGCGGGCCACCTGGATGGGGTCCCTGTGGGCAAATTGGGGG  3960
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Db  3901  CCCTGTACACAGGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG  3960
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Qy  3961  GAGGTGCTGTGGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA  4015
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  GAGGTGCTGTGGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA  4015

RESULT 11
PCT-US99-07160-1
; Sequence 1, Application PC/TUS9907160
; GENERAL INFORMATION:
;  APPLICANT: Cech, Thomas R.
;  APPLICANT: Lingner, Joachim
;  APPLICANT: Nakamura, Toru
;  APPLICANT: Chapman, Karen B.
;  APPLICANT: Morin, Gregg B.
;  APPLICANT: Harley, Calvin B.
;  APPLICANT: Andrews, William H.
;  APPLICANT: Geron Corporation
;  APPLICANT: University Technology Corporation
; TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting
; TITLE OF INVENTION: Telomerase Reverse Transcriptase
; FILE REFERENCE: 015389-003610PC
; CURRENT APPLICATION NUMBER: PCT/US99/07160
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER: US 08/724,643
; EARLIER FILING DATE: 1996-10-01
; EARLIER APPLICATION NUMBER: US 08/844,419
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: US 08/846,017
; EARLIER FILING DATE: 1997-04-25
; EARLIER APPLICATION NUMBER: US 08/851,843
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: US 08/854,050
; EARLIER FILING DATE: 1997-05-09
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 09/052,919
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
PCT-US99-07160-1

Query Match      100.0%;  Score 4015;  DB 2;  Length 4015;
Best Local Similarity  100.0%;
Matches 4015;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1  GCAGGCGTCGCGTCCCGCTGCCGAGCCGTGCGCTCCCGCTGCCGAGCCGTGCGGATGCC  60
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Db     1  GCAGGCGTCGCGTCCCGCTGCCGAGCCGTGCGCTCCCGCTGCCGAGCCGTGCGGATGCC  60
Qy    61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCGCTGCCGAGCCGTGCGGATGCC  120
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Qy  2281 TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340
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Db  2281 TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGGA 2340

Qy  2341 CGTCTCTACCTTGACAGACTCCAGCCTCCAGCCGTCACAGTTCGTGGCTCACCTGCAGA 2400
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Db  2341 CGTCTCTACCTTGACAGACTCCAGCCTCCAGCCGTCACAGTTCGTGGCTCACCTGCAGGA 2400

Qy  2401 GACCAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG 2460
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Db  2401 GACCAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG 2460

Qy  2461 CAGTGGCCTCTTCGACGTCTTCATCTTCGACGTCTTCATCTGCCACCACGGTGCCACAGGG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGTGGCCTCTTCGACGTCTTCATCTTCGACGTCTTCATCTGCCACCACGGTGCCATCAGGGG 2520

Qy  2521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCCACGCTGCTCTG 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG 2580

Qy  2581 CAGCCTGTGCTACGGCGACATGGAGAACAAGAGCTGTTTGCGGGGACTTCGGCGGGACGGGCT 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CAGCCTGTGCTACGGCGACATGGAGAACAAGAGCTGTTTGCGGGGATTCGGCGGGACGGGCT 2640

Qy  2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGCAAAAC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 GCTCCTGCGTTGGTGGATGATTTCTTGTTGGTGCACCTCACCTCACCCACGCGCAAAAC 2700

Qy  2701 CTTCCTCAGGACCCGGTCCGAGTGTCCCTGAGTATGCCCGGACTCGCGTGGTGAACTTGCGGAA 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CTTCCTCAGGACCCGGTCCGAGTGTCCCTGAGTATGCCCGGACTCGCGTGGTGAACTTGCGGAA 2760

Qy  2761 GACAGTGGTGAACTTCCCTGTAGAACGAGAGGCCCTGGGTGGCACGGCTTTGTTCAGAT 2820
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Db  2761 GACAGTGGTGAACTTCCCTGTAGAACGAGAGGCCCTGGGTGGCACGGCTTTGTTGTTCAGAT 2820

Qy  2821 GCCGGCCCACGGCCTATTCCCCTGTGCGCGCCTGCTGCTGGATACCCGGACCCTGGAGGT 2880
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Db  2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTGTGCTGCAGCTCCACCTTCAACCG 2940

Qy  2941 CGGCTTCAAGGCTGGGAGGAACAATGCGTCGCGCAAACTCTTTGGGGTTCTTGCGGGTGAAGTG 3000
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Db  2941 CGGCTTCAAGGCTGGGAGGAACAATGCGTCGCGCAAACTCTTTGGGGTTCTTGCGGGTGAAGTG 3000

Qy  3001 TCACAGCCTGTTCTGTTTCTGGATTTGCAGTGGAGTGAACAGCCTCCAGACGGTGTGACCAACATCTA 3060
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Db  3061 CAAGATCCTCTGCGCTGCAGGCGTACAGGTTCACGCATGTGCTGCTGCAGCTCCCAGTTTCA 3120

Qy  3121 TCAGCAAGTTTGGAAGAACCCACATTTTCCTGCGCGTCATCTCTGACACGGGCTCCCT 3180
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Qy  3181 CTGCTACTCCATCCATCCTGAAAGCCAAGACGCCAGGATGTGTCGCTCCTGGGGGCGCGC 3240
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Db  3181 CTGCTACTCCATCCATCCTGAAAGCCAAGACGCCAGGATGTCGCTCCTGGGGGCGCGC 3240

Qy  3241 CGGGCCCTCTGCCCTCCGAGGCGTGCAGTGGCTGGTGCTGCTGCCAAGCATTCCTGCTCAAGCT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CGGGCCCTCTGCCCTCCGAGGCGTGCAGTGGCTGGTGCTGCTGCCAAGCATTCCTGCTCAAGCT 3300

Qy  3301 GACTCGACACCGTGTCCACTCGCCCAGGACCCGGAGCCACACTGCGCTACTGCGTGCGCG 3360
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Db  3301 GACTCGACACCGTGTCCACTCGCCCAGGACCCGGAGCCACACTGCGCTACTGCGTGCGCA 3360

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Qy  1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCCTGTTTCTGCTGAGCTGCTGCTGGGAACCACGCGGCA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCCTGTTTCTGCTGAGCTGCTGCTGGGAACCACGCGGCCA 1260

Qy  1261 GTGCCCTACGGGGTGCTCCCTCAAGACGCACTCCCGCCGCTGCGGGCTGCGCGTCACCCCAGC 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GTGCCCCTACGGGGTGCTCCCTCAAGACGCACTCCCGCCGCTGCGGGCTGCGCGTCACCCCAGC 1320

Qy  1321 AGCCGGTGTCTGTGCCCGGAGAAGCCCAGGGCTCGTGTGGGGCGCCCCCGAGGAGGAGGA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 AGCCGGTGTCTGTGCCCGGAGAAGCCCAGGGCTCGTGTGGGGCGCCCCCGAGGAGGAGGA 1380

Qy  1381 CACAGACCCCCGTGCCGCTGGTGCAGTCTCCCGCCAGCACAGACCCCTGCGAGGTGTA 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CACAGACCCCCGTGCCGCTGGTGCAGTCTCCGCCAGCACAGACCCCTGCGAGGTGTA 1440

Qy  1441 CGGCTTCGTGCGGGCCTGCCTGGCTGGTGCCCCGGCTCTGGGGCTCCCAGGCA 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CGGCTTCGTGCGGGCCTGCCTGGCTGGTGCCCCGGCTCTGGGGCTCCCAGGCA 1500

Qy  1501 CAACGAACGCCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 CAACGAACGCCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

Qy  1561 GCTCCTGCGCTGCAGGAGCGTGACGTGGAAGATGACGCTGCGCGGACTGCGCTTGGCTGCCGCAG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1621 GAGCCCAGGGGTTGGCTGTGTTCCGGGCCAGAGCACCGTCTCGCGTGAGGAGATCCTGGC 1680

Qy  1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGTGTTGTACGTCAGTGTCTTTCTTTTA 1740
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Db  1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGTGTTGTACGTCAGTGTCTTTCTTTTA 1740

Qy  1741 TGTCACGGAGACCACGTTTCAAAAGAACACAGGCTCTCTTTTTCTACCGGAGAGTGTCTGGAGG 1800
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Qy  1801 CAAGTTGCAAAGCATTGGAATCAGAGAGCGCACTTGAAGAGGGTGCAGCTGCGGGAGCGTGTC 1860
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Db  1801 CAAGTTGCAAAGCATTGGAATCAGAGAGCGCACTTGAAGAGGGTGCAGCTGCGGGAGCGTGTC 1860

Qy  1861 GGAAGCAGAGGTCAGCGCAGCATCGGGAAGCCAGCCAGCCCTGCGACTCCG 1920
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Db  1861 GGAAGCAGAGGTCAGCGCAGCATCGGGAAGCCAGCCAGCCCTGCGACTCCG 1920

Qy  1921 CTTCATCCCCAAGCCTGACGGGCTGCCGCCGATTGTGAACATGCTCGTCGGGAGC 1980
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Qy  1981 CAGAACGTTCCGCAGAGAAAAGAGGGGCGGCCGAGCGTCTCACCTCGAAGGCCACTGTT 2040
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Db  1981 CAGAACGTTCCGCAGAGAAAAGAGGGGCGGCCGAGCGTCTCACCTCGAAGGCCACTGTT 2040

Qy  2041 CAGCGGTGCTCAACTACGAGCGGGCCTCCTGTGCGCCCAGGACCCG 2100
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Qy  2101 CCTTGCAGCGATATCCGGAGGTCATCGGAGTCATCAAACCCCCAGGGACCCG 2160
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Db  2101 CCTTGGACGATATCCGGAGGTCATCGGAGTCATCAAACCCCCAGGGACCCG 2160

Qy  2161 GCCGCCCTCGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCCGCTACGACACCATCCCCCA 2220
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Db  2161 GCCGCCCTCGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCCGCTACGACACCATCCCCCA 2220

Qy  2221 GGACAGGTCATCACGGAGGTCATCGGCCAGAGCATCAAACCCCAGAGAACACTACTGCGTGCG 2280
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Db   3361 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   GCTGAGTCGGAAGTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCCAGCCAGGCCGGC 3420

Qy   3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA 3480
Db   3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA 3480

Qy   3481 GAGCAGACACCAGCAGCCCTGTCACGCCGGCCTCTACGTCCAGGGAGGGAGGGGCGGCC 3540
Db   3481 GAGCAGACACCAGCAGCCCTGTCACGCCGGCCTCTACGTCCAGGGAGGGAGGGGCGGCC 3540

Qy   3541 CACACCCAGGCCCGCCACCGCCACCCGCTGAGTGAGTGTTTGGCCGAGGCCTG 3600
Db   3541 CACACCCAGGCCCGCCACCGCCACCCGCTGAGTGAGTGTTTGGCCGAGGCCTG 3600

Qy   3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCCGAGTGTCAGCCAAGGGCT 3660
Db   3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCCGAGTGTCAGCCAAGGGCT 3660

Qy   3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGCCTGGCCGTCCTCCACCCCCA 3720
Db   3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGCCTGGCCGTCCTCCACCCCCA 3720

Qy   3721 GGGCCAGCTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
Db   3721 GGGCCAGCTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780

Qy   3781 CCAGATTCGCCATTGTTCACCCGTTGCCTTCACCATCCTCGGGAATTGGAGTGACCAAAGGTGTG 3840
Db   3781 CCAGATTCGCCATTGTTCACCCGTTGCCTTCACCATCCTCGGGAATTGGAGTGACCAAAGGTGTG 3840

Qy   3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGAATTGGAGTGACCAAAGGTGTG 3900
Db   3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGAATTGGAGTGACCAAAGGTGTG 3900

Qy   3901 CCCTGTACACAGGCCGGAGACCCGGAGGACCCTGGGTCCGTGGGTGGTCAAATTGGGGG 3960
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Qy   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAA 4015
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RESULT 12
US-08-974-549-1
; Sequence 1, Application US/08974549
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 726
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hTRT"
; OTHER INFORMATION: /note= "human telomerase reverse
; OTHER INFORMATION: transcriptase (hTRT) catalytic protein
; OTHER INFORMATION: component"
US-08-974-549-1

Query Match   100.0%; Score 4015; DB 14; Length 4015;
Best Local Similarity   100.0%;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCTGGCCCCGGCCACCCCCGCGATGCC 60
Db   1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCTGGCCCCGGCCACCCCCGCGATGCC 60

Qy   61 GGGCGGCTCCCCGCTGCCGAGCCGTGCCTGCTCCCTGCGCGTCCGCTCCCTGCGCGTCCGCTCCGCGAGGTGCT 120
Db   61 GGGCGGCTCCCCGCTGCCGAGCCGTGCCTGCTCCCTGCGCGTCCGCTCCCTGCGCGTCCGCTCCGCGAGGTGCT 120

Qy   121 GCCGCTGCCAGTTCGTGCGGCGCCGGCCGGCCCTGGCGGCCCTGGGCGGCGG 180
Db   121 GCCGCTGCCAGTTCGTGCGGCGCCGGCCGGCCCTGGCGGCCCTGGGCGGCGG 180

Qy   181 GGACCCCGGCGGCTTCCGCGGCCGGCCAGTGCGCTGCCGGCTGCCTGGTGCGTGCGCCGGGGGACGC 240
Db   181 GGACCCCGGCGGCTTCCGCGGCCGGCCAGTGCGCTGCCGGCTGCCTGGTGCGTGCGCCGGGGGACGC 240

This page is a dense DNA sequence alignment presented in two blocks, each consisting of paired query (Qy) and database (Db) sequence rows with alignment bars (||||) between them, labeled with sequence position numbers.

Left block (positions 241–1380):

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Qy   241  ACGGCCGCCCCCCGCCGCCCTCCTTCCGCCCCAGGCTGTCCTGCCTGAAGGAGCTGGTGGC  300
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Db   241  ACGGCCGCCCCCCGCCGCCCTCCTTCCGCCCCAGGCTGTCCTGCCTGAAGGAGCTGGTGGC  300

Qy   301  CCGAGTGCTGCAGAGCGGTGCGCCGGGGCCCCCCGAGCGCGCGAAGAACGTGCTGGCCTTCGC  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CCGAGTGCTGCAGAGCGGTGCGCCGGGGCCCCCCGAGCGCGCGAAGAACGTGCTGGCCTTCGC  360

Qy   361  GCTTGCTGGACGGGGCCCGCGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA  420
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Db   361  GCTTGCTGGACGGGGCCCGCGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA  420

Qy   421  CCTGCCCAACACGTGACCGACGCACTGCGGGGCGGGGCCGTGGGGGCTGCTGCTGCGG  480
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Db   421  CCTGCCCAACACGTGACCGACGCACTGCGGGGCGGGGCCGTGGGGGCTGCTGCTGCGG  480

Qy   481  CCCGTGGGCGACGACGTGCTGTTCACCTGCTGGCACGCTGCGCGCCGCTCTTTGCTGCTGGT  540
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Qy   541  GGCTCCCAGCTGCGCCCTACCAGGTGTGCGGGGCCCGTGTACCAGCTCGGCCCTGCCAC  600
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Db   541  GGCTCCCAGCTGCGCCCTACCAGGTGTGCGGGGCCCGTGTACCAGCTCGGCCCTGCCAC  600

Qy   601  TCAGGCCCGCCCGCCCACACGCTAGTGACCCCGAAGGCGTCTGGGATGCGAACGGGC  660
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Qy   661  CTGGAACCATAGCGTCAGGGAGGCCGGGGCCGGGCCTGCCCCTGGGCCTGCCCAGCCCGGGTGCGCGC  720
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Db   661  CTGGAACCATAGCGTCAGGGAGGCCGGGGCCGGGCCTGCCCCTGGGCCTGCCCAGCCCGGGTGCGGAG  720

Qy   721  GAGGCGCGGGGGCCAGTGACCGTGGTTTCGTGTGTCACCAAGTCTGCCCAGAGGGTCTGGGGCCGTGGCGC  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  GAGGCGCGGGGGCCAGTGACCGTGGTTTCGTGTGTCACCAAGTCTGCCCAGAGGGGTCTGGGGCCGTGGCGC  780

Qy   781  TGCCCTGAGCCCGGAGCCGACGGCCGTTGGGCAGGGTCCGTTGGGCAGGGTCCGTTGGGCAGGGGTCGGGAC  840
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Qy   841  GCGTGGACCGAGTGACCGTGGTTTCTGTGTCACCTGACGCTGCCCACCTCCTCAGGCGACAAGGAGCAGCTGCGG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GCGTGGACCGAGTGACCGTGGTTTCTGTGTCACCTGACGCTGCCCACCTCCTCAGGCGACAAGGAGCAGCTGCGG  900

Qy   901  CACCTCTTTGGAGGGTGCGCCTCTCTGGCACGGCCGCCACTCCACCCATCCGTGGGCCGCCA  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CACCTCTTTGGAGGGTGCGCCTCTCTGGCACGGCCGCCACTCCACCCATCCGTGGGCCGCCA  960

Qy   961  GCACCACGCGGGGCCCCCATCCACATCGGGCCACCAGGTCCCTGGGACGCCCAGGCCCTGTCC  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  GCACCACGCGGGGCCCCCATCCACATCGGGCCACCAGGTCCCTGGGACGCCCAGGCCCTGTCC  1020

Qy  1021  CCCCAGAGCCTACGGCCCCCCGTTTCTGAGCTGCGCCAGGCTGCTCAAGGAGCAGCTGCG  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  CCCCAGAGCCTACGGCCCCCCGTTTCTGAGCTGCGCCAGGCTGCTCAAGGAGCAGCTGCG  1080

Qy  1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCGACTGGCCGCTGGCCGCTCGTCGGA  1140
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Db  1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCGACTGGCCGCTGGCCGCTCGTCGGA  1140

Qy  1141  GACCATCTTTCTGGGTTCCAGGGCCCTGGAATGCCAAGGCTCCCCGCAGGTTGCCCCGGCCT  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GACCATCTTTCTGGGTTCCAGGGCCCTGGAATGCCAAGGCTCCCCGCAGGTTGCCCCGGCCT  1200

Qy  1201  GCGCCAGCCTACTGCCAAATGCGGCCCCGTTTCTGGAGCTGCTTGGGAACCACGCGGCA  1260
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Db  1201  GCGCCAGCCTACTGCCAAATGCGGCCCCGTTTCTGGAGCTGCTTGGGAACCACGCGGCA  1260

Qy  1261  GTCCCCTACGGGGTGCTCCTCAAGACGCACTGCGCCCGCTGCGAGCTGCGCGTCACCCCAGC  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  GTCCCCTACGGGGTGCTCCTCAAGACGCACTGCGCCCGCTGCGAGCTGCGCGTCACCCCAGC  1320

Qy  1321  AGCGGTGTCGTGTGCCCGGAGAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAGGA  1380
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Right block (positions 1321–2460):

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Db  1321  AGCCGGTGTCGTGTGCCCGGAGAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAGGA  1380

Qy  1381  CACAGACCCCGTCGGCTCTGGTGCAGCTGCTCTCCCGCCAGCACAGCAGCCCTGGCCAGGTGTA  1440
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Db  1381  CACAGACCCCGTCGGCTCTGGTGCAGCTGCTCTCCCGCCAGCACAGCAGCCCTGGCCAGGTGTGA  1440

Qy  1441  CGGCTTCGTGCGGGGCCTGCTGCCTGCGCCGCCGCGCCTGGTGCCCCGCCTCTGGGGCGTCCAGGCA  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  CGGCTTCGTGCGGGGCCTGCTGCCTGCGCCGCCGCGCCTGGTGCCCCGCCTCTGGGGGTCCAGGCA  1500

Qy  1501  CAACGAACCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  CAACGAACCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560

Qy  1561  GCTCTCGCTGCAGGAGCTGACGTGCGGGACTGCGGGACTGCGGGACTGCGGGGCTGCGCGCAG  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  GCTCTCGCTGCAGGAGCTGACGTGCGGGACTGCGGGACTGCGGGACTGCGGGGCTGCGCGCAG  1620

Qy  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCGCTCTGCGTGAGGAGATCCTGGC  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCGCTCTGCGTGAGGAGATCCTGGC  1680

Qy  1681  CAAGTTCCTGCACTGGCTGTGATGAGTGTGTACGTCGTCTGAGCTCGTGAGCGTCTCAGGTCTTCTTTTA  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CAAGTTCCTGCACTGGCTGTGATGAGTGTGTACGTCGTCTGAGCTCGTGAGCGTCTCAGGTCTTCTTTTA  1740

Qy  1741  TGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  TGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG  1800

Qy  1801  CAAGTTGCAAAGCATTCAGAATCAGACACAGACACTTGAAGAGGGTCAGCTGCGGGAGCTGTC  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  CAAGTTGCAAAGCATTCAGAATCAGACACAGACACTTGAAGAGGGTCAGCTGCGGGAGCTGTC  1860

Qy  1861  GGAAGCAGAGGTCAGGCAGCATGGGCATGGGCCGCCCGCCCCGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  GGAAGCAGAGGTCAGGCAGCATGGGCATGGGCCGCCCGCCCCGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1920

Qy  1921  CTTCATCCCCAAGCCTGACGCCTGCGGGGCTGCGGGGCCAGGTGTGCGTGCGTGTGCGTGTGCGTGGGTGAAGGCACTGTT  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CTTCATCCCCAAGCCTGACGCCTGCGGGGCTGCGGGGCCAGGTGTGCGTGCGTGTGCGTGTGCGTGGGTGAAGGCACTGTT  1980

Qy  1981  CAGAACGTTCCGCAGAGAAAGAGGGGCCCGGCCGTCTCACCTCGGGGTGAAGGGTCGGGCCA  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAGAACGTTCCGCAGAGAAAGAGGGGCCCGGCCGTCTCACCTCGGGGTGAAGGGTCGTGTT  2040

Qy  2041  CAGCCTGCTCAACTACGAGCGGGGCGCCCGCGGGCCCTCGTGTCTGTGGG  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CAGCCTGCTCAACTACGAGCGGGGCGCCCGCGGGCCCTCGTGTCTGTGGG  2100

Qy  2101  CCTGGACGATATCCACCAGAGGCCGCCACCTTGCGTGCGTGCGTGTGCGTGGGGCCCAGGACCC  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTGGACGATATCCACCAGAGGCCGCCACCTTGCGTGCGTGCGTGTGCGTGGGGCCCAGGACCC  2160

Qy  2161  GCCGCCTGAGCGTGTACTTTGTCAAGGTGACACCATCCCCCA  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCCGCCTGAGCGTGTACTTTGTCAAGGTGACACCATCCCCCA  2220

Qy  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGCG  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGCG  2280

Qy  2281  TCGGTATGCCGTGGTCCAGAAGGCCGCACGTCCGAAGGCCTTCAAGAGCCA  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCGGTATGCCGTGGTCCAGAAGGCCGCACGTCCGAAGGCCTTCAAGAGCCA  2340

Qy  2341  CGTCTCTACCTTGACAGACCTTCACCTGCACCTGGGCTCCACCTGCAGGA  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGTCTCTACCTTGACAGACCTTCACCTGCACCTGGGCTCCACCTGCAGGA  2400

Qy  2401  GACCAGCCCCGCTGAGGGATGCGCTCGTCATCGAGCAGAGCTCCCTGAATGAGGCCAG  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2401 GACCAGCCCCGCTGAGGGATGCCGTCTGCTCATCGAGCAGAGCTTCCTCCCTGAATGAGGCCAG 2460

Qy  2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCCATCAGGGG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCCATCAGGGG 2520

Qy  2521 CAAGTCCTACGTCCAGTGCCCAGGGCTCCATCTCTCCACGCTGCTCTG 2580
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Db  2521 CAAGTCCTACGTCCAGGGGATCCCCAGGGATCCCATCTCTCCACGCTGCTCTG 2580

Qy  2581 CAGGCTGTGTCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGGGGACGGGCT 2640
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Db  2581 CAGCTGTGTCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGGGGACGGGCT 2640

Qy  2641 GCTCCTGCGCGTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACCGCGAAAAC 2700
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Qy  2701 CTTCCTCAGGACACCCTGGTCCGTGCGTGGTGACTTGCGGAA 2760
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Db  2701 CTTCCTCAGGACACCCTGGTCCGAGTGTGCGTGGTGACTTGCGGAA 2760

Qy  2761 GACAGTGGTGAACTTCCCTGTGAGAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820
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Qy  2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCCAGTCTCACCTTCAACCG 2940
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Db  2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCCAGTCTCACCTTCAACCG 2940

Qy  2941 CGGCTTCAAGGCTGGGAGGAACAATGCGTCGCAACATGCGTCGCAAACTCTTTGGGGTCTTGGGGCTGAAGTG 3000
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Db  2941 CGGCTTCAAGGCTGGGAGGAACAATGCGTCGCAACATGCGTCGCAAACTCTTTGGGGTCTTGGGGCTGAAGTG 3000

Qy  3001 TCACAGCCTGTTTCTGGATTGCAGGTGAACAGCCTCCAGAGCGTGCACCAACATCTA 3060
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Db  3001 TCACAGCCTGTTTCTGGATTGCAGGTGAACAGCCTCCAGAGCGTGCACCAACATCTA 3060

Qy  3061 CAAGATCCTCCTGCTCCAGGCGTACAGGTTTCACCGCATGTGTGCTGCAGTCCCATTTCA 3120
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Db  3061 CAAGATCCTCCTGCTCCAGGCGTACAGGTTTCACCGCATGTGTGCTGCAGTCCCATTTCA 3120

Qy  3121 TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGCGCCTCCCT 3180
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Db  3121 TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGCGCCTCCCT 3180

Qy  3181 CTGCTACTCCATCTGAAAGCCAGGGGATGTCGCTGGGGTCGGGGCCAAGGGGCCGGC 3240
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Db  3181 CTGCTACTCCATCTGAAAGCCAGGGGATGTCGCTGGGGTCGGGGCCAAGGGGCCGGC 3240

Qy  3241 CGGCCCCTCCGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
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Db  3241 CGGCCCCTGCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy  3301 GACTCGACACCGTGCACGTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360
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Qy  3361 GCTGAGTCGGAAGTCCCGGGGACGCGACTGCCCTGGAGCGCGACCCCGGC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 GCTGAGTCGGAAGTCCCGGGGACGCGACTGCCCTGGAGCGCGACCCCGGC 3420

Qy  3421 ACTGCCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCCAGAGCCAGGCCGA 3480
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Db  3421 ACTGCCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCCACAGCCAGGCCGA 3480

Qy  3481 GAGCAGACACCAGCACCACGTCCGCGGCTCTACGTCCCAGGGAGGAGGAGGGCGGGCC 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GAGCAGACACCAGCACCACGTCCGCGGCTCTACGTCCCAGGGAGGAGGAGGGCGGGCC 3540
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Qy  3541 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCAGGGCCTG 3600
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Db  3541 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCAGGGCCTG 3600

Qy  3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGCCGCTGAGCGAGTGCCAAGGGCT 3660
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Qy  3661 GAGTGTCCAGCAGCACCTGCCGTCTCACTTCCCACAGGCTGCGGCTCGGCTCCACCCCA 3720
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Db  3661 GAGTGTCCAGCAGCACCTGCCGTCTTCACTTCCCACAGGCTGCGGCTCGGCTCCACCCCCA 3720

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Db  3781 CCAGATTCGCCATTGTTCACCCCCTTCCCTTCCTTGCCTTCCTTCCACCCCACCATCC 3840

Qy  3841 AGTGTGGGACCCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG 3900
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Qy  3901 CCCTGTACCAGGCGGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGTCAAATTGGGGG 3960
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PRIOR APPLICATION DATA:
  APPLICATION NUMBER: WO PCT/US97/17618
  FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: WO PCT/US97/17885
  FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/974,549
  FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/974,584
  FILING DATE: 19-NOV-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph T.
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-003300US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 4015 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  FEATURE:
  NAME/KEY: CDS
  LOCATION: 56..3454
  OTHER INFORMATION: /product= "human telomerase reverse
  OTHER INFORMATION: transcriptase (hTRT)"

US-09-052-864-1

Query Match   100.0%;   Score 4015;   DB 15;   Length 4015;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 4015;   Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCGTGGCCCTGCCCGATGCC 60
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Db   1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCGTGGCCCTGCCCGATGCC 60

Qy   61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120

Qy   121 GCCGCTGGCCACGTTCGTGCGCGCCCTGGGCCCCAGGGCCCCGGCTGGTGCAGCGCGCG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCCGCTGGCCACGTTCGTGCGCGCCCTGGGCCCCAGGGCCCCGGCTGGTGCAGCGCGCG 180

Qy   181 GGACCCGGCGGGCCGCTTCCGCGGCGCTGGTGCGCGCGCTGGTGTGCGTGCCCTGGGACGC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACCCGGCGGGCCGCTTCCGCGGCGCTGGTGCGCGCGCTGGTGTGCGTGCCCTGGGACGC 240

Qy   241 ACGGCGCGGTTCGTGCGCGCGCCCCTCCTTCCGCGAGCGCGCGCGCCCCCCCGAGGAGCTGTGGCTGGCGGC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACGGCGCGGTTCGTGCGCGCGCCCCTCCTTCCGCGAGCGCGCGCGCCCCCCCGAGGAGCTGTGGCTGGCGGC 300

Qy   301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGGCGCGAAGCGCGCGCGAAGCGTGCCGGCTTCGGCTTCGC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   361 GCTGCTGGACGGGGCCCCGCGGGGCGCCCCCGAGGCCTTCACCACCAGCGTGCCGCAGCTA 420
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Db   361 GCTGCTGGACGGGGCCCCGCGGGGCGCCCCCGAGGCCTTCACCACCAGCGTGCCGCAGCTA 420

Qy   421 CCTGCCCAACACGTGACCGACGCCACTGGTGGGGGAGCGTGGGGGTCGCGGCCATGCCGG 480
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Qy   481 CCGCTGGGCGGCGACGACGTGCTGGTTCACCTGCGCGCTCTTTGTTGTGGT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCTCTTCGCTGCGCGACGACGTGCTGGTTCACCTGCGCGCTCTTTGTTGTGGT 540

Qy   541 GGCTCCCAGCTGCGCCTGCTGCGCACGAGGTGTGCGGGGCCGGCCGCCGGCTGACCCACC 600
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Db   541 GGCTCCCAGCTGCGCCTGCTGCGCACGAGGTGTGCGGGGCCGGCCGCCGGCTGACCCACC 600

Qy   601 TCAGGCCCGGCCCCGCCCCACACGCGCTAGTGCACCCGTCTTGGGATGCCGAACGGGC 660
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Qy   721 GAGGCGCGGCGGGCCAGTGCCAGCCCGAAGTCTGCCGTTGCCCAGGAGGCCCAGGCGTGCGGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   841 GCGTGGACCGAGTGACCGTGGTTTCTGTTCTGTGTCACCTGCCAGACCCGCCGAAGAAGC 900
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Db   841 GCGTGGACCGAGTGACCGTGGTTTCTGTTCTGTGTCACCTGCCAGACCCGCCGAAGAAGC 900

Qy   901 CACCTCTTTGGAGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCA 960
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Db   901 CACCTCTTTGGAGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCA 960

Qy   961 GCACCACGGCGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGACACCGCCTTGTCC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTGAGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTGAGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA 1080

Qy   1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGGCCTCGGAGGCTCGTGGA 1140
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Db   1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGGCCTCGGAGGCTCGTGGA 1140

Qy   1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGTTGCCCGCCT 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGTTGCCCGCCT 1200

Qy   1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGTTTCTGGAGCTGTTCTGGAACCACGCGCCA 1260
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Db   1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGTTTCTGGAGCTGTTCTGGAACCACGCGCCA 1260

Qy   1261 GTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCGTGTGGTGCCCTGGGACGC 1320
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Qy   1321 AGCCGGTGTCTGTGCCCGTCGCCTGCTGCCGCGAAGGAGCGTGGCTGGCTGGCTGGC 1380
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Qy   1381 CACAGACCCCGTCGCCTGGTGCAGCTGCCGCGAAGACGTGCTGGCCTTCGGCTTCGC 1440
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Qy   1441 CGGCTTCGTGTGGCGCCTGCCCGGCTGGTGCTGCCGCCGGCTGGTGCCTCCAGGCA 1500
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Qy   1501 CAACGAACGCGCTGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
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Qy   1561 GCTCTCGCTGCTCCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCGTTGGCTGCGCGGCAG 1620
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Db 1681 CAAGTTCCTCACTGCTGCTGCGTGATGAGTGTGTACGTCGTCGAGCTGCTCTTTCTTTTA 1740

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Db 1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860

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Qy 2161 GCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCCGTACGACACCATCCCCCA 2220
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Qy 2821 GCCGGCCCACGGCCTATTCCCCTGGTGCGTGCGCCCTGCTGCTGCGTGGATACCCGGAGGT 2880
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RESULT 14
US-09-402-181A-1
; Sequence 1, Application US/09402181A
  GENERAL INFORMATION:
       APPLICANT: Cech, Thomas R.
                  Lingner, Joachim
                  Nakamura, Toru
                  Chapman, Karen B.
                  Morin, Gregg B.
                  Harley, Calvin B.
                  Andrews, William H.
       TITLE OF INVENTION: Human Telomerase Catalytic Subunit
       NUMBER OF SEQUENCES: 633
       CORRESPONDENCE ADDRESS:
            ADDRESSEE: Townsend and Townsend and Crew LLP
            STREET: Two Embarcadero Center, Eighth Floor
            CITY: San Francisco
            STATE: California
            COUNTRY: USA
            ZIP: 94111-3834
       COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/402,181A
            FILING DATE: 29-Sep-1997
            CLASSIFICATION: <Unknown>
       PRIOR APPLICATION DATA:
            APPLICATION NUMBER: US 08/724,643
            FILING DATE: 01-OCT-1996
            APPLICATION NUMBER: US 08/844,419
            FILING DATE: 18-APR-1997
            APPLICATION NUMBER: US 08/846,017
            FILING DATE: 25-APR-1997
            APPLICATION NUMBER: US 08/851,843
            FILING DATE: 06-MAY-1997
            APPLICATION NUMBER: US 08/854,050
            FILING DATE: 09-MAY-1997
            APPLICATION NUMBER: US 08/911,312
            FILING DATE: 14-AUG-1997
            APPLICATION NUMBER: US 08/912,951
            FILING DATE: 14-AUG-1997
            APPLICATION NUMBER: US 08/915,503
            FILING DATE: 14-AUG-1997
            APPLICATION NUMBER: WO PCT/US97/17885
            FILING DATE: 01-OCT-1997
       ATTORNEY/AGENT INFORMATION:
            NAME: Ausenhus, Scott L.
            REGISTRATION NUMBER: 42,271
            REFERENCE/DOCKET NUMBER: 015389-002620US
       TELECOMMUNICATION INFORMATION:
            TELEPHONE: (415) 576-0200
            TELEFAX: (415) 576-0300
  INFORMATION FOR SEQ ID NO: 1:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 4015 base pairs
            TYPE: nucleic acid
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Query Match          100.0%;  Score 4015;  DB 21;  Length 4015;
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Matches 4015;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db 541  GGCTCCCAGCTGCGCCTACCAGGTGCGGGGCCACCGGTGTACCAGCTCGGCGCTGCCAC  600

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Qy 2041  CAGCGTGCTCAACTACGAGCGGCGGCGGCCGGCCTCGTGTCTGGG  2100
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Qy 2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGACGGGGCGCCGTACGACACCATCCCCCA  2220
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Qy 2221  GGACAGGGCTCACCGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCG  2280
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94111-3834
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/402,181B
    FILING DATE: 29-Sep-1997
    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/724,643
    FILING DATE: 01-OCT-1996
    APPLICATION NUMBER: US 08/844,419
    FILING DATE: 18-APR-1997
    APPLICATION NUMBER: US 08/846,017
    FILING DATE: 25-APR-1997
    APPLICATION NUMBER: US 08/851,843
    FILING DATE: 06-MAY-1997
    APPLICATION NUMBER: US 08/854,050
    FILING DATE: 09-MAY-1997
    APPLICATION NUMBER: US 08/911,312
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: US 08/912,951
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: US 08/915,503
    FILING DATE: 14-AUG-1997
    APPLICATION NUMBER: WO PCT/US97/17885
    FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
    NAME: Ausenhus, Scott L.
    REGISTRATION NUMBER: 42,271
    REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
    LENGTH: 4015 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
    NAME/KEY: CDS
    LOCATION: 56..3454
    OTHER INFORMATION: /product= "hTRT"
    /note= "human telomerase reverse
    transcriptase (hTRT) catalytic protein
    component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-402-181B-1
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Best Local Similarity 100.0%;  Pred. No. 0;
Matches 4015;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db   TCACAGCCGTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060

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Qy   TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180
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Qy   GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGTCACTCAGGACAGCCCAGACGCA 3360
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Qy   GCTGAGTCGGAAGCTCCCGGGACGCGTGACTGCCCTGGAGGCCGCGCAGCCAACCCGGC 3420
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Qy   CCAGATTCGCCATTGTTCACCCCTCGCCCTCCTTTGCCTTCACCCCCACCATCC 3840
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RESULT 15
US-09-402-181B-1
; Sequence 1, Application US/09402181B
; GENERAL INFORMATION:
;    APPLICANT: Cech, Thomas R.
;            Lingner, Joachim
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 21:58:59 ; Search time 7768 seconds
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Title: US-10-054-295-224
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Searched: 22781392 seqs, 1152238056 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1		806	20.1	925	12	BM453198	BM453198 AGENCOURT
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4		445	11.1	492	12	BM824748	BM824748 K-EST0096
5		419	10.4	851	12	BG917907	BG917907 602820830
6		416	10.4	416	6	AW276315	AW276315 xr10b12.x
7	c	385.8	9.6	389	9	AA281296	AA281296 zt08g02.r
8		322	8.0	599	10	BB618671	BB618671 BB618671
9		317.8	7.9	664	13	BQ258274	BQ258274 NISC_kp11
10	c	305.4	7.6	340	9	AA811084	AA811084 oa85c05.s
11		290.8	7.2	614	10	BB651920	BB651920 BB651920
12	c	284.4	7.1	315	9	AA748707	AA748707 ny02e05.s
13		267	6.7	866	10	BE371943	BE371943 601217728
14		252.2	6.3	715	10	BE396925	BE396925 601290610
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16		248.8	6.2	679	10	BE396606	BE396606 601289077
17		243.2	6.1	649	10	BE514070	BE514070 601316575
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27	c	140	3.5	148	9	AI824948	AI824948 wb04c01.x
28		132	3.3	641	28	AZ972318	AZ972318 2M0246F07
29		128.8	3.2	875	13	BU122597	BU122597 603148441
30		123.8	3.1	813	10	BG198331	BG198331 RST17589
31		116.8	2.9	632	14	CA353864	CA353864 625469 NC
32		114.8	2.9	739	13	BX315053	BX315053 BX315053
33		113.4	2.8	568	9	Bx521269	Bx521269 RZPD Mus
34		111.8	2.8	534	9	AW318894	AW318894 un09a02.y
35		107.4	2.7	366	10	BF511837	BF511837 UI-H-BI4-
36		107.4	2.7	519	10	BF802688	BF802688 PM4-CI007
37		107	2.7	1610	29	B2569386	B2569386 pacs2-164
38		106.8	2.7	835	13	BU111946	BU111946 603127372
39		104.2	2.6	862	13	BU224024	BU224024 603798349
40	c	100.6	2.5	862	29	AG036151	AG036151 Pan trog1
41		100.4	2.5	1341	29	AG030611	AG030611 Pan trog1
42		98.4	2.5	1116	29	B2569478	B2569478 pacs2-164
43	c	97.8	2.4	1120	29	AG136785	AG136785 Pan trog1
44		97.4	2.4	1126	29	AG064051	AG064051 Pan trog1
45	c	97.4	2.4	1160	29	AG043473	AG043473 Pan trog1

ALIGNMENTS

RESULT 1
BM453198
LOCUS   BM453198   925 bp   mRNA   linear   EST 05-FEB-2002
DEFINITION   AGENCOURT_6387556 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5529840
             5', mRNA sequence.
ACCESSION   BM453198
VERSION   BM453198.1   GI:18502238
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 925)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM12208 row: p column: 01
             High quality sequence stop: 646.

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FEATURES          Location/Qualifiers
     source       1..925
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:5529840"
                  /tissue_type="leiomyosarcoma"
                  /lab_host="DH10B (phage-resistant)"
                  /clone_lib="NIH_MGC_71"
                  /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                   Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                   Average insert size 2.1 kb. "
BASE COUNT      172 a       290 c       276 g       187 t
ORIGIN

Query Match      20.1%;   Score 806;   DB 12;   Length 925;
Best Local Similarity   99.2%;   Pred. No. 2.9e-150;
Matches  821;   Conservative    0;   Mismatches   5;   Indels   2;   Gaps    1;

Qy   2149 GGGCCAGGAGACCCGCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGTACGA 2208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 GGGCCAGGAGACCCGCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGTACGA 61

Qy   2209 CACCATCCCCAGGACAGCCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACAC 2268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 CACCATTCCCCAGGACAGCCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACAC 121

Qy   2269 GTACTGCGTGCCGTCGGTATGCCGTGGTCCAGAAGGCGCGCCATGGGCACGTCCGCAAGGC 2328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 GTACTGCGTCGGTATGCCGTGGTCCAGAAGGCGCGCCATGGGCACGTCCGCAAGGC 181

Qy   2329 CTTCAAGAGCCACGTCTCTTCACCTTGACAGACCTCCAGCAGTTCGTGCGCTACATGCGCACGTTCGTGGC 2388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 CTTCAAGAGCCACGTCTCTCACCTTGACAGACCTCCAGCAGTTCGTGCGCTACATGCGCACGTTCGTGGC 241

Qy   2389 TCACCTGCAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCT 2448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 TCACCTGCAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCT 301

Qy   2449 GAATGAGGCCAGCAGTGCCCTCTTCGACGTCTTCGACGTCTTCCACCACGCCGT 2508
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 GAATGAGGCCAGCAGTGCCCTCTTCGACGTCTTCGACGTCTTCCACCACGCCGT 361

Qy   2509 GCGGCATCAGGGCAAGTCCTACGTCCAGTGCCCAGGGGATCCCGCAGGCGTCCCATCCTCTC 2568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 GCGGCATCAGGGCAAGTCCTACGTCCAGTGCCCAGGGGATCCCGCAGGCGTCCCATCCTCTC 421

Qy   2569 CACGGTGCTCTGCAGCCTGTCTACGGCGCACATGGAGAACAAGCTGTTTGCGGGGATTCG 2628
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 CACGGTGCTCTGCAGCCTGTCTACGGCGCACATGGAGAACAAGCTGTTTGCGGGGATTCG 481

Qy   2629 GACGGGACGGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCAC 2688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 GGGGACGGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCAC 541

Qy   2689 CCACGCGAAAACCTTCCTCAGGACCCTGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGT 2748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 CCACGCGAAAACCTTCCTCAGGACCCTGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGT 601

Qy   2749 GAACTTGCGGAAGACAGTGTGAACTTCCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGC 2808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    602 GAACTTGCGGAAGACAGTGTGAACTTCCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGC 661

Qy   2809 TTTTGTTCAGATGCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCG 2868
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Db    662 TTTTGTTCAGATGCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCG 721

Qy   2869 GACCCTGGAGGTGCAGAGGCGACTACTCCACGTCTTCCATCCAGAGCCAGTCT 2928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    722 GACCCTGGAGGTGCAGAGGCGACTACTCCACGTCTTCCATCCAGAGCCAGTCT 781

Qy   2929 CACCTTCAACCGCGGCCTTCAA--GGCTGGGAGGAACATGCGTCGCAA 2974
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Db     782 CACCTTCAACCGCGGCCTTCAAAGGCTGGGAGGAACATGCGTCGCCAAA 829

RESULT 2
LOCUS        BU702370
DEFINITION   BU702370
             UI-M-FIO-byx-f-12-0-UI.r1 NIH_BMAP_FIO Mus musculus cDNA clone
             IMAGE:6400523 5', mRNA sequence.
ACCESSION    BU702370
VERSION      BU702370.1   GI:23627105
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 851)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/,
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished
  COMMENT    Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at
             http://image.llnl.gov
             This clone was contributed by the Brain Molecular Anatomy Project
             (BMAP)
             Seq primer: pYX-5.
FEATURES          Location/Qualifiers
     source       1..851
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="C57BL/6"
                  /db_xref="taxon:10090"
                  /clone="IMAGE: 6400523"
                  /tissue_type="whole brain"
                  /dev_stage="embryo 12.5dpc"
                  /lab_host="DH10B (T1 phage resistant)"
                  /clone_lib="NIH_BMAP_FIO"
                  /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                   Site_2: Not I; The library was constructed according
                   Bonaldo, Lennon and Soares. Genome Research, 6:791-806,
                   1996. Denatured RNA was size fractionated on a 1% agarose
                   gel.First strand cDNA synthesis was primed with oligo-dT
                   primer containing a Not I site. Double strand cDNA was
                   size selected according to mRNA size fraction, ligated
                   with EcoR I adaptor, digested with NotI and then cloned
                   directionally into pYX-Asc vector. The library tag
                   sequence located between the Not I site and the polyA tail
                   is CAGCCACGAC. This library was created for the University
                   Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                   Developing Mouse Nervous System', supported by National
                   Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                   program coordinator."
BASE COUNT      180 a       227 c       221 g       220 t       3 others
ORIGIN

Query Match      12.5%;   Score 500.2;   DB 13;   Length 851;
Best Local Similarity   75.1%;   Pred. No. 2.5e-89;
Matches  638;   Conservative    0;   Mismatches  206;   Indels    6;   Gaps    1;

Qy   2262 AGAACACGTACTGCGTGCCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCC 2321
          ||  ||||||  || ||| |||||||| | || ||||||||| |||||| ||| ||||| |
Db      1 AGCGCACGTACTGTATCCGCCAGTATGCAGTGGTCCGGAAGCCAGTGGTCCGGAGATAGCCAAGGCCAAGTCC 60

Qy   2322 GCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCACGTCCTTGACAGTACATGCGACAGT 2381
          |||| |||||| || ||||| | |  | ||| |
Db     61 ACAAGTCCTTTAGGAGACAGCAGGTCACCACCCTCTCTGACCTCCAGCCATACATGCGCAGT 120

Qy   2382 TCGTGCTCACCTGCAG------GAGACCAGCCCGCCGTGAGGGATGCGTCGTCATCGAGC 2435
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Db    121  TCCTTAAGCATCTGCAGGATTCAGATGCCAGTGCACTGCCTTCGACGCTCTTCCTACGCTTCCATGT  180
           ||  ||  || ||||||   |||||  ||||||    |||||  ||| |||||||||  ||||||||||

Qy   2436  AGAGCTCCTCCGACCTGAATGAGGCCAGCAGTGGCCTCTTCCTGCCTTCCTTCGACGCTCTTCCTGC  2495
           |||  ||| |||||||   ||| ||||||||||||   |||||  || |||||||||  ||||||||||
Db    181  AGAGCATCTCATGATGAATGAGAGCAGCAGCAGCCTGTTGACTTCTTCCTGCCACTTCCTGC  240

Qy   2496  GCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTGCCAGGGATCCCCCAGG  2555
           |  |||   || ||||   || ||  || || |  ||||||||  |||| |||| ||||
Db    241  GTCACAGTGTCGTAAAGATTGGTGACAGGTGCTATACGCAGTGCCAGGGCATCCCCCAGG  300

Qy   2556  GCTCCATCCTCCACGCTGCTCGCAGCCTGCTACGGCGACATGGAGAACAAGCTGT  2615
           | |||  || ||||  ||||||||||||  ||| ||  ||||||||||||||||||
Db    301  GCTCCAGCCATCCACCCTGCTCTGCAGTCTGTTCGGAGACATGGAGAACAAGCTGT  360

Qy   2616  TTGCCGGGATTCGGCGGCGAGACGGCTGCTCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGA  2675
           |||||||  ||| |||| ||||||||||||   | |||  ||||| |||| || |||||||| ||
Db    361  TTGCTCAGGTGCAGCGGGATGGGTTCTTTGTCTTTTACGTTTGTGATGACTTTCTGTGTGTGA  420

Qy   2676  CACCTCACCTCACCCCACGCGGAAAACCTTCCTCAGGACACCTGGTCCGAGGTGTCCCTGAGT  2735
           | |||||| |||   |||||   |||||| |||||||||||||||   || |  || |||||||
Db    421  CGCCTCACTTGGACCAAGCAAAAAACCTTCCTCAGCACACCTGGTCCCATGGCGTTTCCTGAGT  480

Qy   2736  ATGGCTGCGTGGTGTGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCC  2795
           |||| ||| || |  || | || ||  ||||||  ||||||||   || |  ||
Db    481  ATGGGTGCATGATAAACTTGCAGAAGACAGTGGTGAACTTCCCTGTGGAGCCTGGTACCC  540

Qy   2796  TGGGGTGCACGGGCTTTTGTTCAGATGCCCAGGCCCCATTCCCCTGGTTCGCGGCCTGC  2855
           ||||    ||| | |||||  || ||   ||  ||| ||||| ||||||| ||||||||
Db    541  TGGGGTGGTGCAGCTCCATACCAGCTGGCCTGCTCACTGCGTTTCCTGTTCGCGGGCTGC  600

Qy   2856  TGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCCGGACCTCCA  2915
           || |||||    ||| | |||||||| ||||    || |||   ||||||
Db    601  TGCTGGACACTCAGACTTTGGAGGTGTTCTGTGACTACTCCAGGACCTCAA  660

Qy   2916  TCAGAGCCAGTGTCTCACCTTCACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAAC  2975
           |||||||||||  | |||| |||||| || ||  ||| | |||||   ||||| ||||  |
Db    661  TTAAGACGAGCCTCCACCTTCCAGAGTGTCTTCCAGAGTCGTCAAGCGGATTGCGGAACANGC  720

Qy   2976  TCTTTGGGGTTGCGCGGTGAAGTGTCACAGCCCTGTTTCTGGATTTGCAGTGAACAGCC  3035
           || |||||| |||||||||||||| ||| |||   | ||   ||| |||||||||||||
Db    721  TCCTGTGGGTCTTGCGGTTGAAGTGTCACGGGCTATTTCTGCTCTCGCTGCGTGAACAGCC  780

Qy   3036  TCCAGACGGGTGTGCACCAACATCTACAGAGATCCTCCGCTGCCAGGCGTACAGGTTTCACG  3095
           |||||  || || |||| ||||  || ||||  |||||||||| ||||   |||||||  |
Db    781  TCCAGACAGTCTGCATCAATCAATATATACAAGATCTTCCTGCTTCANGGCTACAGGTTCCATG  840

Qy   3096  CATGTGTGCT  3105
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Db    841  CATGTGTGAT  850
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RESULT 3
AW270031/C
LOCUS   AW270031   468 bp   mRNA   linear   EST 03-JAN-2000
DEFINITION xv57e03.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2817244 3',
            mRNA sequence.
ACCESSION   AW270031
VERSION   AW270031.1 GI:6657061
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 468)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 416.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2817244"
                     /tissue_type="two pooled squamous cell carcinomas"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu28"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.   Primer: Oligo dT.
                     Library constructed by Life Technologies."
BASE COUNT   100 a   137 c   144 g   86 t   1 others
ORIGIN

Query Match   11.6%; Score 465.4; DB 9; Length 468;
Best Local Similarity   99.6%; Pred. No. 1.8e-82;
Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy   3543  CACCCAGGCCCGCACCGCTGGGAGTCTGAGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCA  3602
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Db    468  CACCCAGGCCCGCACCGCTGGGAGTCTGAGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCA  409

Qy   3603  TGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGAGGCTGAGGCGAGTGTCCAGCCAAGGGCTGA  3662
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Db    408  TGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGAGGCTGAGGCGAGTGTCCAGCCAAGGGCTGA  349

Qy   3663  GTGTCCAGCACACTGCCGTCGCTCTTCACTTCCCCACAGGCTGGCCGCTGGCCGTCCACCCAGG  3722
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    348  GTGTCCAGCACACTGCCGTCGCTCTTCACTTCNCCACAGGCTGGCCGCTGGCCGTCCACCCAGG  289

Qy   3723  GCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCC  3782
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    288  GCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCC  229

Qy   3783  AGATTCGGCCATTGTTCACCCCTGCCTTCGCCTTTGCCTTCCACCCATCCAG  3842
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Db    228  AGATTCGGCCATTGTTCACCCCTGCCTTCGCCTTTGCCTTCCACCCACCATCCAG  169

Qy   3843  GTGGAGACCCTGAGAAGGACCCTGGGAGTCTCGGGAATTGGAGTGACCAAAGTGTGCC  3902
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Db    168  GTGGAGACCCTGAGAAGGACCCTGGGAGTCTCGGGAATTGGAGTGACCAAAGTGTGCC  109

Qy   3903  CTGTACACAGGCGAGGAGACCCTGACACCTGGATGGGGGTCCCGTGGTCAAATTGGGGGGA  3962
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Db    108  CTGTACACAGGCGAGGAGACCCTGACACCTGGATGGGGGTCCCGTGGTCAAATTGGGGGGA  49

Qy   3963  GGTGCTGTGGGAGTAAAATACTGAATATATGAATATAGAGTTTTCAGTTTTGAA  4010
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    48  GGTGCTGTGGGAGTAAAATACTGAATATATGAATATAGAGTTTTCAGTTTTGAA  1
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RESULT 4
BM824748
LOCUS   BM824748   492 bp   mRNA   linear   EST 06-MAR-2002
DEFINITION K-EST0096335 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-99-E07
            5', mRNA sequence.
ACCESSION   BM824748
VERSION   BM824748.1 GI:19181161
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 492)

AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
           Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
           Kim,Y.S.
TITLE   21C Frontier Korean EST Project 2001
JOURNAL   Unpublished
COMMENT   Contact: Kim YS
           Genome Research Center
           Korea Research Institute of Bioscience & Biotechnology
           52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
           Tel: +82-42-860-4470
           Fax: +82-42-860-4409
           Email: yongsung@mail.kribb.re.kr
           Plate: 99 row: E column: 07
           High quality sequence stop: 492.
FEATURES   Location/Qualifiers
     source   1..492
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="S22SNU16n1-99-E07"
                    /sex="F"
                    /tissue_type="Ascites"
                    /cell_type="Lymphoblast-like"
                    /cell_line="SNU-16"
                    /lab_host="DH10B"
                    /clone_lib="S22SNU16n1"
                    /note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
                    Site_2: NotI; The S22SNU16 library was contributed by the
                    Soares laboratory and it was constructed as described by the
                    Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
                    Research 6(9): 791-806. RNA was prepared from harvested
                    cells of SNU-16 culture. SNU-16 cell was obtained from
                    Korean Cell Line Bank (KCLB). SNU-16 was established from
                    ascitic fluids of Korean patients by Park J.G. et al.
                    (1990), Cancer Res 50: 2773-2780."
BASE COUNT   96 a   152 c   131 g   113 t
ORIGIN

Query Match   11.1%;   Score 445;   DB 12;   Length 492;
Best Local Similarity   100.0%;   Pred. No. 2.1e-78;
Matches   445; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy 2768 GTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAGATGCCGGCC 2827
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Db   1 GTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAGATGCCGGCC 60

Qy 2828 CACGGCCTATTCCCCTGTGCCGGCCTCGATACCCGGACCCTGGAGGTGCAGAGC 2887
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CACGGCCTATTCCCCTGTGCCGGCCTCGATACCCGGACCCTGGAGGTGCAGAGC 120

Qy 2888 GACTACTCCAGTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTC 2947
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACTACTCCAGTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTC 180

Qy 2948 AAGGCTGGGAGGAACAATGCGTCCGCAAACTCTTTGGGGCTGAAGTGTCACAGC 3007
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AAGGCTGGGAGGAACAATGCGTCCGCAAACTCTTTGGGGCTGAAGTGTCACAGC 240

Qy 3008 CTGTTTCTGGATTTGCAGTGAACAGCCTCCAGACGGTGCACCAACATCTACAAGATC 3067
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CTGTTTCTGGATTTGCAGTGAACAGCCTCCAGACGGTGCACCAACATCTACAAGATC 300

Qy 3068 CTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTCTGCAGCTCCCATTTCATCAGCAA 3127
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTCTGCAGCTCCCATTTCATCAGCAA 360

Qy 3128 GTTTGGAAGAAGAACCCCACATTTTTCCTGCGCGTCATCTGACACGGCCTCCCCTGCTAC 3187
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTTTGGAAGAAGAACCCCACATTTTTCCTGCGCGTCATCTGACACGGCCTCCCCTGCTAC 420

Qy 3188 TCCATCCTGAAAGCCAAGAACGCAG 3212
         |||||||||||||||||||||||||
Db   421 TCCATCCTGAAAGCCAAGAACGCAG 445

RESULT 5
BG917907
LOCUS   BG917907   851 bp   mRNA   linear   EST 05-JUN-2001
DEFINITION 602820030F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4949887 5',
            mRNA sequence.
ACCESSION   BG917907
VERSION   BG917907.1   GI:14298383
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 851)
  AUTHORS   NIH-MGC http://mgc.ncl.nih.gov/,
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10903 row: k column: 08
            High quality sequence stop: 753.
FEATURES   Location/Qualifiers
     source   1..851
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="FVB/N"
                    /db_xref="taxon:10090"
                    /clone="IMAGE:4949887"
                    /sex="female, virgin"
                    /tissue_type="infiltrating ductal carcinoma"
                    /dev_stage="5 months"
                    /lab_host="DH10B"
                    /clone_lib="NCI_CGAP_Mam6"
                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                    Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                    Library constructed by Life Technologies. Investigator
                    providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT   184 a   238 c   214 g   215 t
ORIGIN

Query Match   10.4%;   Score 419;   DB 12;   Length 851;
Best Local Similarity   71.9%;   Pred. No. 3.8e-73;
Matches   579; Conservative   0;   Mismatches   215;   Indels   11;   Gaps   2;

Qy 2651 TTGGTGGATGATTTCTTGTTGGTGACACCTCACCCACGCGGAAACCTTCCTCAGG 2710
         ||| |||| ||||| |||||||||| ||||||| | ||| ||||||||||||
Db   38 TTGTGTGATGACTTTCTGTAGGTGACGCGCCTCACTTGGACCAAGCAAAAACCTTCCTCAGC 97

Qy 2711 ACCCTGGTCCGAGTGTCCCCTGAGTATGGCGTCGTGGTGGTGAACTTGCGGAAGACAGTGGTG 2770
         |||||||| ||| ||| ||| ||||| |||||||| ||| ||| ||| | ||||| ||||||
Db   98 ACCCTGGTCCATGCCTTCCTGAGTATGGCGTCATGATGGTGTGCATGATGAAACTTGCAGAAGACAGTGGTG 157

Qy 2771 AACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAGATGCCGGCCCAC 2830
         ||||||||| | ||||||||||||||||||||||||||| ||||||| |||||| |||
Db   158 AACTTCCCTGTGGAGGACGAGGCCCTGGGTGGTGCAGCTCCCATACCAGCTGCCTGCTCAC 217

Qy 2831 GGCCTATTCCCCTGCTGCGCGTGATACCCGGACCCTGGAGGTGCAGAGCGAC 2890
         |||| || ||| | ||| ||| ||| ||||| || |||||| |||||| ||
Db   218 TGCCTGTTCCCTGCTGCGTGTGGCTTGCGTGCTGCGGACACTCAGACTCTGTGTGAC 277

Qy 2891 TACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAG 2950
         ||||| ||| | || ||||||| |||| |||||||| | ||| |||||| |||||||||
Db   278 TACTCAGGTTATGCCCAGGACCTCCAATTAAGACGAGGCCCTCACCCTTCACCTTCCAGAGTGTCTTCAAA 337

Qy 2951 GCTGGGAGGAACAATGCGTCCGCAAACTCTTTGGGGTCTTCGCGGCTGAAGTGTCACAGCCTG 3010
         |||||| ||||||||||||| | |
Db   338

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              /clone_lib="NCI_CGAP_Lu28"
              /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
               Site_2: NotI; Cloned unidirectional. Primer: Oligo dT.
               Library constructed by Life Technologies."

BASE COUNT         90 a        118 c       130 g        78 t
ORIGIN

Query Match      10.4%;   Score 416;   DB 9;   Length 416;
Best Local Similarity   100.0%;   Pred. No. 1.2e-72;
Matches 416;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    3594 AGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCGAGTGTCCAGCC 3653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     416 AGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCGAGTGTCCAGCC  357

Qy    3654 AAGGGCTGAGTGTCCAGCACACTGCCGTCTCACTTCCCCACCAGGAGGCTGGCCGGTCGGCTC 3713
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     356 AAGGGCTGAGTGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACCAGGAGGCTGGCCGGGCTC  297

Qy    3714 CACCCCCAGGAGGCCAGCTTTTTCCTCCACCAGGAGCCCGGCTTCCACTCCCCACCATAGGAATAG 3773
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     296 CACCCCCAGGGCCAGCTTTTTCCTCCACCAGGAGCCCGGCTTCCACTCCCCACCATAGGAATAG  237

Qy    3774 TCCATCCCAGATTCGCCATTGTTCACCCTCGCGCCTCCTTTGCCTTCCACCCCC 3833
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     236 TCCATCCCAGATTCGCCATTGTTCACCCTCGCGCCTCCTTTGCCTTCCACCCCC  177

Qy    3834 ACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGTCTGGGAATTTGGAGTGACCAA 3893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     176 ACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGTCTGGGAATTTGGAGTGACCAA  117

Qy    3894 AGTGTGCCCTGTACACAGGCAGGCGGAGGAAAATACTGAATATGAATATGAGTTTTTCAGTTTTGA 3953
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     116 AGTGTGCCCTGTACACAGGCAGGCGGAGGAAAATACTGAATATGAATATGAGTTTTTCAGTTTTGA   57

Qy    3954 TTGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGA 4009
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      56 TTGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGA 1
```

```
RESULT 7
AA281296
LOCUS       AA281296          389 bp     mRNA      linear    EST 14-AUG-1997
DEFINITION  zt08g02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5',
            mRNA sequence.
ACCESSION   AA281296
VERSION     AA281296.1  GI:1924194
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 389)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 2187   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 385.
FEATURES             Location/Qualifiers
     source          1..389
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:712562"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GCB1"
```

```
Db     338 |||||| || ||||| |||| ||  ||  |||||||||||   ||
           GCTGGGAAGACCATGCGGAACAAGCTCCTGTCCGTCCGGTCTTGCGGTTGAAGTGTCACGGTCTA 397

Qy    3011 TTTCTGGATTTGCAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTC 3070
           |||| || |||||||||||||| |||||   ||| ||||||||||||||||||
Db     398 TTTCTAGACTTGCAGTGAACAGCCTCCAGACAGCAGTCTGCATCAATATATACAAGATCTTC 457

Qy    3071 CTGCTGCAGGCGTACAGGTTTCACGGACGTGCTGCTGCCAGCTGCGCAGCTCCCATTTCATCAGCAAGTT 3130
           ||||| ||||| |||||||| || ||||||||||| || ||||| ||||||||||||||||||||
Db     458 CTGCTTCAGGCCTACAGGTTTCCATGCATGTGATTCAGCATGTTTCCCTTTGACCAGCGTGTT 517

Qy    3131 TGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCCTGCTACTCC 3190
           |||||||||||| ||||| || || || |||||| || ||||| ||| |||| |
Db     518 AGGAAGAACCTCACATTCTTTCTGCGGCATCATCTCCAGCATCCTCCAGCATCCTGCTGCTATGCT 577

Qy    3191 ATCCTGAAAGCCAAGAACCCAGGGATTGTCCGCTGGGGCCAAGGGCCGCCGGCCCCTCTG 3250
           |||||||| ||||||||||| ||||| |||| ||| |||| ||||
Db     578 ATCCTGAAGGTCAAGAATCCAGGAATGACACTAAAGGCCTCTGGCTC----CTT 627

Qy    3251 CCCTCCGAGGCCGTGCAGTGGCGTGTGCCACCAAGCATTCCT-GCTCAAGCTGACTCGACA 3309
           |||||| |||| |||||| ||| ||||||||||||||  ||||||
Db     628 TCCTCCTGAAGCCGGACCGACATTGGCTCTGCTACCAGGCCTTCCTGGCTCAAGCTGGCTGCTCA 687

Qy    3310 CCGTGTCACCTACGTGCCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCGTGAGTCG 3369
           ||||| |||| ||| || || ||| || |||||  ||||
Db     688 TTCTGTCATCTACAAATGTCTCCTGGGACCTCTGAGGACAGCAGCCCAAAAACCGCTGTGCCG 747

Qy    3370 GAAGGTCCCGGGGACGACGGCTGACTGCCCTGGAGGCGCAGCCAACCCGGCCCACTGCCCTC 3429
           |||| |||| |||| || ||| ||||| || || |||
Db     748 GAAGCTCGCAGAGGCGACAATGACCATGCCTTACAGCTGCAGCTGGCCACCGAGACCTAAGGAC 807

Qy    3430 AGACTTCAAGACCATCCTGGACTGA 3454
           ||||| ||||| |||||||
Db     808 AGACTTCAAGACCATTGGGACTAA 832
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RESULT 6
AW276315/c
LOCUS       AW276315          416 bp     mRNA      linear    EST 03-JAN-2000
DEFINITION  xr10b12.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2759711 3',
            mRNA sequence.
ACCESSION   AW276315
VERSION     AW276315.1  GI:6663345
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 416)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 413.
FEATURES             Location/Qualifiers
     source          1..416
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2759711"
                     /tissue_type="two pooled squamous cell carcinomas"
                     /lab_host="DH10B"
```

Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M. Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
,Y. and Hayashizaki,Y.
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES   Location/Qualifiers
source   1..599
                   /organism="Mus musculus"
                   /mol_type="mRNA"
                   /strain="C57BL/6J"
                   /db_xref="taxon:10090"
                   /clone="5730412M20"
                   /sex="mixed"
                   /dev_stage="8 days embryo"
                   /lab_host="DH10B"
                   /clone_lib="RIKEN full-length enriched, 8 days embryo"
                   /note="Site_1: SalI: Site_2: BamHI; cDNA library was
                   prepared and sequenced in Mouse Genome Encyclopedia
                   Project of Genome Exploration Research Group in Riken
                   Genomic Sciences Center and Genome Science Laboratory in
                   RIKEN. Division of Experimental Animal Research in Riken
                   contributed to prepare mouse tissues. 1st strand cDNA was
                   primed with a primer [5'
                   GAGAGAGAAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTTTVN 3'], cDNA was
                   prepared by using trehalose thermo-activated reverse
                   transcriptase and subsequently enriched for full-length by
                   cap-trapper. cDNA went through one round of subtraction to
                   Rot = 100.0 Second strand cDNA was prepared with the
                   primer adapter of sequence [5'
                   GAGAGAGAATTCTCGAGTTAATTAAATTAARTCCCCCCCCCCCC 3']. cDNA
                   was cloned into the XhoI and BamHI sites. Vector: a
                   modified pBluescript KS(+) after bulk excision from Lambda
                   FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

BASE COUNT   91 a   185 c   181 g   142 t
ORIGIN

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCGAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT   87 a   102 c   123 g   77 t
ORIGIN

Query Match   9.6%;   Score 385.8;   DB 9;   Length 389;
Best Local Similarity 99.5%;   Pred. No. 1.3e-66;
Matches   387;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Qy   1679 GCCAAGTCCTGCACTGGCTGATGAGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTT 1738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTT 60

Qy   1739 TATGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTTCTCACCGGAAGAGTGTCTGG 1798
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TATGTCACGGAGACCACGTTTCAAAAGAACACAGGCTCTTTTTCTCACCGGAAGAGTGTCTGG 120

Qy   1799 AGCAAGTTGCAAAGCATTGGAATCAGACACTTGAAGAGGTGCCAGCTGCGGGAGCTG 1858
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCAAGTTGCAAAGCATTGGAATCAGACACTTGAAGAGGTGCAGCTGCGGGACGTG 180

Qy   1859 TCGGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTC 1918
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCGGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTC 240

Qy   1919 CGCTTCATCCCCAAGCCTGACGGGCTGCGGCCCGATTGTGAAACATGGACTACGTCGTGGGA 1978
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CGCTTCATCCCCAAGCCTGACGGGCTGCGGCCCGATTGTGAAACATGGACTACGTCGTGGGA 300

Qy   1979 GCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCCTCTCACCCTGAGGGTGAAGGCACTG 2038
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCCTCTCACCCTGAGGGTGAAGGCACTG 360

Qy   2039 TTCAGCGTGCTCAACTACCAGCCGGCGCCG 2067
           ||||||||||||||||||||||||||
Db   361 TTCAGCGTGCTCAACTACCAGCCGGCGCCG 389

RESULT 8
BB618671
LOCUS   BB618671   599 bp   mRNA   linear   EST 26-OCT-2001
DEFINITION   BB618671 RIKEN full-length enriched, 8 days embryo Mus musculus
                cDNA clone 5730412M20 5', mRNA sequence.
ACCESSION   BB618671
VERSION   BB618671.1   GI:16458173
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 599)
AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
                ,Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Ito,M., Kawai,J., Konno,M., Kouda
                ,M., Koya,S., Matsuyama,M., Miyazaki,A., Nomura,K., Ohno,M.,
                Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
                ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
                Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
                Muramatsu,M. and Hayashizaki,Y.
TITLE   RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL   Unpublished
COMMENT   Contact: Yoshihide Hayashizaki
                Laboratory for Genome Exploration Research Group, RIKEN Genomic

---

Query Match   8.0%;   Score 322;   DB 10;   Length 599;
Best Local Similarity 74.9%;   Pred. No. 7.3e-54;
Matches   403;   Conservative   0;   Mismatches   135;   Indels   0;   Gaps   0;

Qy   2 CAGGCGCTGCGTCCTGCTGCCACGTGGGAGCCCCTGGCCCCCGGCCACCCCGGCGATGCCG 61
           || ||| || ||||||| | ||| ||||| | |||| | |||||| ||||||| | |||
Db   61 CACCCTTGCATCTTGGTTCCCGCACGTGGGAGGCCCCATCCCGGCCTTGAGCAACATGACC 120

Qy   62 CGGCTCCCCGCTACCGGCCGTGCCGCTCCTGCTGCGGACGTCCCTGCCACTACCGCACGGTG 121
           ||||||||| || |||| ||||| ||||| |||||||||| ||||||||||| ||||||||

```
SalI/NotI sites using the following 5' adaptor:
5'-TCGACCCACGCGTCCG-3'. Size-selected for average insert
size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
University)."

BASE COUNT      155 a       177 c       183 g       149 t
ORIGIN

        Query Match         7.9%;    Score 317.8;   DB 13;   Length 664;
        Best Local Similarity   68.3%;   Pred. No. 5.2e-53;
        Matches   479;   Conservative    0;  Mismatches 177;  Indels 45;  Gaps  1;

Qy    1108  GCCCAGCCTGACTGCGCTCGGAGCTCGTGGAGCACCATCTTTCTGGGTTCCAGGCCCTG 1167
            |||-| ||||||| ||-|| |||||||| || ||||||||||||-|| |||||||||
Db       9  GCCTAACTTGACTGGGCCCAGGACTGGTGGAGATCATCTTTCTGGGTCACAAGCCTAG   68

Qy    1168  GATGCCAGGGACTCCCCGCAGGTTGCCCCGCTACTGCACCGCAAAATGCCGGCC 1227
            |-||| |||||||||-|-|| |||||||| | ||||||||| |||||||||||
Db      69  GACATCAGGACCACTCTGCACGACACACCGTCTATCGCGTGCGATACTGGCAGATGCGGCC  128

Qy    1228  CCTGTTTCTGGAGCTGCTTGGGAACCACCACCGCCAGTGCCCTCACCGGGGTGCCTCCTCAAGAC 1287
            ||| | |||||||| || |-| ||||| ||||||| |||| || ||||||||||
Db     129  CCTGTTCAACAGCTGCTGGTGAACCATGCAGCAGAGTGCCAATATGTCAGACTCCTCCAGGTC  188

Qy    1288  GCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTCGTGCCCGGAGAAGCC 1347
            || |||||| || |||| |||||| | |||||||||||||||| |
Db     189  ACATTGCAGTTTCGAACAGCCAAACCAACAGGTGACAGATGCCT-------------  232

Qy    1348  CCAGGGCTCTTGTGCGGGCCCCCCGTCGCCCTGGTCGCAGCT 1407
            | | ||| |||| |||||||| |||||||||||||||
Db     233  ------------------------------TGAACACCAGCCACCGCACCTCATGGATTT  263

Qy    1408  GCTCCGGCCAGCACAGCAGCCGGCTTCGTGCGGGGCCTTCGTCCTGCGCCG 1467
            |||||||||| |||||| |||| ||||||||| ||||| |||||
Db     264  GCTCCGCCTGCACAGCAGTCCTCGGACTCCAGTATATGGTTTTCTCGGGCCTGTCTCTGCAA  323

Qy    1468  GCTGGTGCCCCAGGCCTTCGTGGGGTCCAGGCACGACGCGCTTCCTCCAGGAACAC 1527
            | |||| ||| ||| |||||| ||||| | ||||| ||
Db     324  GGTCGTGTCGCCTAGTCTCTGGGTACCAGGCCACAATGAGCGCGCCGCTTCTTTTAAGAACTT  383

Qy    1528  CAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTACGGAGGCTGACGTGGAA 1587
            |||||||||||||| |||||| || |||| || ||||| |||||||||
Db     384  AAAGAAGTTCATCTCGTTGGGAAATACCGCCAAGCTACACTCAGGAACGATGTGGAA  443

Qy    1588  GATGAGCGTGCGGGACTGGCCTTGGCTGCGCTGCCCAGGGGTTGGCTGTGTTCCGGC 1647
            |||| || ||| ||| ||| || ||||||| ||||||||| | |||| | ||
Db     444  GATGAAAGTAGAGGATTGCCACTGCGTCCGCAGCCCAGGGAAGGACCGTGTCCCCGC  503

Qy    1648  CGCAGAGCACCGTCGTCGTGAGGAGATCCTGGCCCAAGTTCCTGCACTGCTGATGAGTGT 1707
            |||||||||| || ||||||||| |||| || |||||| | |||||||
Db     504  TGCAGACACCGTCGAGGGAGGAGGATCCTGGCTACGGTTCCTGCTGTTCCTGGCTGATGGACAC  563

Qy    1708  GTACGTCGTCGAGCTGCTCCAGGTGTCTTTTATGTCACCGGAGACCACGTTCAAAAGAA 1767
            || ||| |||| |||||| |||||||| |||||||||
Db     564  ATACGTGGTACAGCGTCGCTTAGGTCATTCTTTACATCACAGAGAGCACAATTCCAGAAGAA  623

Qy    1768  CAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGC 1808
            |||||| || |||||||||| ||||||| | |||||||||
Db     624  CAGGCTCTTCTTCTACCGTAAGAGTGTGTGGAGCAAGCTGC  664

RESULT 9
BQ258274
LOCUS        BQ258274               664 bp    mRNA    linear   EST 06-MAY-2002
DEFINITION   NISC_kp1lg04.q3 Baker mouse embryo e7.5 Mus musculus cDNA clone
             IMAGE:5409222, mRNA sequence.
ACCESSION    BQ258274
VERSION      BQ258274.1   GI:20459030
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 664)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             cDNA Library Preparation: J. Baker (Stanford University)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
             Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             info@image.llnl.gov
             MGI:1845958
             Plate: LLAM12043  row: N  column: 7
             Seq primer: Sp6 primer.
FEATURES             Location/Qualifiers
     source          1..664
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CD-1"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5409222"
                     /tissue_type="embryo, late gastrula"
                     /dev_stage="embryo, 7.5 dpc"
                     /lab_host="XL1-Blue"
                     /clone_lib="Baker mouse embryo e7.5"
                     /note="Vector: pCS105; Site_1: NotI; Site_2: SalI; cDNA
                     made by oligo-dT priming. Directionally cloned into

Db     121  CGCGGCTCCTCGTTGCCCGCCGGTGCGCCTCTCTGCTCGCGCAGCCGATACCGGAGGTGTGG  180

Qy     122  CCGCTGGCCACGTTCGTGCGGGGCCTGGGGCCCAGGGCTGCGGCGGCTGCGGCTGCAGCGCGGG  181
            ||||||| || ||-|| ||||||| ||||||||| || ||||||| ||-|| ||||
Db     181  CCGCTGCCAACCTTTGTGCGGCGCCTGGGGCTGGGGCCCGAGGGCAGGGCGGCTTGTGCAACCGGG  240

Qy     182  GACCCGCGGCTTTCCGCGCGCTGGTGGCTGGTGTGCCTGGTGCGCCCTGGGGACGCA  241
            ||||||| ||||| ||||| | ||-||| |||| ||||| |||| ||-|| |||-||
Db     241  GACCCGAAGATCTACCCGCACTTTGGTTGCCCCATAGTGTGCCATGTGCATGCACTGGGGCTCA  300

Qy     242  CGGGCCCCCCCGCCCCTTCGCCAGGTGTCCTGCCAGGTGTCCTGCCGAAGAGCTGGTGGCC  301
            | ||| ||-|| ||||| || |||||||||| |||||||| |||||||||| ||||||||
Db     301  CAGCCTCCACCTGCCCACCTTTCCTTCCACCAGGTGTCATCCCTGAAAGAGCTGGTGGCC  360

Qy     302  CGAGTGCTGCAGAGGCTGTGCAGACGCGGCGAAGAACGTGCTGGCCTTCGGCTTCGCG  361
            | ||-||||| |||||| |||||||||| || |||| ||
Db     361  AGGGTTGTGCAGAGACTCTGCGAGACGCGCAACGAGAGAAACGTGCTGGCTTTTGGCTTTGAG  420

Qy     362  CTGCTGGACAGGGGCCCCCGCGGGGGCCCCCCGAGGGCCTTCACCACCAGCGTGCGCAGCTAC  421
            || ||| |||| |||||||||||||||| |-||| ||||||| || ||||||||| |||||||
Db     421  CTGCTTAACGAGGCCAGAGGCGGGCCCTCCATGGGCCTGTGGTCACTAGCGTGCGTAGCTAC  480

Qy     422  CTGCCCAACACGGTGACCGACGACACTGCGGGGCGGGGGCGTGGGGGTGGGGGTCGTGCTGCGC  481
            ||||||||| || ||-|| | ||||||||| || ||||| | |||||||||||||||||
Db     481  TTGCCCAACACTGTTATTGACACCCTGCGTGTGTCAGTGGTGCATGGATGCTACTGTTGAGC  540

Qy     482  CGCGTGGGCGACGACGTGCTGTTCACCTGCTGCACGCTGCGCGCCTCTTTGTGCTGG  539
            || |||||||||||||||||| |||||| | |||| |||| |||-|| |||-|| |||
Db     541  CGAGTGGGCGACGACCTGCTGTTCACCTGCTGCACACTGCTGCGCACCGTGCTCTTTATCTTCTGG  598
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AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
             Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Seq primer: -40m13 fwd. ET from Amersham
             Insert Length: 2249    Std Error: 0.00
             High quality sequence stop: 331.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1319048"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GCB1"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGAGGGCGCCTCCATTTTTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      73 a      86 c      100 g      81 t
ORIGIN

Query Match     7.6%;   Score 305.4;   DB 9;   Length 340;
Best Local Similarity  99.1%;   Pred No. 1.3e-50;
Matches  328;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   2;

Qy   3685 TCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCCAGGGCCAGCTTTTCCTCACCAGGAG 3744
          ||||||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db    340 TCACTTCCCCACAGG-TGGCGCTCGGCTCCACCCCCAGGGCCAGCTTTTCCTCACCAGGAG  282

Qy   3745 CCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCAGATTCGGCCATTGTTCACCCCT 3804
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 CCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCAGATTCGGCCATTGTTCACCCCT  222

Qy   3805 CGCCCTGCCCTCCTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAGGACCC 3864
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    221 CGCCCTGCCCTCCTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAGGACCC  162

Qy   3865 TGGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTG 3924
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 TGGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTG  102

Qy   3925 CACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGGAGGTGCTGTGGGAGTAAAATACT 3984
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 CACCTGGATGGGGGT-CCTGTGGGTCAAATTGGGGGGGAGGTGCTGTGGGAGTAAAATACT   43

Qy   3985 GAATATATGAGTTTTCAGTTTTGAAAAAAA 4015
          ||||||||||||||||||||||||||||||
Db     42 GAATATATGAGTTTTCAGTTTTGAAAAAAA 12

RESULT 11
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BB651920
LOCUS        BB651920    614 bp    mRNA    linear    EST 26-OCT-2001
DEFINITION   BB651920 RIKEN full-length enriched, ES cells Mus musculus cDNA
             clone C330020G14 5', mRNA sequence.
ACCESSION    BB651920
VERSION      BB651920.1    GI:16486058
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 614)
AUTHORS      Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
             , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
             ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
             Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
             ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
             Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
             Muramatsu,M. and Hayashizaki,Y.
TITLE        RIKEN Mouse ESTs (Arakawa,T. et al. 2001)
JOURNAL      Unpublished
COMMENT      Contact: Yoshihide Hayashizaki
             Laboratory for Genome Exploration Research Group, RIKEN Genomic
             Sciences Center(GSC), Yokohama Institute
             The Institute of Physical and Chemical Research (RIKEN)
             1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
             Tel: 81-45-503-9222
             Fax: 81-45-503-9216
             Email: genome-res@gsc.riken.go.jp,
             URL:http://genome.gsc.riken.go.jp/
             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
             ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new
             genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
             Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
             ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
             Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer. Genome Res.
             10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
             ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
             encyclopedia: real-time sequence clustering for construction of a
             nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
             ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
             Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
             Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
             further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1..614
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="C330020G14"
                     /cell_type="ES cells"
                     /lab_host="SOLR"
                     /clone_lib="RIKEN full-length enriched, ES cells"
                     /note="Site_1: XhoI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'-
                     GAGAGAGAAGAGATCCAAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was
```

prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 5.0 and subtraction to Rot = 25.0. Second strand
cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGAGGATTCGAGTTAATTAAATTAATCCCCCCCCCC 3'].

BASE COUNT   93 a   191 c   188 g   142 t
ORIGIN

Query Match   7.2%;   Score 290.8; DB 10; Length 614;
Best Local Similarity 74.7%; Pred. No. 1.2e-47;
Matches 378; Conservative   0; Mismatches 127; Indels   1; Gaps   1;

Qy   2 CAGGGCTGGCTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCACCCCCCGGATGCCG   61
           || ||||| |||| | |||| | | || || ||||||
Db   61 CACCCTTGCATCTTGGTTCCCGCACGTGGGAGGCCCATCCCGGCCTTGAGCACAATGACC 120

Qy   62 CGCGGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTTGCGCAGCCACTACCCGAGGTGCTG 121
           |||||| || |||| | |||||| ||||||||||| |||| |||| |||| |||||
Db   121 CGCGGCTCCTCGTTGCCCCCGGCGTGCTCTCTGCTGCGCGCCGCCGAGCCGGAGGTGTGG 180

Qy   122 CCGGTGGCCACGTTCGTGCGCGCCTGGGCCTCGGGGCTGGCCGGCTGGTGCAGCGCGGG 181
           || ||||||| ||| ||| |||||||| ||||||| |||||| |||||| |||||||||
Db   181 CCGCTGGCAACCTTTGTGCGGGCCGCCCGAGGGCAGGGCGGCTTGTGCAACCCGGG 240

Qy   182 GACCCGGCGGCTTCCGCCGTGGTGCCCAGTGCTGCGGTGCCCGTGCCCTGGCGACCGCA 241
           |||||| | |||| | ||| ||| ||||||||| |||||| ||||| || |||| |||
Db   241 GACCCGAAGATCTACCGCACTTTGTTGCCCAATGCCTCAGTGTGCATGCACTGGGGCTCA 300

Qy   242 CGGCCGCCCCCCGCCGCCGCCCCTCCTTCCGCCAGTGTCTCTGCGCCCAGTGTCGTGGCC 301
           | ||| || ||||||| |||||| |||| |||||||| |||| |||||||||| |||||||
Db   301 CAGCCTCCACCTGCCGCCACCTTTCCTTCCTTCCACCAGTGTCATCCCTGAAAGAGCTGGGCC 360

Qy   302 CGAGTGCTGCGAGAGCGTGTGCGAGCGCGGCGGAGAACGTGCTGGCCTTCGGCTTCGCG 361
           || ||||||| || ||| || |||||| |||| || ||| ||||| |||| |||||||
Db   361 AGGGTTGTGCAGAGACTCTCGGAGCGCAACGAGAGAAACGTGCTGCGTTTTGGCTTTGAG 420

Qy   362 CTGCTGGACGGGGCCCGGGCGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTAC 421
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Db   421 CTGCTTAACGAGGCCAGAGGCGGGCCTCCCATGCGGGGCCTTCGTGGTGCGTAGCTAC 480

Qy   422 CTGCCCAACACGGTGACGACGACTCGCGGGACGCGGGGCCTCGCTGCGC 481
           |||||||| | |||| | ||||| || ||||| |||| | ||| ||||
Db   481 TTGCCCAACACTGTTATTGAGACCCTGCGTGTCAGTGGTGGTCAGTGATGATGCGCTACTGTTGAGC 540

Qy   482 CGCGT-GGGCGACGACGTGCTGGTTC 506
           ||||| |||||||||||| || ||||
Db   541 CGAGTGGGGCGACGACCTGCTGGGTC 566

RESULT 12
AA748707/c
LOCUS   AA748707   315 bp   mRNA   linear   EST 18-FEB-1998
DEFINITION   ny02e05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1270592 3',
             mRNA sequence.
ACCESSION   AA748707
VERSION   AA748707.1   GI:2788665
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 315)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
             Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1226   Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 281.

FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:1270592"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GCB1"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Eco RI; Site_2: Not I; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCGAGCTGGAGCGGCCGCGCTCATTTTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT   68 a   95 c   87 g   65 t
ORIGIN

Query Match   7.1%;   Score 284.4; DB 9; Length 315;
Best Local Similarity 96.2%; Pred. No. 1.9e-46;
Matches 302; Conservative   0; Mismatches 11; Indels   1; Gaps   1;

Qy   3703 GCGCTCGGCTCCACCCCAGGAGCAGCGTTTCCTCACCAGGAGCCGGCTTCCACTCCCCA 3762
           |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   314 GCGCTCGGCTCCACCCCAGGAGCAGCTTTTCTCACCAGGAGCCGGCTTCCACTCCCCA   255

Qy   3763 CATAGGAATAGTCCATCCCAGATTCGCCATTGTTCACCCCTCACCCCTCCTTGC 3822
           |||||||||||||||||||||||| |||||||||||||||||||||||| | |||
Db   254 CATAGGAATAGTCCATCCCAGATTCGCCATTGTTCACCCCTCACCCCTCCGTGGTTGG   195

Qy   3823 CTTCC-ACCCCACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGATT 3881
           |||| |||||||||||||||||||||||||||||||||||||||||||
Db   194 GGGCCGGCGGGCCCCCACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGATT   135

Qy   3882 TGGAGTGACCAAAGGTGTGCCCGTGTACCACAGGCCGAGGACCCTGCACCTGGATGGGGGGTCC 3941
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   134 TGGAGTGACCAAAGGTGTGCCCGTGTACCACAGGCCGAGGACCCTGCACCTGGATGGGGGGTCC   75

Qy   3942 CTGTGGGTCAAATTGGGGGGAGGTGCTGGGAGTAAAATACTGAATATGAGTTTTC 4001
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   74 CTGTGGGTCAAATTGGGGGGAGGTGCTGGGAGTAAAATACTGAATATGAGTTTTC 4001

Qy   4002 AGTTTTGAAAAAAA 4015
           ||||||||||||||
Db   14 AGTTTTGAAAAAAA 1

RESULT 13
BE371943
LOCUS   BE371943   866 bp   mRNA   linear   EST 21-JUL-2000
DEFINITION   601217728F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586614 5',
             mRNA sequence.
ACCESSION   BE371943
VERSION   BE371943.1   GI:9317215
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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LOCUS           BE396925                  715 bp    mRNA    linear  EST 21-JUL-2000
DEFINITION      601290610F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3621050 5',
                mRNA sequence.
ACCESSION       BE396925
VERSION         BE396925.1  GI:9342290
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 715)
AUTHORS         NIH-MGC http://mgc.nci.nih.gov/.
TITLE           National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL         Unpublished
COMMENT         Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
                cDNA Library Preparation: Ling Hong/Rubin Laboratory
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                Plate: LLCM294  row: c  column: 03
                High quality sequence stop: 634.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3621050"
                     /tissue_type="Burkitt lymphoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_8"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT        119 a        164 c        266 g        166 t
ORIGIN
```

```
Query Match          6.3%;       Score 252.2;  DB 10;   Length 715;
Best Local Similarity  93.9%;   Pred. No. 6.3e-40;
Matches    307;    Conservative   0;  Mismatches  13;  Indels    7;  Gaps     4;

Qy   1627  AGGGGTTGGCGTGTTCCGGCCGCAGAGACACCGTCTGCGTGAGAGATCCTGGCCAAGTT  1686
                 |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    372  AGGGGTTGGCGTGTTCCGGCCGCAGAGACACCGTCTGCGTGAGAGATCCTGGCCAAGTT   431

Qy   1687  CCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTTCGTTCTT-TATGTCA  1745
                 ||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    432  CCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTATATGTCA   491

Qy   1746  CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCCGGAAGAGTGTCTGGAGCAAGT  1805
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492  CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCCGGAAGAGTGTCTGGAGCAAGT   551

Qy   1806  TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCT-GTCGGAA  1864
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Db    552  TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTAGTCGGAA   611

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Db    669  TTCATCCCCAAGCTGAAGGGCTGCGGC   695
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REFERENCE       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS         1  (bases 1 to 866)
TITLE           NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL         National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT         Unpublished
                Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLAM8748  row: h  column: 07
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BASE COUNT        157 a        231 c        253 g        225 t
ORIGIN
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Query Match          6.7%;       Score 267;    DB 10;   Length 866;
Best Local Similarity  75.2%;   Pred. No. 7.4e-43;
Matches    333;    Conservative   0;  Mismatches 110;  Indels    0;  Gaps     0;

Qy   2466  GCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCCGCATCAGGGGCAAGT  2525
                 |||||| ||| ||| |  |||| | |||  ||| || |  | ||||||||||| ||
Db      2  GCCTGTTTGACTTCTTCCTGCACTTCCTGCAGTGTCGTAAAGATTGGTGACAGGT    61

Qy   2526  CCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCC  2585
                 ||||||||||||||||||||| | ||||  | |||||||||||||| ||| |||||
Db     62  GCTATACGCAGTGCCAGGGCATCCCCCAAGGTCCCAAAGGCTCCAGCCTATCCACCTGCTCTGCAGTC   121

Qy   2586  TGTGCTACGGCGACATGGAGACAAAGCTGTTTGCGGGGATTCGGCGGACGGGCTGCTCC  2645
                 ||| | ||||| ||||||||||| |||||||||| | |||  |  | ||| |||| |
Db    122  TGTGTTTCGGAGACATGGAGAACAAGCTGTGTTTGCTGAGGTGCAGCAGGATGGGTTGCTTT   181

Qy   2646  TGCGTTTGGTGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAAACCTTCC  2705
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Db    242  TCAGCACCCTGCTCCATGGCCGTTCCTGAGTATGAATGGCATGATAAACTTGCAGAAGACAG   301

Qy   2766  TGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGCTGGCACCGCTTTTGTTCAGATGCCGG  2825
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Db    422  GTGACTACTCAGGGTAAGCACAG   444
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RESULT 14
BE396925

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RESULT 15
AA311750
LOCUS       AA311750            409 bp    mRNA      linear    EST 19-APR-1997
DEFINITION  EST182469 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA
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ACCESSION   AA311750
VERSION     AA311750.1  GI:1964077
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
            ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
            ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
            Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
            ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
            Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
            Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.
            , Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
            Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
            Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
            ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
            Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
   MEDLINE  96026280
    PUBMED  7566098
COMMENT     Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
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ORIGIN
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Best Local Similarity  97.7%;  Pred. No. 1.8e-39;
Matches  252;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy  2649 GTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCCACGCGAAAACCTTCCTCA 2708
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Db     1 GTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCCACGCGAAAACCTTCCTCA   60

Qy  2709 GGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCCTGCGGTGGTGAAGACAGTGG 2768
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Db    61 GGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCCTGCGGTGGTGAAGACAGTGG  120

Qy  2769 TGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGCCC 2828
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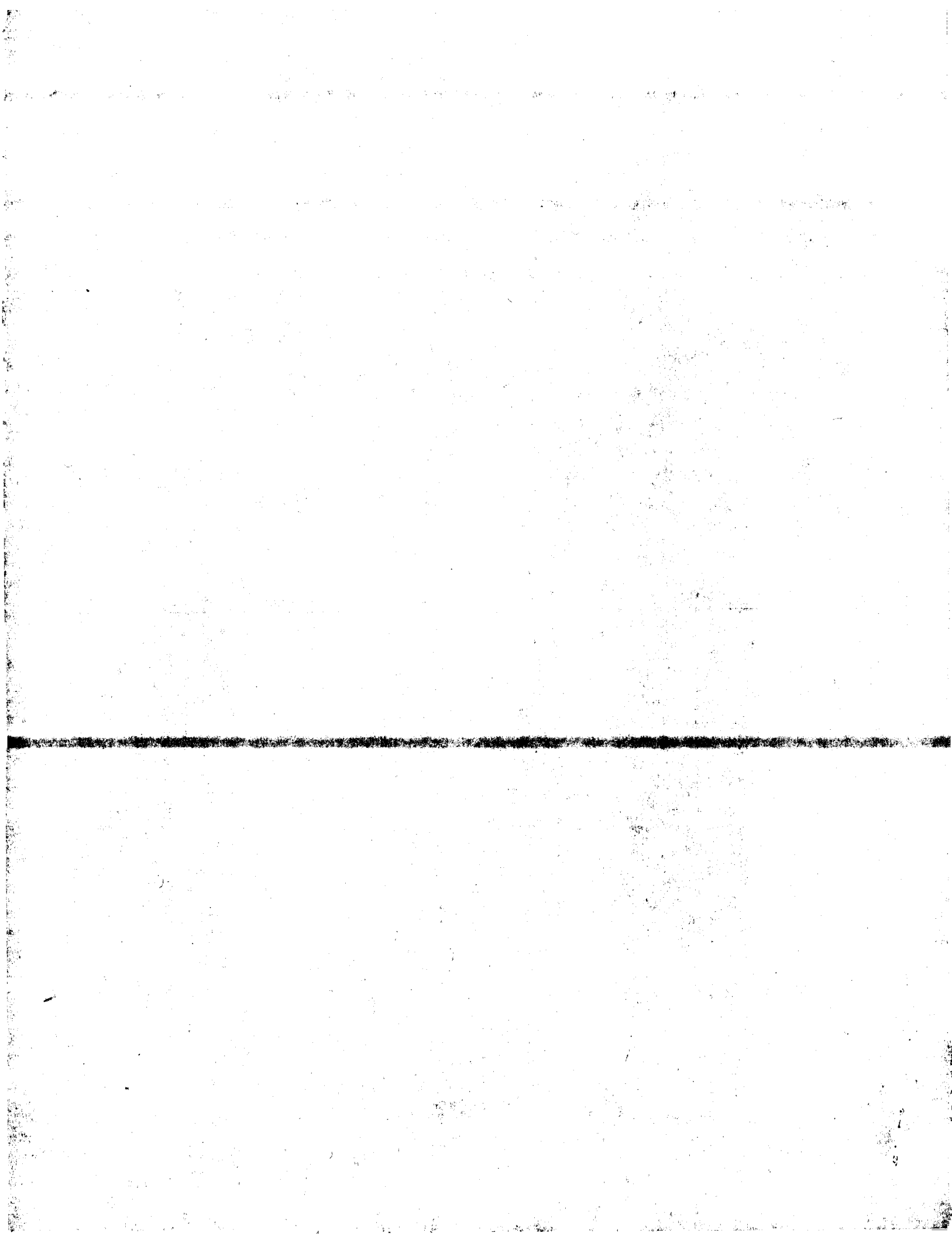
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Db   121 TGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTNTTCAGATGCCGGCCC  180
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Qy  2829 ACGGCCTATTCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCG 2888
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Db   181 ACGGCNTATTCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCG  240

Qy  2889 ACTACTCCAGCTATGCCC 2906
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Search completed: October 15, 2003, 04:34:47
Job time : 7781 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: October 14, 2003, 21:56:28 ; Search time 14222 Seconds
(without alignments)
11549.160 Million cell updates/sec

Title: US-10-054-295-224
Perfect score: 4015
Sequence: 1 GCAGCGCTGCGTGCCTGCTGC.........TTTTTCAGTTTTGAAAAAAA 4015

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
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4: gb_om:*
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6: gb_pat:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	4015	100.0	4015	6	AR175848	AR175848 Sequence
3	4015	100.0	4015	6	AR182221	AR182221 Sequence
4	4015	100.0	4015	6	AR224455	AR224455 Sequence
5	4015	100.0	4015	6	AR226390	AR226390 Sequence
6	4015	100.0	4015	6	AR243328	AR243328 Sequence
7	4015	100.0	4015	6	AR263555	AR263555 Sequence
8	4015	100.0	4015	6	AR265996	AR265996 Sequence
9	4015	100.0	4015	6	AX019310	AX019310 Sequence
10	4015	100.0	4015	6	AX133979	AX133979 Sequence
11	4015	100.0	4015	6	AX552695	AX552695 Sequence
12	4015	100.0	4015	6	BD011044	BD011044 Human tel
13	4015	100.0	4015	6	BD015832	BD015832 Quantitat
14	4015	100.0	4015	6	BD082985	BD082985 Method fo
15	4015	100.0	4015	6	BD131727	BD131727 Method fo
16	4015	100.0	4015	6	E36793	E36793 Human telom
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18	4015	100.0	4042	6	AX001446	AX001446 Sequence
19	4015	100.0	4042	6	AX003121	AX003121 Sequence
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21	4015	100.0	4070	6	AX391846	AX391846 Sequence
22	4008.6	99.8	4037	6	BD011070	BD011070 Human tel
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24	4002	99.7	4027	9	AF018167	AF018167 Homo sapi
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28	3849.2	95.9	4029	6	E36818	E36818 Human telom
29	3641	90.7	3855	6	AR243330	AR243330 Sequence
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31	3641	90.7	3855	6	E36795	E36795 Human telom
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33	3400	84.7	13766	6	AX553919	AX553919 Sequence
34	3399	84.7	3399	6	AX481414	AX481414 Sequence
35	3396	84.6	3396	6	BD091553	BD091553 Adult bon
36	3396	84.6	3396	6	BD094749	BD094749 The cell
37	3396	84.4	3396	6	BD096291	BD096291 Cells cap
38	3388	84.4	8742	9	AX553924	AX553924 Sequence
39	3011	75.0	3210	9	AB085628	AB085628 Homo sapi
40	2637	65.7	3028	9	AB086379	AB086379 Homo sapi
41	2555	63.6	2992	9	AB086950	AB086950 Homo sapi
42	2335.4	58.2	2357	6	E22277	E22277 Higher anim
43	1961.4	48.9	2175	6	E22279	E22279 Higher anim
44	1960.4	48.8	2176	6	AR243329	AR243329 Sequence
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ALIGNMENTS

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DEFINITION   Sequence 224 from patent US 6093809.
ACCESSION   AR104587
VERSION   AR104587.1   GI:12817295
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 4015)
  AUTHORS   Cech,T.R. and Lingner,J.
  TITLE   Telomerase
  JOURNAL   Patent: US 6093809-A 224 25-JUL-2000;
FEATURES   Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

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Best Local Similarity  100.0%;  Pred. No. 0;
Matches 4015;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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LOCUS       AR175848                4015 bp    DNA            linear   PAT 17-DEC-2001
DEFINITION  Sequence 224 from patent US 6309867.
ACCESSION   AR175848
VERSION     AR175848.1  GI:17917147
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4015)
  AUTHORS   Cech,T.R. and Nakamura,T.
  TITLE     Telomerase
  JOURNAL   Patent: US 6309867-A 224  30-OCT-2001;
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ORIGIN

Query Match        100.0%;  Score 4015;  DB 6;  Length 4015;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 4015;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db       1 GCAGCGCTGCGTCCTGCTGCCGCACGTGGGAAGCCCTGCCCCGGCCACCCCGCGATGCC      60

Qy      61 GCGGCTCCCCGCCTGCCGAGCCGTGCGCTGCCTCCCTGCTCGCCGCCACTACCGCGAGGTGCT     120
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Db      61 GCGGCTCCCCGCCTGCCGAGCCGTGCGCTGCCTCCCTGCTCGCCGCCACTACCGCGAGGTGCT     120

Qy     121 GCCGTGGCCACGTTCGTGCGGCGCCTGGGGCGGCCCCAGGGCTGCGGGCTGGTGCAGCGCGG     180
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Db     121 GCCGTGGCCACGTTCGTGCGGCGCCTGGGGCGGCCCCAGGGCTGCGGGCTGGTGCAGCGCGG     180

Qy     181 GGACCCCGGCGGCTTTCCGCCGCTGGTGGTCCCAGTGCCTGGTGTGCGTGCCCTTGGGACGC     240
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Qy     241 ACGGCCGCGCCCCGCCCCTCCTTCGCCGTCCAGGTGTCCTGCCTGGAAGGACTGGTTGGCGG     300
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Qy     361 GCTGCTGGACGGGGCCCCGCGGGGGCCCCGAGGGCCTTCACCACCAGCGTGCGCAGCTA     420
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Qy     421 CCTGCCCACACGTGACCAGCAGCGTGACGACGCACGCGGGGCGGGGCCGTGGGGCGCTGCTCGG     480
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Qy     781 TGCCCCTGAGCCGGAGCCGGACGCGACGGTGCGGCGCGGGGTCCGTTGGGCAGGGGTCCAGGAC     840
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Db     781 TGCCCCTGAGCCGGAGCCGGACGCGACGGTGCGGCGCGGGGTCCGTTGGGCAGGGGTCCAGGAC     840

Qy     841 GCGGTGGACCCGAGTGACCGTGGTTTCTGTGGTGTGTCACCTGCCAGACCCGCCGGAAGAAGC     900
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Db     961 GCACCACGCGGCGGCCCCATCCACATGCGGCCACCACGTCCCTGGACACGCCACCGCCTGTCC    1020

Qy    1021 CCCGGTGTACGCGCGAGACCAAGCACTTCCTCACTCCTCTACTCCTCAGCGCGACAAGGAGCAGCTGCG    1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCCGGTGTACGCGCGAGACCAAGCACTTCCTCACTCCTCTACTCCTCAGCGCGACAAGGAGCAGCTGCG    1080

Qy    1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCCAGCCTGACTGGCGCTGGCGGCTCCGGAGGCTCGTGGA    1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCCAGCCTGACTGGCGCTGGCGGCTCCGGAGGCTCGTGGA    1140

Qy    1141 GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGGACTCCCCGCCAGGTTGCCCCGCCT    1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGGACTCCCCGCCAGGTTGCCCCGCCT    1200

Qy    1201 GCCCCAGCGCTACTGGCCAAATGGGCCCCGTGTTTCTGGAGCTGCTTGGGAACCACGCGCCA    1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GCCCCAGCGCTACTGGCCAAATGGGCCCCGTGTTTCTGGAGCTGCTTGGGAACCACGCGCCA    1260

Qy    1261 GTGCCCCTACGGGTGCTGCCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTGCACCCCAGC    1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGCCCCTACGGGTGCTGCCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTGCACCCCAGC    1320

Qy    1321 AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGTGGCGGCCCCCGAGGAGGAGGA    1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGTGGCGGCCCCCGAGGAGGAGGA    1380

Qy    1381 CACAGACCCCGTGCCGTCAGCTGCCGCTGGAGCCCGGGCAGCAGCCCCTGGCAGGTGTA    1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CACAGACCCCGTGCCGTCAGCTGCCGCTGGAGCCCGGGCAGCAGCCCCTGGCAGGTGTA    1440

Qy    1441 CGGCTTCGTGCGGGCCTGCCTGGCGTGCCCCCAGGCCTCTGGGGCTCCAGGCA    1500
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Db    1441 CGGCTTCGTGCGGGCCTGCCTGGCGTGCCCCCAGGCCTCTGGGGCTCCAGGCA    1500

Qy    1501 CAACGAACGGCCGCTTCCTCAGGAACACCACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA    1560
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Db    1501 CAACGAACGGCCGCTTCCTCAGGAACACCACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA    1560

Qy    1561 GCTCTCGCTGCGAGGAGCTGACGTGGAAGATGAGCGTGCGGCGACTGGCGCTTGGCTGCGCAG    1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GCTCTCGCTGCGAGGAGCTGACGTGGAAGATGAGCGTGCGGCGACTGGCGCTTGGCTGCGCAG    1620

Qy    1621 GAGCCCAGGGTTGGCTGTGTTCCGCGGACCGTCGTGCGTGAGGAGATCTGGC    1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GAGCCCAGGGTTGGCTGTGTTCCGCGGACCGTCGTGCGTGAGGAGATCTGGC    1680

Qy    1681 CAAGTTCGTGCACTGCGCTGATGAGTGTGTACGTCGTGATGCTGCTCAGTGCTCTTTTCTTTTA    1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 CAAGTTCGTGCACTGCGCTGATGAGTGTGTACGTCGTGATGCTGCTCAGTGCTCTTTTCTTTTA    1740

Qy    1741 TGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG    1800
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Db    1741 TGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG    1800

Qy    1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTCGCAGCTGCGTC    1860
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Db    1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTCGCAGCTGCGTC    1860

Qy    1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCGCCCTGCGACGTCCAGACTCCG    1920
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Db    1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCGCCCTGCGACGTCCAGACTCCG    1920

Qy    1921 CTTCATCCCAAGCCTGACGGCTGCGCGCCGATTGTGAACATGACTACGTCGTGGGAGC    1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 CTTCATCCCAAGCCTGACGGCTGCGCGCCGATTGTGAACATGACTACGTCGTGGGAGC    1980

Qy    1981 CAGAACGTTCCGCAGAGAAAAGAGAGGGCCGAGAGCGTCCACCTCGAGGGTGAAGGCACTGTT    2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CAGAACGTTCCGCAGAGAAAAGAGAGGGCCGAGAGCGTCCACCTCGAGGGTGAAGGCACTGTT    2040
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Qy   2041 CAGCGTGCTCAACTACGAGCGGGCGGCGCCCGGCCTCCTGTGGCTGCTGGG 2100
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Db   2041 CAGCGTGCTCAACTACGAGCGGGCGGCGCCCGGCCTCCTGTGGCTGCTGGG 2100

Qy   2101 CCTGGACGATATCCACAGGAGGCCTGGCGCACCTTCGTCGTGCGGGCCGAGGACCC 2160
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Db   2101 CCTGGACGATATCCACAGGAGGCCTGGCGCACCTTCGTCGTGCGGGCCGAGGACCC 2160

Qy   2161 GCGGCCTGAGCTGTACTTTGTCAAGGTGACGGGCGTACGACACACCATCCCCCA 2220
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Db   2161 GCCGGCCTGAGCTGTACTTTGTCAAGGTGACGGGCGTACGACACACCATCCCCCA 2220

Qy   2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCG 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCG 2280

Qy   2281 TCGGTATGCCGTGGTCAGAAGGCCGCGCCCATGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TCGGTATGCCGTGGTCAGAAGGCCGCGCCCATGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340

Qy   2341 CGTCTCTACCTTGACAGACCTCCAGCGCGTACATGCGACAGTTCGTGCTCACCTGCAGGA 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CGTCTCTACCTTGACAGACCTCCAGCGCGTACATGCGACAGTTCGTGCTCACCTGCAGGA 2400

Qy   2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG 2460
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Db   2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG 2460

Qy   2461 CAGTGGCCTTCTTCGACGTCTTCCTACGGGATCCCCAGGGGTCCATCCTCTCCACCGCTCTCTG 2520
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Db   2521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCCAGAGTGTCGGGGGACTGTCCAAGGGCT 2580

Qy   2581 CAGCCTGTGTGCTACGGCGACACAAGCTGTTTGCGGGGATTCGGCGGGACGGGGCT 2640
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Db   2581 CAGCCTGTGTGCTACGGCGACACAAGCTGTTTGCGGGGATTCGGCGGGACGGGGCT 2640

Qy   2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTGTGGTGACACCTCACCTCACCACGCGAAAAC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTGTGGTGACACCTCACCTCACCACGCGAAAAC 2700

Qy   2701 CTTCCTCAGGACCCGTGTCCGAGGTGTCGGTGGTGAACTTGCCGGAA 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTTCCTCAGGACCCGTGTCCGAGGTGTCGGTGGTGAACTTGCCGGAA 2760

Qy   2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGCCCTGGGTGGTCACGGCTTTGTTCAGAT 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGCCCTGGGTGGTCACGGCTTTGTTCAGAT 2820

Qy   2821 GCCGGCCCACGGCCTATTCCCCGGTGCGGCCGCTGCTCGATACCCGGACCCTGGAGGT 2880
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Db   2821 GCCGGCCCACGGCCTATTCCCCGGTGCGGCCGCTGCTCGATACCCGGACCCTGGAGGT 2880

Qy   2881 GCAGAGCGACTACTCCAGCTATGCCCATCAGAGCGACTTCACCTTCAACCG 2940
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Db   2881 GCAGAGCGACTACTCCAGCTATGCCCATCAGAGCGACTTCACCTTCAACCG 2940

Qy   3001 TCACAGCCTGTTTCTTGGATTTGCAGGTGAACAGCGTGCACCAACATCTA 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TCACAGCCTGTTTCTTGGATTTGCAGGTGAACAGCGTGCACCAACATCTA 3060

Qy   3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTCTGCAGCTCCCATTTCA 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTCTGCAGCTCCCATTTCA 3120

Qy   3121 TCAGCAAGTTTGGAAGAACCCCACATTTTCTCGCGCGTCATCTCTGACACGGCCTCCCCT 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 TCAGCAAGTTTGGAAGAACCCCACATTTTCTCGCGCGTCATCTCTGACACGGCCTCCCCT 3180
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RESULT 3
AR182221

LOCUS   AR182221   4015 bp   DNA   linear   PAT 20-APR-2002
DEFINITION   Sequence 1 from patent US 6337200.
ACCESSION   AR182221
VERSION   AR182221.1 GI:20225137
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
               Unclassified.
REFERENCE   1 (bases 1 to 4015)
  AUTHORS   Morin,G.B.
  TITLE   Human telomerase catalytic subunit variants

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JOURNAL     Patent: US 6337200-A 1 08-JAN-2002;
FEATURES            Location/Qualifiers
 source     1 .4015
                    /organism="unknown"
BASE COUNT  663 a      1363 c     1275 g      714 t
ORIGIN

Query Match        100.0%;   Score 4015;   DB 6;   Length 4015;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 4015;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
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Qy      1 GCAGCGCTGCGTCCTGCGTCGCACGTGGGAAGCCTGGCCCCCGATGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAGCGCTGCGTCCTGCGTCGCACGTGGGAAGCCTGGCCCCCGATGCC 60

Qy     61 GCGCGCTCCCCGCGTGCCGAGCCGTCGGCCTCCGCTGCTCGCGCGCCG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGCGCTCCCCGCGTGCCGAGCCGTCGGCCTCCGCTGCTCGCGCGCCG 120

Qy    121 GCCGCTGGCCACGTTCGTGCGGCGGCCTCGGGGTGCGTGGTGGTGGTGG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCGCTGGCCACGTTCGTGCGGCGGCCTCGGGGTGCGTGGTGGTGGTGG 180

Qy    181 GGACCCGGGGCTTTCCGCGCGTGGTGCCCAGTGCGTGGTGTCCCTGGGACGC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGACCCGGGGCTTTCCGCGCGTGGTGCCCAGTGCGTGGTGTCCCTGGGACGC 240

Qy    241 ACGGCGCGCCCCGCGCCCCCCGCGCCCGCCTCCTTCCGCCCAGGTGTTCTGC 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACGGCGCGCCCCGCGCCCCCCGCGCCCGCCTCCTTCCGCCCAGGTGTTCTGC 300

Qy    301 CCGAGTGCTGCAGAGCGTGCGAGGCCGCGGGCCACTGCGGGGAGCCGCGC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGAGTGCTGCAGAGCGTGCGAGGCCGCGGGCCACTGCGGGGAGCCGCGC 360

Qy    361 GCTGCTGGACGGGGCGGGGGGCCCCGGGGGGCCTTCACCACCAGCGTGCGCAGCTA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTGCTGGACGGGGCGGGGGGCCCCGGGGGGCCTTCACCACCAGCGTGCGCAGCTA 420

Qy    421 CCTGCCCAACACGGTGACCGACGGGGGCGGGGAGCCGGTGGGGCGTGCTGCTGCG 480
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Db    421 CCTGCCCAACACGGTGACCGACGGGGGCGGGGAGCCGGTGGGGCGTGCTGCTGCG 480

Qy    481 CCGCGTGGGCGACCACGTCTGGTTCACCTGGCGCACGCTGCCGCCTCTTGTGCTGT 540
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Db    481 CCGCGTGGGCGACCACGTCTGGTTCACCTGGCGCACGCTGCCGCCTCTTGTGCTGT 540

Qy    541 GGTCCCCAGCTGCGGCCTACCAGGTGTGCGGGGCCGCGCCGTGCCCAGCTCGGG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGTCCCCAGCTGCGGCCTACCAGGTGTGCGGGGCCGCGCCGTGCCCAGCTCGGG 600

Qy    601 TGCCCCTGAGCCGGACGGAGGCGGACGCCCGGTTGGGCAGGGGTCTCGGGGATG 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGCCCCTGAGCCGGACGGAGGCGGACGCCCGGTTGGGCAGGGGTCTCGGGGATG 660

Qy    661 CTGGAACCATAGCCTCAGGGAGGCCGGGGGTCCCCGGGGTCCCCGCTGCCCAGG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGGAACCATAGCCTCAGGGAGGCCGGGGGTCCCCGGGGTCCCCGCTGCCCAGG 720

Qy    721 GAGGCGCGGGGCAGTGCCGCAGCCGAAGTCTGCCGTTGCCCAAGAGGCGTGGCGC 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GAGGCGCGGGGCAGTGCCGCAGCCGAAGTCTGCCGTTGCCCAAGAGGCGTGGCGC 780

Qy    781 TGCCCCTGAGCCGGACGGCGGAGGCCAGGGTCTGGCAGGGGTCTCCACCCGGGGC 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TGCCCCTGAGCCGGACGGCGGAGGCCAGGGTCTGGCAGGGGTCTCCACCCGGGGC 840

Qy    841 GCGTGGACCGGACCGTGGTTTCGTGTGGTCACCTGCCAGAGCCGCCGAAGAAGC 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCGTGGACCGGACCGTGGTTTCGTGTGGTCACCTGCCAGAGCCGCCGAAGAAGC 900

Qy    901 CACCTCTTTGGAGGTGCGGCTCTCTGGCACGGCGCACCACCCATCCGTGGGCCGCCA 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACCTCTTTGGAGGTGCGGCTCTCTGGCACGGCGCACCACCCATCCGTGGGCCGCCA 960

Qy    961 GCACCACGCGGGCGCCCCCATCCCACCCACATCGCGGCCACCAGTCCCTGGGACA 1020
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Db    961 GCACCACGCGGGCGCCCCCATCCCACCCACATCGCGGCCACCAGTCCCTGGGACA 1020

Qy   1021 CCGGGTGTACGCCGGAGACCAAGCACTTCCTCCTACTCCTCAGGCGGACAAGGAG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCGGGTGTACGCCGGAGACCAAGCACTTCCTCCTACTCCTCAGGCGGACAAGGAG 1080

Qy   1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCCGTCGGAGGCTC 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCCGTCGGAGGCTC 1140

Qy   1141 GACCATCTTTCTGGTTCCGGTTCCAGGCCCTGGATGCCAGGGGACTCCCCGCGGC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GACCATCTTTCTGGTTCCGGTTCCAGGCCCTGGATGCCAGGGGACTCCCCGCGGC 1200

Qy   1201 GCCCCAGGGCTACTGGGCAAATGCGGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GCCCCAGGGCTACTGGGCAAATGCGGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC 1260

Qy   1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCGCCGTGCGAGCTGGGACGC 1320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCGCCGTGCGAGCTGGGACGC 1320

Qy   1321 AGCCGGTGTGTGCCCGCGCCTCGTGTGCCCCGAGGGCTCGTGTGCCCCGAGGAGGAGA 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGCCGGTGTGTGCCCGCGCCTCGTGTGCCCCGAGGGCTCGTGTGCCCCGAGGAGGAGA 1380

Qy   1381 CACAGACCCCCGTCGCGCTCGTGGCTGCCCGCCTGGTGCCCCGGCTCCCAGGCTTCGC 1440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CACAGACCCCCGTCGCGCTCGTGGCTGCCCGCCTGGTGCCCCGGCTCCCAGGCTTCGC 1440

Qy   1441 CGGCTTCGTGCGGGGCCTGGTGCGGGGCTCGTGTGCCCCCAGGGCTCCTCCCAGGCA 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CGGCTTCGTGCGGGGCCTGGTGCGGGGCTCGTGTGCCCCCAGGGCTCCTCCCAGGCA 1500

Qy   1501 CAACGAAGCGCGTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
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Db   1501 CAACGAAGCGCGTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

Qy   1561 GCTCTCGCGTGCAGGAGCTGACGTGGAAGATGAGCGTGGCGGACTGCGCTTGGCGTGCGTGT 1620
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Db   1561 GCTCTCGCGTGCAGGAGCTGACGTGGAAGATGAGCGTGGCGGACTGCGCTTGGCGTGCGTGT 1620

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            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1861 GGAAGCAGAGGTCAGGCAGCCATCGGGAAGCCAGGGCCCGCCTGCTGAGCTTCCGAGACTCCG 1920
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Qy   1921 CTTCATCCCCAAGCCTGCGCGGCCTGCGGCCCGCGATTGTGAACATGACTACGTCGTGGGAGC 1980
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Db   1921 CTTCATCCCCAAGCCTGCGCGGCCTGCGGCCCGCGATTGTGAACATGACTACGTCGTGGGAGC 1980

Qy   1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGCAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGCAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040
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Qy 2041 CAGCGTGCTCAACTACGAGCGGGCGCGGGCCCCGGCCTCCTCGGGCGCCTCTGTGCTGGG 2100
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db 2041 CAGCGTGCTCAACTACGAGCGGGCGCGGGCCCCGGCCTCCTCGGGCGCCTCTGTGCTGGG 2100

Qy 2101 CCTGGACGATATCCACACGGCCTGGCCGTGCGTGTGGGGCCCAGGACCC 2160
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Qy 2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA 2220
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Db 2161 GCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA 2220

Qy 2221 GGACAGGCTCACGGAGGTCATGCCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2221 GGACAGGCTCACGGAGGTCATGCCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG 2280

Qy 2281 TCGGTATGCCGTGGTCCAGAAGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340
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Db 2341 CGTCTCTACCTTGACAGACCTCCAGCCTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400

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Db 2401 GACCAGCCGCGTGAGGGATGCCGTCGTCATGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460

Qy 2461 CAGTGGGCCTCTTCGACGTCTTCATGTGCCACACCGCGTCGGCCATCAGGGG 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2461 CAGTGGGCCTCTTCGACGTCTTCATGTGCCACACCGCGTCGGCCATCAGGGG 2520

Qy 2521 CAAGTCCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCCTCTGCTGCTCTG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 2581 CAGCCGTGTGCTACGGCACATGAGAACAAAGCTGTTTGCTGGGGATTCGGCGGGACGGGCT 2640
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Db 2581 CAGCCGTGTGCTACGGCACATGAGAACAAAGCTGTTTGCTGGGGATTCGGCGGGACGGGCT 2640

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          |||||||||||||||||||||||||||||||||||||||||||||
Db 2821 GCGGGCCACGCGTATTCCCGTGTCGTCTGCGTGGACCCTGGAGGT 2880

Qy 2881 GCAGAGGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCCAGTCTCACCTTCAACCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2881 GCAGAGGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCCAGTCTCACCTTCAACCG 2940

Qy 2941 CGGCTTCAAGGCTGGAGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2941 CGGCTTCAAGGCTGGAGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000

Qy 3001 TCACAGCCTGTTTCTGGATTTGCAGTTGAACAGCCTCCAGACCGTGCACCAACATCTA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3001 TCACAGCCTGTTTCTGGATTTGCAGTTGAACAGCCTCCAGACCGTGCACCAACATCTA 3060

Qy 3061 CAAGATCCTCCTGCTCGCAGGCGTACAGGTTTCACGCATGTGTCTGCAGCTCCCATTTCA 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3061 CAAGATCCTCCTGCTCGCAGGCGTACAGGTTTCACGCATGTGTCTGCAGCTCCCATTTCA 3120

Qy 3121 TCAGCAAGTTTGGAAGAACCCACATTTTCCTGCGGCGTCATCTCTGACACGGCGCTCCCT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3121 TCAGCAAGTTTGGAAGAACCCACATTTTCCTGCGGCGTCATCTCTGACACGGCGCTCCCT 3180

Qy 3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGAGATGTCGGGGCGCCAAGGGGCGCCGC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGAGATGTCGGGGCGCCAAGGGGCGCCGC 3240

Qy 3241 CGGCCCCTCTGCCCTCCGAGGCGTGCAGTGCGTGTTGCCACCAAGCATTCCTGCTCAAGCT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3241 CGGCCCCTCTGCCCTCCGAGGCGTGCAGTGCGTGTTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy 3301 GACTCGACACCGTGCACTACGTGCCACTCCTCAGGGTCACTCAGGACAGCCCAGACGCA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3301 GACTCGACACCGTGCACTACGTGCCACTCCTCAGGGTCACTCAGGACAGCCCAGACGCA 3360

Qy 3361 GCTGAGTCGGAAGCTCCCGGGACGTCCCGTGACTGCCCTGCCCTGAGGCCGGCCAACCCGGC 3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3361 GCTGAGTCGGAAGCTCCCGGGACGTCCCGTGACTGCCCTGCCCTGAGGCCGGCCAACCCGGC 3420

Qy 3421 ACTGCCCTACAGACTTCAAGACCATCCTGGACTGATGGCCACCGCGCCCACAGCCAGGCCGA 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3421 ACTGCCCTACAGACTTCAAGACCATCCTGGACTGATGGCCACCGCGCCCACAGCCAGGCCGA 3480

Qy 3481 GAGCAGACACCAGCAGCCCTGTCAGCGGCCTCTACGTCCCAGGGAGGAGGGGGCGGCC 3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3481 GAGCAGACACCAGCAGCCCTGTCAGCGGCCTCTACGTCCCAGGGAGGAGGGGGCGGCC 3540

Qy 3541 CACACCCAGGCCGACCACCGGCCTGAGTGAGTGGCCTGAGGGCCTGAGGCCCAAGGCTG 3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3541 CACACCCAGGCCGACCACCGGCCTGAGTGAGTGGCCTGAGGGCCTGAGGCCCAAGGCTG 3600

Qy 3601 CATGTCCGGCTGAAGGCTGAGGTCCGGCGTGTCCGGCGAGTGTCCAGCCAAGGGCT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3601 CATGTCCGGCTGAAGGCTGAGGTCCGGCGTGTCCGGCGAGTGTCCAGCCAAGGGCT 3660

Qy 3661 GAGTGTCCAGCACACCTGCGTCTCACTTCCCCCACCAGGAGAGCCTCCACTCCCACCCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3661 GAGTGTCCAGCACACCTGCGTCTCACTTCCCCCACCAGGAGAGCCTCCACTCCCACCCCA 3720

Qy 3721 GGGCCAGCGTTTTCCTCACCAGGAGAGCCCGGCTTCCACTCCCCACATAGGAGGAATCCATCC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3721 GGGCCAGCGTTTTCCTCACCAGGAGAGCCCGGCTTCCACTCCCCACATAGGAGGAATCCATCC 3780

Qy 3781 CCAGAATTCGCCATTGTTCACCCCTGCCTTGTTCACCCTCCTTGCCTTCCACCCCACCATCC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3781 CCAGAATTCGCCATTGTTCACCCCTGCCTTGTTCACCCTCCTTGCCTTCCACCCCACCATCC 3840

Qy 3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGAGTGACCAAAGTGTG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGAGTGACCAAAGTGTG 3900

Qy 3901 CCCTGTACACAGGCGAGGAGGACCCTGCACCTGGTCCCTGTGGTCAAATTGGGGG 3960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3901 CCCTGTACACAGGCGAGGAGGACCCTGCACCTGGTCCCTGTGGTCAAATTGGGGG 3960

Qy 3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015

TITLE   Dendritic cell vaccine containing telomerase reverse transcriptase
            for the treatment of cancer
JOURNAL   Patent: US 6440735-A 1 27-AUG-2002;
FEATURES   source
                1..4015
                Location/Qualifiers
                /organism="unknown"
BASE COUNT   663 a   1363 c   1275 g   714 t
ORIGIN

Query Match   100.0%;   Score 4015;   DB 6;   Length 4015;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 GCAGGCTGCGTCCTGCTGCCGACGTGGGAAGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGGCGATGCC   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GCAGGCTGCGTCCTGCTGCCGACGTGGGAAGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGGCGATGCC   60

Qy   61 GCGCGCTCCCGCTGCCGAGCGCGTGCGCTCCCTGCTCGCCGCCACTACCCGCGAGTGCT  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCGCGCTCCCGCTGCCGAGCGCGTGCGCTCCCTGCTCGCCGCCACTACCCGCGAGTGCT  120

Qy  121 GCCGTGGCCACGTTCGTGCGGCGCGCCCCCAGGGCGTGGGCGGCGTGGTGCGCGCGCGG  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GCCGTGGCCACGTTCGTGCGGCGCGCCCCCAGGGCGTGGGCGGCGTGGTGCGCGCGCGG  180

Qy  181 GGACCCGCGGCGTTTCCCGCGCGCGCGTGGTGGCCCAGTGTGCCGTGTGCCCTGGGACGC  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GGACCCGCGGCGTTTCCCGCGCGCGCGTGGTGGCCCAGTGTGCCGTGTGCCCTGGGACGC  240

Qy  241 ACGGCGGCCCCGCCGCGCGCCCCCGGCCGCTCCTTCCGCGCTGCCTCCGCGAGTGCTGGC  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ACGGCGGCCCCGCCGCGCGCCCCCGGCCGCTCCTTCCGCGCTGCCTCCGCGAGTGCTGGC  300

Qy  301 CCGAGTGCTGCAGAGGCGCGGGGGCCCCGGGGGCCCCCGAGGGCTTCGGCCTTCGC  360
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Db  301 CCGAGTGCTGCAGAGGCGCGGGGGCCCCGGGGGCCCCCGAGGGCTTCGGCCTTCGC  360

Qy  361 GCTGCTGGACGGGGCCCCGGGGGCGGGGGCCCCCCGAGGGCGTCGCGCAGCTA  420
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Db  361 GCTGCTGGACGGGGCCCCGGGGGCGGGGGCCCCCCGAGGGCGTCGCGCAGCTA  420

Qy  421 CCTGCCCAACACGGTGACCGACGCCACTGCGGGCGGGGCGGGCTGCTGCG  480
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CCTGCCCAACACGGTGACCGACGCCACTGCGGGCGGGGCGGGCTGCTGCG  480

Qy  481 CCGGCTGGGGCGACGCGGGCAGCGTGTCACCTGGTCGTGGTTTGTGCTGGT  540
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 CCGGCTGGGGCGACGCGGGCAGCGTGTCACCTGGTCGTGGTTTGTGCTGGT  540

Qy  541 GGCTCCCAGCGTGCGCCTACCAGGTGCGGGCGCCGCCGTGTACCAGCTCGGCCGCTGCCAC  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GGCTCCCAGCGTGCGCCTACCAGGTGCGGGCGCCGCCGTGTACCAGCTCGGCCGCTGCCAC  600

Qy  601 TCAGGCCCGGCCGCCCCCACCACGCCAGTGCAGCGGCGTCTCGGGATGCGGAACGGGC  660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TCAGGCCCGGCCGCCCCCACCACGCCAGTGCAGCGGCGTCTCGGGATGCGGAACGGGC  660

Qy  661 CTGGAACCATAGCGTCAGGGAGGAGGCGGGGTCCCCAGCCCGGGGTGCGAG  720
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Db  661 CTGGAACCATAGCGTCAGGGAGGAGGCGGGGTCCCCAGCCCGGGGTGCGAG  720

Qy  721 GAGGCGGGGGCGGGGCCAGCGTGTGCCAGCCCGGAGCTCTGCGAGTCGCGC  780
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Db  721 GAGGCGGGGGCGGGGCCAGCGTGTGCCAGCCCGGAGCTCTGCGAGTCGCGC  780

Qy  781 TGCCCCTGAGCCGCGGACGACCCGTTGGGCCACCTTGGGGTGTGTGTTCACCTGGTCTGTGTGTCACCGTGC  840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 TGCCCCTGAGCCGCGGACGACCCGTTGGGCCACCTTGGGGTGTGTGTTCACCTGGTCTGTGTGTCACCGTGC  840

Qy  841 GCGTGACCGAGTGACCGTTTCGTGGTCACCTGGTGTCACCTGCACCTGGTCACCGAGACCAGGAAGC  900
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Db  841 GCGTGACCGAGTGACCGTTTCGTGGTCACCTGGTGTCACCTGCACCTGGTCACCGAGACCAGGAAGC  900
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Qy  901 CACCCTCTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCACCCACCATCCGTGGGCCGCCA   960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 CACCCTCTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCACCCATCCCACCCGTGGGCCGCCA   960

Qy  961 GCACCACGCGGGCGCCCCCATCCACATCGGCGGGCCCCCATCCACATCCACCACGTCCCTGGACACGCCTTGTCC  1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 GCACCACGCGGGCGCCCCCATCCACATCGGCGGGCCCCCATCCACATCCACCACGTCCCTGGACACGCCTTGTCC  1020

Qy 1021 CCGGGTGTACGCCGAGACCAAGCACTTCCTACTCCTCAGGCGACAAGGAGGAGCAGTCG  1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 CCGGGTGTACGCCGAGACCAAGCACTTCCTACTCCTCAGGCGACAAGGAGGAGCAGTCG  1080

Qy 1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGGCCCAGCCTGACTGGCGCTCGGACGGCTCGTGGA  1140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 GCCCTTCCTCCTACTCAGCTCTCTGAGGGCCCAGCCTGACTGGCGCTCGGACGGCTCGTGGA  1140

Qy 1141 GACCATCTTCTGGGTTCCAGGCCTTGGATGCCAGGACTCCCCGCCCTTGCCCGCCT  1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 GACCATCTTCTGGGTTCCAGGCCTTGGATGCCAGGACTCCCCGCCCTTGCCCGCCT  1200

Qy 1201 GCCCCAGCGCTACTGGCAAATGGGGCCCTGTTTCTGGCAAATCGGGCTGGTGCAGCGCGG  1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 GCCCCAGCGCTACTGGCAAATGGGGCCCTGTTTCTGGCAAATCGGGCTGGTGCAGCGCGG  1260

Qy 1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGCTGCGGCTGCGGCTCACCCCAGC  1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGCTGCGGCTCACCCCAGC  1320

Qy 1321 AGCCGGTGTCTGTGCCCGGGGGAGAAGCCCGTCGTGCAGCTGCCCCAGCCAGCAGCCCTGGCACAGCAGCCCTGGCAGC  1380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 AGCCGGTGTCTGTGCCCGGGGGAGAAGCCCGTCGTGCAGCTGCCCCAGCCAGCAGCCCTGGCACAGCAGCCCTGGCAGC  1380

Qy 1381 CACAGACCCCCGTGCCTGCCTGCGCGGCGCGAAGAAGGCCCTTCGGCCTTCGCAGCTA  1440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 CACAGACCCCCGTGCCTGCCTGCGCGGCGCGAAGAAGGCCCTTCGGCCTTCGCAGCTA  1440

Qy 1441 CGGCTTCGTGCGGCCTGCGCCTGCGCCTGCCCAGGCCTGGTGCCCAGGCTGTGCCCAGGCA  1500
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 CGGCTTCGTGCGGCCTGCGCCTGCGCCTGCCCAGGCCTGGTGCCCAGGCTGTGCCCAGGCA  1500

Qy 1501 CAACGAACGCCGCCGCTTCCTCAGGAGCAGCCGGGGCGGCGGCGGGTTCATCTCCCTGGGAAGCATGCCAA  1560
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Db 1501 CAACGAACGCCGCCGCTTCCTCAGGAGCAGCCGGGGCGGCGGCGGGTTCATCTCCCTGGGAAGCATGCCAA  1560

Qy 1561 GCTCTCGCCTGCGAGGCTGACGTGGAAGATGAGCGTGCGGGACTGCGGCTTGGCTGCGCAG  1620
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1561 GCTCTCGCCTGCGAGGCTGACGTGGAAGATGAGCGTGCGGGACTGCGGCTTGGCTGCGCAG  1620

Qy 1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCGGCCGCCGCAGAGACCACCGGTCGAGCTTGGC  1680
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCGGCCGCCGCAGAGACCACCGGTCGAGCTTGGC  1680

Qy 1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGGTCGAGCTCTTTTCTACCGGAAGAGTGCTGGAG  1740
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Db 1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGGTCGAGCTCTTTTCTACCGGAAGAGTGCTGGAG  1740

Qy 1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCGTCTTTTTCTACCGGAAGAGTGCTGGAG  1800
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Db 1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCGTCTTTTTCTACCGGAAGAGTGCTGGAG  1800

Qy 1801 CAAGTTGCAAAGCATTGGAATCAGAGCACTCGGAGGGGTGCGGGAGCTGTC  1860
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801 CAAGTTGCAAAGCATTGGAATCAGAGCACTTGGAGGGGTGCGGGAGCTGTC  1860

Qy 1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCCCCTGCGCTGACTCCG  1920
        |||||||||||||||||||||||||||||||||||||||||||||||
Db 1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCCCCTGCGCTGACTCCG  1920

Qy 1921 CTTCATCCCCAAGCCTGCACGTGGTTTCGTGTGTGCACCTGCAGAGACCTGCCGAGAAGC  1980
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921 CTTCATCCCCAAGCCTGCACGTGGTTTCGTGTGTGCACCTGCAGAGACCTGCCGAGAAGC  1980

Qy 1981 CAGAAACGTTCCCGCAGAGAAAGAGGGCCGCTCCTCACCTCGAGGGTGAAGGCACTGTT  2040
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Db 1981 CAGAAACGTTCCCGCAGAGAAAGAGGGCCGCTCCTCACCTCGAGGGTGGGGAGC
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Db  3061 CAAGATCCTCCTGCTGCGAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTCA 3120
                                                                       
Qy  3121 TCAGCAAGTTGGAAGAACCCACATTTTCCTGCGCGTCATCTGACACGGCCTCCCT 3180
         ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  3121 TCAGCAAGTTTGGAAGAACCCACATTTTCCTGCGCGTCATCTGACACGGCCTCCCT 3180

Qy  3181  CTGCTACTCCATCCTGAAAGCCAGGATGGTCGCTGGGGCCCAAGGGCGCCGGC 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CTGCTACTCCATCCTGAAAGCCAGGATGGTCGCTGGGGCCCAAGGGCGCCGC 3240

Qy  3241 CGGCCCTCTGCCCTCCGAGGCGTGCAGTGGCGTGCACCAAGCATTCCTGCTCAAGCT 3300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CGGCCCTCTGCCCTCCGAGGCGTGCAGTGGCGTGCACCAAGCATTCCTGCTCAAGCT 3300

Qy  3301 GACTCGACACCGTGTCACCTACGTGCCACTCTGGGGTCACTCCTCAGGACAGCCCAGACACGCA 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GACTCGACACCGTGTCACCTACGTGCCACTCTGGGGTCACTCCTCAGGACAGCACCCAGCGCA 3360

Qy  3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGCACACCTGGGAGGGCCGCCAACCCGGC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGCACACCTGGGAGGGCCGCCAACCCGGC 3420

Qy  3421 ACTCCCTCAGACTTCAAGACCATCCTGACGCCCCTGTCACGCGGGAGGGAGGGCCGGA 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 ACTCCCTCAGACTTCAAGACCATCCTGACGCCCCTGTCACGCGGGAGGGAGGGCCGGA 3480

Qy  3481 GAGCAGACACCAGCAGCCCGCCACCCGGTCTTACGTCCCGGGCTCTACGGGAGGGCGGGCC 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GAGCAGACACCAGCAGCCCGCCACCCGGTCTTACGTCCCGGGCTCTACGGGAGGGCGGGCC 3540

Qy  3541 CACACCCAGGCCCGCCACCCGGAGTCTGAGTGAGTTTGGCGAGGCCTG 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CACACCCAGGCCCGCCACCCGGAGTCTGAGTGAGTTTGGCGAGGCCTG 3600

Qy  3601 CATGTCCGGCTGAAGGCTGAGGCTGAGTGTCCGGCGAGTGTCCAAGGGCT 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CATGTCCGGCTGAAGGCTGAGGCTGAGTGTCCGGCGAGTGTCCAAGGGCT 3660

Qy  3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACCAGGCTGGGCCTCGGCTCCACCCCA 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACCAGGCTGGGCCTCGGCTCCACCCCA 3720

Qy  3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCGCTTCCACCCCCTCGCGCCCTCGCCCATCC 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCGCTTCCACCCCCTCGCGCCCTCGCCCATCC 3780

Qy  3781 CCAGATTCCCCATTGTTCACCCCATGTGCCTTCACCCCTCGCCCTGCCTCCCACCCCACCATCC 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 CCAGATTCCCCATTGTTCACCCCATGTGCCTTCACCCCTCGCCCTGCCTCCCACCCCACCATCC 3840

Qy  3841 AGGTGGAGACCCTGAGAAGGACCCCTGGGAAGTTGGGAGTGACCAAAGGTGTG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 AGGTGGAGACCCTGAGAAGGACCCCTGGGAAGTTGGGAGTGACCAAAGGTGTG 3900

Qy  3901 CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGGGTCAAATTGGGGG 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGGGTCAAATTGGGGG 3960

Qy  3961 GAGGTGCTGTGGGAGTAAAATACTGAATATGAGTTTTTCAGTTTTTGAAAAAA 4015
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Db  3961 GAGGTGCTGTGGGAGTAAAATACTGAATATGAGTTTTTCAGTTTTTGAAAAAA 4015
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RESULT 5
AR226390

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LOCUS       AR226390                4015 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6444650.
ACCESSION   AR226390
VERSION     AR226390.1  GI:27264905
KEYWORDS    
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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Db  1981 CAGAAGGTTCCGCAGAGAAAAGAGGGCCGAGCGGTGAAGGCACTGTT 2040
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Qy  2041 CAGCGTGCTCAACTACGAGCGGGCGGCCGGCGGCGGCCGCCTCTGTCGCTGTGGG 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 CAGCGTGCTCAACTACGAGCGGGCGGCCGGCGGCGGCCGCCTCTGTCGCTGTGGG 2100

Qy  2101 CCTGGACGATATCCACAGAGGGCCTGGCGCACCTTCGTGCTGCGTGCCCAGGACCC 2160
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Db  2101 CCTGGACGATATCCACAGAGGGCCTGGCGCACCTTCGTGCTGCGTGCCCAGGACCC 2160

Qy  2161 GCCGCCTGAGCTGTACTTTGTCAAGTGGATCGGGCGGCGTACGACACACCATCCCCA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCGCCTGAGCTGTACTTTGTCAAGTGGATCGGGCGGCGTACGACACCATCCCCA 2220

Qy  2221 GGACAGGCTCACGGAGTCATCGCCAGCATCATCAAACCCCAGAAACACGTACTGCCTGCCG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GGACAGGCTCACGGAGTCATCGCCAGCATCATCAAACCCCAGAAACACGTACTGCCTGCCG 2280

Qy  2281 TCGGTATGCCGTGGTCCAGAAGGCCACGTCCGCAAGGCCTTCAAGAGCCA 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TCGGTATGCCGTGGTCCAGAAGGCCACGTCCGCAAGGCCTTCAAGAGCCA 2340

Qy  2341 CGTCTCTACCTTGACAGACCTCGTGGCTCACCTGCAGGA 2400
         |||||||||||||||||||||||||||||||||||||||
Db  2341 CGTCTCTACCTTGACAGACCTCGTGGCTCACCTGCAGGA 2400

Qy  2401 GACCAGCCCGCTGAGGCGATGCCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GACCAGCCCGCTGAGGCGATGCCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460

Qy  2461 CAGTGGCCTCTTCGACGTCTTCGACGTCTTCATGTGCCACCACGCCGTGCGCATCAGGGGG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGTGGCCTCTTCGACGTCTTCGACGTCTTCATGTGCCACCACGCCGTGCGCATCAGGGGG 2520

Qy  2521 CAAGTCCTAGTCCAGTGCCAGGGATCCCGCAGGCCTCCATCCTCTTCCACCGCTGCCTG 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CAAGTCCTAGTCCAGTGCCAGGGATCCCGCAGGCCTCCATCCTCTTCCACCGCTGCCTG 2580

Qy  2581 CAGCCTGTGCTACGGCGACACATGGAGAACAAGCTGTTTGCGGGATTCGGCGGGACGGGCT 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CAGCCTGTGCTACGGCGACACATGGAGAACAAGCTGTTTGCGGGATTCGGCGGGACGGGCT 2640

Qy  2641 GCTCCTGCCTGCGTTTGGTGATGATTCTTGTTGGTGACACCTCACCTGGTGGTGAACTTGCGAA 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 GCTCCTGCCTGCGTTTGGTGATGATTCTTGTTGGTGACACCTCACCTGGTGGTGAACTTGCGAA 2700

Qy  2701 CTTCCCTCAGGACCCTGGTCCGAGGTGTGCCCTGAGTATGGGCCCTGGTGGTGAACTTGCGGAA 2760
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Db  2701 CTTCCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGGCCCTGGTGGTGAACTTGCGGAA 2760

Qy  2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGCCCTGGCTGGCACGGTTTGTTGTTCAGAT 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGCCCTGGCTGGCACGGTTTGTTGTTCAGAT 2820

Qy  2821 GCCGGCCACGGCCTAGTCCCCCGGTGCTGCTGGACTCCCATCAGAGCCCAGGACCCTGGAGGT 2880
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Db  2821 GCCGGCCACGGCCTAGTCCCCCGGTGCTGCTGGACTCCCATCAGAGCCCAGGACCCTGGAGGT 2880

Qy  2881 GCAGAGCGACTACTCCCAGCTATGCGGGTGGGGACGACGGTGTGCACCAACACATCTA 2940
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Db  2881 GCAGAGCGACTACTCCCAGCTATGCGGGTGGGGACGACGGTGTGCACCAACACATCTA 2940

Qy  2941 CGGCTTCAAGGCTGGGAGGAACATGCTCGCAAACTCTTTGGGGTCTTGCGGCTGAGTG 3000
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Db  2941 CGGCTTCAAGGCTGGGAGGAACATGCTCGCAAACTCTTTGGGGTCTTGCGGCTGAGTG 3000

Qy  3001 TCACAGCCGTGTTTCTGGATTTGCAGGTGAACAGCCTTCCAGACGCGGTGTGCACCAACATCTA 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 TCACAGCCGTGTTTCTGGATTTGCAGGTGAACAGCCTTCCAGACGCGGTGTGCACCAACATCTA 3060

Qy  3061 CAAGATCCTCCTGCTGCGAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTCA 3120
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REFERENCE    1 (bases 1 to 4015)
AUTHORS      Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
             Harley,C.B. and Andrews,W.H.
TITLE        Antisense compositions for detecting and inhibiting telomerase
             reverse transcriptase
JOURNAL      Patent: US 6444650-A 1 03-SEP-2002;
FEATURES     Location/Qualifiers
  source     1..4015
             /organism="unknown"
BASE COUNT      663 a    1363 c    1275 g    714 t
ORIGIN

Query Match           100.0%;  Score 4015;  DB 6;  Length 4015;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 4015;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy   1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCTGCCCCGGCCCCGCGATGCC   60
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Db   1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCTGCCCCGGCCCCGCGATGCC   60

Qy   61 GCGCGCTCCCGCTGCCGAGCCGGTCGCGCTCCCTGCGCAGCCACTACCGGCCAGAGGTGCT   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCGCGCTCCCGCTGCCGAGCCGGTCGCGCTCCCTGCGCAGCCACTACCGGCCAGAGGTGCT   120

Qy   121 GCCGCTGGCCACGTTCGTGCGCGCCCTGGGGCCCCAGGCGTCGGTCGGTCGCAGCGCGG   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCCGCTGGCCACGTTCGTGCGCGCCCTGGGGCCCCAGGCGTCGGTCGGTCGCAGCGCGGG   180

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Db   1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980

Qy   1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTTCACCTTCACCGCACTGTT 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTTCACCTTCACCGCACTGTT 2040

Qy   2041 CAGCGTGCTCAACTACGAGCGGCGGCCGCGGCCCCGGCCTCCTGGGCGCCTCGTGCTGGG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CAGCGTGCTCAACTACGAGCGGCGGCCGCGGCCCCGGCCTCCTGGGCGCCTCGTGCTGGG 2100

Qy   2101 CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTCGGGCCCAGGACCCC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTCGGGCCCAGGACCCC 2160

Qy   2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGTACGACACCATCCCCCA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGTACGACACCATCCCCCA 2220

Qy   2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCG 2280

Qy   2281 TCGGTATGCCGTGGTCCAGAAGGCCGCACGTCCGCAAGGCCTTCAAGAGCCA 2340
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Db   2281 TCGGTATGCCGTGGTCCAGAAGGCCGCACGTCCGCAAGGCCTTCAAGAGCCA 2340

Qy   2341 CGTCTCTACCTTGACGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400
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Db   2341 CGTCTCTACCTTGACGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400

Qy   2401 GACCAGCCCCGCTGAGGGCGACATGGAGAACAAGCTGTTTGCGGGATTCGGCGGGACGGGCT 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GACCAGCCCCGCTGAGGGCGACATGGAGAACAAGCTGTTTGCGGGATTCGGCGGGACGGGCT 2460

Qy   2461 CAGTGCCGCCTCTTCGACGTCTTCGACGTCCGCTTCATGTGCCACCACCGCGTGCCATCAGGGG 2520
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Db   2461 CAGTGCCGCCTCTTCGACGTCTTCGACGTCCGCTTCATGTGCCACCACCGCGTGCCATCAGGGG 2520

Qy   2521 CAAGTCCTACGTGCCAGGGATCCCGCAGGGATCGGCGGGATTCGGCGGGACCAAGGGGCT 2580
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Db   2521 CAAGTCCTACGTGCCAGGGATCCCGCAGGGATCGGCGGGATTCGGCGGGACCAAGGGGCT 2580

Qy   2581 CAGCCGTGTGTACGGCGACAATGGAGAACAAGCTGTTTGCGGGATTCGGCGGGACGGGCT 2640
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Db   2581 CAGCCGTGTGTACGGCGACAATGGAGAACAAGCTGTTTGCGGGATTCGGCGGGACGGGCT 2640

Qy   2641 GCTCCTGCGCTTGGTCCGAGGGTGCGCGGCCTACCTCACCTCACCCGGACCCTGGAGGT 2700
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Qy   2701 CTTCCTCAGGACCCTGGTGAACTTCCCGAGGTGTCGGTATGCTCGTGTCGGTGAACTTGCCGGAA 2760
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Db   2761 GACAGTGGTGAACTCCCTGTAGAAGACGAGGCCTGGGTGGCACGGCTTTTGTTCAGAT 2820

Qy   2821 GCCGGCCCACGGCCTATTCCCCGGTTGCGCGGCCTGCTGCTCGATACCGGGACCCTGGAGGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GCCGGCCCACGGCCTATTCCCCGGTTGCGCGGCCTGCTGCTCGATACCGGGACCCTGGAGGT 2880

Qy   2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTTCACCTTCACCTTCAACCCG 2940
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Db   2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTTCACCTTCACCTTCAACCCG 2940

Qy   2941 CGGCTTCAAGGCTGGGAGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTCGCGGCTGAAGTG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCGTCCCAGAACGGTGTGCACCAACATCTA 3060
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Db   3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCGTCCCAGAACGGTGTGCACCAACATCTA 3060
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Qy   3061 CAAGATCCTCCTGCTGCTGCGGCCGTACAGGTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120
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Db   3061 CAAGATCCTCCTGCTGCTGCGGCCGTACAGGTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120

Qy   3121 TCAGCAAGTTGGAAGAACCCACCATTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180
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Db   3121 TCAGCAAGTTGGAAGAACCCACCATTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180

Qy   3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGAGATGTCGCTGGGGCCCAAGGGCGCCGC 3240
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Db   3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGAGATGTCGCTGGGGCCCAAGGGCGCCGC 3240

Qy   3241 CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCGTGCCACCAAGCCATTCCTGCTCAAGCT 3300
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Db   3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360

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Qy   3481 GAGCAGACACCAGCGCCCGCACCCGCTCTACGTCCCAGGAGGGAGGGCGGCGCC 3540
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Qy   3721 GGGCCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCCCGCCCTGGATGGGGGTCCCTGTGGGT 3780
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Qy   3781 CCAGATTCGCACCCCATTGTTCACCCCCATCCCCTTGCTTCCACCCCCACCATCC 3840
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Qy   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA 4015
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SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1  (bases 1 to 4015)
AUTHORS    Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
           Harley,C.B. and Andrews,W.H.
TITLE      Human telomerase catalytic subunit: diagnostic and therapeutic
           methods
JOURNAL    Patent: US 6475789-A 1 05-NOV-2002;
FEATURES   Location/Qualifiers
  source   1..4015
           /organism="unknown"
BASE COUNT      663 a     1363 c     1275 g      714 t
ORIGIN

Query Match        100.0%;  Score 4015;  DB 6;  Length 4015;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 4015;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Db    1  GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCTGGCCCCCGCCCCCGCCCCCGCGATGCC   60

Qy   61  GCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCGCGCAGCCACTACCGGCCGAGGTGCT  120
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Db   61  GCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCGCGCAGCCACTACCGGCCGAGGTGCT  120

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Qy  181  GGACCCGGCGGCCTTCCGCGCGCTGGTGCTGCCCAGTGCCTGGTGGTGCGCCCTGGGACGC  240
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Db  181  GGACCCGGCGGCCTTCCGCGCGCTGGTGCTGCCCAGTGCCTGGTGGTGCGCCCTGGGACGC  240

Qy  241  ACGGCGCTGGACGGCGGGCCCCGCGCGCCCCTCCTTCCGCGAGCGTGTCCTGCCCAGGAGCTGGTGGC  300
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Db  241  ACGGCGCTGGACGGCGGGCCCCGCGCGCCCCTCCTTCCGCGAGCGTGTCCTGCCCAGGAGCTGGTGGC  300

Qy  301  CCGAGTGCTGCAGAGGCTGTGCGAGCGACGTGCTGGTTCAACGTGCTGGCCTTCGGCCTTCGC  360
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Db  301  CCGAGTGCTGCAGAGGCTGTGCGAGCGACGTGCTGGTTCAACGTGCTGGCCTTCGGCCTTCGC  360

Qy  361  GCTGCTGGACGGGGGCCCGCGGGGCCCCCGGGGGCCCCCGAGGGCCTTCACCACCAGCTGCGCAGCTA  420
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Db  361  GCTGCTGGACGGGGGCCCGCGGGGCCCCCGGGGGCCCCCGAGGGCCTTCACCACCAGCTGCGCAGCTA  420

Qy  421  CCTGCCCAACACGGTGACCGACGCCTGCGGGCCGGGAGCCGTGGGGCTGCGGGGCTGCTGCGG  480
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Db  421  CCTGCCCAACACGGTGACCGACGCCTGCGGGCCGGGAGCCGTGGGGCTGCGGGGCTGCTGCGG  480

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Db  481  CCCGGTGGGCGACGACGTGCTGGTTCACCTGCTGGTTCACGTGCTGCGCGCTCTTTGTGCTGT  540

Qy  541  GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCGTGTACCAGCTCGGCGCCTGCCAC  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCGTGTACCAGCTCGGCGCCTGCCAC  600

Qy  601  TCAGGCCGGCCGCCCCCCACACGCTAGTGGACCCCGGGTCTGGGATGCGGAACGGGC  660
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Db  601  CTGGAACCATAGCGTCAGGGAGGCCGCCCCCGGGTCTCCAGAGGGCGCCGGAG  720

Qy  661  CTGGAACCATAGCGTCAGGGAGGCCGCCCCCGGGTCTCCAGAGGGCGCCGGAG  720
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Db  661  CTGGAACCATAGCGTCAGGGAGGCCGCCCCCGGGTCTCCAGAGGGCGCCGGAG  720

Qy  721  GAGGCGCGGGGAGTGCCAGTCGCCCAAGTCTGCCGTTGCCGTTGCCCTGGCCGCC  780
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Db  721  GAGGCGCGGGGAGTGCCAGTCGCCCAAGTCTGCCGTTGCCGTTGCCCTGGCCGCC  780

Qy  781  TGCCCCTGAGCCGGAGCGGACGGCCCGTTGGGCAGGGGTCCTGGGCTGCCACCCCGGGCCAGGAC  840
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Db  781  TGCCCCTGAGCCGGAGCGGACGGCCCGTTGGGCAGGGGTCCTGGGCTGCCACCCCGGGCCAGGAC  840
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Db  841  GCGTGGACCAGTGACCGGTTTCGTGGTGTCACCTGCGAAGAGC  900
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Qy  841  GCGTGGACCAGTGACCGGTTTCGTGGTGTCACCTGCGAAGAGC  900

Qy  901  CACCTCTTGGAGGGTGCGGCTCTCTGGCACGCGGCCACCGCCACCCACCCATCCGTGGGCCGCCA  960
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Db  901  CACCTCTTTGGAGGGTGCGGCTCTCTGGCACGCGGCCACCGCCACCCACCCATCCGTGGGCCGCCA  960

Qy  961  GCACCACGCGGCGCCCCATCCACATCCACATCGCGGCCACCACGCTTCCTGGGACACGCTGTTCC  1020
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Db  961  GCACCACGCGGCGCCCCATCCACATCCACATCGCGGCCACCACGCTTCCTGGGACACGCTGTTCC  1020

Qy 1021  CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGGCGACACAGGAGCAGCTCGG  1080
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Db 1021  CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGGCGACACAGGAGCAGCTCGCG  1080

Qy 1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGGCCCAGCCTGACTGGCCGCTGGCCGCTCGTGGA  1140
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Db 1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGGCCCAGCCTGACTGGCCGCTGGCCGCTCGTGGA  1140

Qy 1141  GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCGCAGGTTGCCCCGCCT  1200
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Db 1141  GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCGCAGGTTGCCCCGCCT  1200

Qy 1201  GCCCCAGCCTACTGGCAAATGCGGCCCCGTGTTTCTGGAGCTGCTTGGGAACCACGCGCA  1260
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Db 1201  GCCCCAGCCTACTGGCAAATGCGGCCCCGTGTTTCTGGAGCTGCTTGGGAACCACGCGCA  1260

Qy 1261  GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGCAGCCACCCCAGC  1320
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Db 1261  GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGCAGCCACCCCAGC  1320

Qy 1321  AGCCGGTGTCGTGCCCGGGAGAAGCCCCCAGGGCTCTGTGGCGCCCCGAGGAGGAGGA  1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321  AGCCGGTGTCGTGCCCGGGAGAAGCCCCCAGGGCTCTGTGGCGCCCCGAGGAGGAGGA  1380

Qy 1381  CACAGACCCCGTGCTCGCCGCCTGTGGCAGCGGCACCAGCCCTGCCAGGTGTA  1440
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Db 1381  CACAGACCCCGTGCTCGCCGCCTGTGGCAGCGGCACCAGCCCTGCCAGGTGTA  1440

Qy 1441  CGGCTTCGTGCGGGCCTGCTGGCCTGCGCCTGCCGCCTGGTGCCCCAGGCTGGTGCCCAGGCA  1500
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Db 1441  CGGCTTCGTGCGGGCCTGCTGGCCTGCGCCTGCCGCCTGGTGCCCCAGGCTGGTGCCCAGGCA  1500

Qy 1501  CAACGAACGGCGCTTCCTCCAGGAACACCAAGAGTTCATCTCCTGGGAAGCATGCCAA  1560
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Db 1501  CAACGAACGGCGCTTCCTCCAGGAACACCAAGAGTTCATCTCCTGGGAAGCATGCCAA  1560

Qy 1561  GCTCTCGCTGCCAGGAGCGTGACGTGGAAGATGAGCCGTGCGCGTTGGCGTGCGCAG  1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1561  GCTCTCGCTGCCAGGAGCGTGACGTGGAAGATGAGCCGTGCGCGTTGGCGTGCGCAG  1620

Qy 1621  GAGCCCAGGGGTTGGCGTGTGTTCCGCGGCCTGCTGGCGCACCGGTGGAGAATCCTGGC  1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1621  GAGCCCAGGGGTTGGCGTGTGTTCCGCGGCCTGCTGGCGCACCGGTGGAGAATCCTGGC  1680

Qy 1681  CAAGTTCCTGCACTGGCTGATGAGTGTGTCGTGCACGTCGTGCTCTTTTTCTCTTTTA  1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681  CAAGTTCCTGCACTGGCTGATGAGTGTGTCGTGCACGTCGTGCTCTTTTTCTCTTTTA  1740

Qy 1741  TGTCACGGAGACCACGTTCAAAAGAACAGGAACAGCACTTGAAGAGGGTGCTGCGGAGTGTC  1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741  TGTCACGGAGACCACGTTCAAAAGAACAGGAACAGCACTTGAAGAGGGTGCTGCGGAGTGTC  1800

Qy 1801  CAAGTTGCAAAGCATTGGAATCAGACAGACTTGAAGAGGGTGCTGCGGAGTGTC  1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801  CAAGTTGCAAAGCATTGGAATCAGACAGACTTGAAGAGGGTGCTGCGGAGTGTC  1860

Qy 1861  GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCGCCGCCGCCACCCGCCCTGACGTCCGAGACTCCG  1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1861  GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCGCCGCCGCCACCCGCCCTGACGTCCGAGACTCCG  1920
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Qy   1921  CTTCATCCCAAGCCTGACGGGCTGCGGGCCGATTGTGAAACATGGACTACGTCGTGGGAGC  1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  CTTCATCCCAAGCCTGACGGGCTGCGGGCCGATTGTGAAACATGGACTACGTCGTGGGAGC  1980

Qy   1981  CAGAACGTTCCGCAGAGAAAGAGGGCGGGCGCGGGCGTCCGAGGGTGAAGGCACTGTT     2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  CAGAACGTTCCGCAGAGAAAGAGGGCGGGCGCGGGCGTCCGAGGGTGAAGGCACTGTT     2040

Qy   2041  CAGCGTGCTCAACTACGAGCGGGCGGGCGCGGGCCGCTCCTGGGCGCCTCGTGCTGGG     2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  CAGCGTGCTCAACTACGAGCGGGCGGGCGCGGGCCGCTCCTGGGCGCCTCGTGCTGGG     2100

Qy   2101  CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGCGGGCCCAGGACCC     2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGCGGGCCCAGGACCC     2160

Qy   2161  GCCGGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCCGCTACGACACCATCCCCCA  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GCCGGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCCGCTACGACACCATCCCCCA  2220

Qy   2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACACGTACTGCGTGCG  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACACGTACTGCGTGCG  2280

Qy   2281  TCGGTATGCCGTGGTCCAGAAGGCCGCGCACGTCCGCAAGGCCTTCAAGAGACCCA        2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  TCGGTATGCCGTGGTCCAGAAGGCCGCGCACGTCCGCAAGGCCTTCAAGAGACCCA        2340

Qy   2341  CGTCTCTACCTTGACAGACCTCCAGCCGTACAATGCCAGTTCGTGCTCACCTGCAGGA     2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  CGTCTCTACCTTGACAGACCTCCAGCCGTACAATGCCAGTTCGTGCTCACCTGCAGGA     2400

Qy   2401  GACCAGCCCGCTCTTCGACGTCTTCCTACGCTCGTCATCGTCGAGCAGAGAGTCCTCCTCCTGAATGAGGCCAG  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  GACCAGCCCGCTCTTCGACGTCTTCCTACGCTCGTCATCGTCGAGCAGAGAGTCCTCCTCCTGAATGAGGCCAG  2460

Qy   2461  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTCCACCACGCCGTGCCATCAGGGG      2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTCCACCACGCCGTGCCATCAGGGG      2520

Qy   2521  CAAGTCCTACGTCCAGTGCCAGTCCCGGGATCCCCATCCTCTCCCACGCTGCTCTG       2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  CAAGTCCTACGTCCAGTGCCAGTCCCGGGATCCCCATCCTCTCCCACGCTGCTCTG       2580

Qy   2581  CAGCCTGTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  CAGCCTGTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT  2640

Qy   2641  GCTCCTGCGTTGGTGGATGATTCTTGTGTTGTGACACCTCACCTGCACCACGCGGAAAAC     2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  GCTCCTGCGTTGGTGGATGATTCTTGTGTTGTGACACCTCACCTGCACCACGCGGAAAAC     2700

Qy   2701  CTTCCTCAGGACCCGTGCCGAGGGTGCGCGTGGCGTATGGCGCTGCGTGGTGAACTTGCCGGA  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  CTTCCTCAGGACCCGTGCCGAGGGTGCGCGTGGCGTATGGCGCTGCGTGGTGAACTTGCCGGA  2760

Qy   2761  GCTCCTGGTGAACTTCCCTGTAGAAGACGAGCCCCTGGGTGGTGCCACGGCTTTTGTTGTTCAGAT  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  GCTCCTGGTGAACTTCCCTGTAGAAGACGAGCCCCTGGGTGGTGCCACGGCTTTTGTTGTTCAGAT  2820

Qy   2821  GCCGGCCCACGCCTATTCCCCGGTGCGGCCTGCGTGCTGCTCGATACCCGGAGGGT       2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  GCCGGCCCACGCCTATTCCCCGGTGCGGCCTGCGTGCTGCTCGATACCCGGAGGGT       2880

Qy   2881  GCAGAGCGACTACTCCAGCTATCCCCGGTGGGAGGAACATCTCTTTGGGGTCTTGCGGCTGAAGTG  2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  GCAGAGCGACTACTCCAGCTATCCCCGGTGGGAGGAACATCTCTTTGGGGTCTTGCGGCTGAAGTG  2940

Qy   2941  CGGCTTCAAGGCTCGGGAGGAACATCTCTTTGGGGTCTTGCGGCTGAAGTG             3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  CGGCTTCAAGGCTCGGGAGGAACATCTCTTTGGGGTCTTGCGGCTGAAGTG             3000
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Qy   3001  TCACAGCCTGTTTCTGATTTGGAGGTGAACAGCCTCCAGACGCGTGTCCACCAACATCTA   3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  TCACAGCCTGTTTCTGATTTGGAGGTGAACAGCCTCCAGACGCGTGTCCACCAACATCTA   3060

Qy   3061  CAAGATCCTCCTGCCTCGAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCCATTTCA   3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  CAAGATCCTCCTGCCTCGAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCCATTTCA   3120

Qy   3121  TCAGCAAGTTGGAAGAACCCCACATTTTCTCGCGGCGTCATCCTGACACGGCCTCCCT     3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  TCAGCAAGTTGGAAGAACCCCACATTTTCTCGCGGCGTCATCCTGACACGGCCTCCCT     3180

Qy   3181  CTGCTACTCCATCCTGAAAGCCAGGAGACGCAAGAACGCAGGGATGTCGCTGGGGCGCCGGC   3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  CTGCTACTCCATCCTGAAAGCCAGGAGACGCAAGAACGCAGGGATGTCGCTGGGGCGCCGGC   3240

Qy   3241  CGGCCCTCGTGCCCTCCGAGGCCGTGCAGTGGCGTGTGCCACCAAGCATTCCTGCTCAAGCT   3300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241  CGGCCCTCGTGCCCTCCGAGGCCGTGCAGTGGCGTGTGCCACCAAGCATTCCTGCTCAAGCT   3300

Qy   3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGTCACTCAGGACGCCCAGCACGCA    3360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGTCACTCAGGACGCCCAGCACGCA    3360

Qy   3361  GCTGAGTCGGAAGCTCCCGGGACGAGCCGTGACTCGTCGCCCTGGAGGCCGCAACCCGGC   3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361  GCTGAGTCGGAAGCTCCCGGGACGAGCCGTGACTCGTCGCCCTGGAGGCCGCAACCCGGC   3420

Qy   3421  ACTGCCCTCAGACTTCAGAGACCCTGACTCCTGACTGATGCGCACCGCACCCGACCAGCCCGA  3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  ACTGCCCTCAGACTTCAGAGACCCTGACTCCTGACTGATGCGCACCGCACCCGACCAGGCCGA  3480

Qy   3481  GAGCAGACACCAGCAGCCCGTGTCTACGTCCCGGCTCTACGTCGAGTGAGGAGGGGGGCC    3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  GAGCAGACACCAGCAGCCCGTGTCTTCACTTCACTCGACTAGGAGGAGGGGGGGCGGCC    3540

Qy   3541  CACACCCAGGCCCGACCCGCACCGCTGTGAGGCTGAGTGTTTGGCGCAGGCCTG        3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  CACACCCAGGCCCGACCCGCACCGCTGTGAGGCTGAGTGTTTGGCGCAGGCCTG        3600

Qy   3601  CATGTCCGGCTGAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAGGGCT     3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  CATGTCCGGCTGAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAGGGCT     3660

Qy   3661  GAGTGTCCAGCAGCACACCTGCGTCTTCACTTCCCCACAGGCTGGCGCTCCACCCCA      3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  GAGTGTCCAGCAGCACACCTGCGTCTTCACTTCCCCACAGGCTGGCGCTCCACCCCA      3720

Qy   3721  GGGCCAGCTTTTCTCCACCAGGAGCCCGCTTCCACTCCCCACATAGGAATAGTCCATCC    3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  GGGCCAGCTTTTCTCCACCAGGAGCCCGCTTCCACTCCCCACATAGGAATAGTCCATCC    3780

Qy   3781  CCAGAATTCGCCATTGTTCACCCCTGCCTTCCACCCTGCCTTCCACCCACCATCC        3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781  CCAGAATTCGCCATTGTTCACCCCTGCCTTCCACCCTGCCTTCCACCCACCATCC        3840

Qy   3841  AGGTGGAGCCCTGAGAAGGACCCCTGGGAGCTCTGGAGTTGGAGTGACCAAAGGTGTG     3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841  AGGTGGAGCCCTGAGAAGGACCCCTGGGAGCTCTGGAGTTGGAGTGACCAAAGGTGTG     3900

Qy   3901  CCCTGTACACAGGCGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA      3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901  CCCTGTACACAGGCGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA      3960

Qy   3961  GAGGTGCTGTGGGGAGTAAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA       4015
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961  GAGGTGCTGTGGGGAGTAAAAATACTGAATATATGAGTTTTTCAGTTTTGGGGG         4015
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RESULT 7
AR263555

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ACCESSION    AR263555
VERSION      AR263555.1  GI:28075300
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 4015)
  AUTHORS    Monia,B.P., Gaarde,W.A. and Wancewicz,E.
  TITLE      Antisense inhibition of tert expression
  JOURNAL    Patent: US 6331399-A 3 18-DEC-2001;
FEATURES             Location/Qualifiers
     source          1..4015
                     /organism="unknown"
BASE COUNT      663 a    1363 c    1275 g    714 t
ORIGIN

Query Match         100.0%;    Score 4015;    DB 6;  Length 4015;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 4015;  Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;
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Qy       1 GCAGCGCTGCGTCCTGCGTGCGCACGTGGGAAGCCCTGGCCCCCGGATCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCAGCGCTGCGTCCTGCGTGCGCACGTGGGAAGCCCTGGCCCCCGGATCC 60

Qy      61 GCGGCGCTCCCCGCGTGCGCCGAGCCGTGCGCTCCCCTGCTCGCCAGCCACTACCGCGAGGTGCT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCGCGCTCCCCGCGTGCGCCGAGCCGTGCGCTCCCCTGCTCGCCAGCCACTACCGCGAGGTGCT 120

Qy     121 GCCGCTGGCCACGTCGTGCGGACGGCCCTGGGCGTCGTGGCTGGCAGCGCGG 180
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGCTGGCCACGTCGTGCGGACGGCCCTGGGCGTCGTGGCTGGCAGCGCGG 180

Qy     181 GGACCCGGGCGGGCTTTCCGGCGGTGCGGTGCCTCGGGACGC 240
           |||||||||||||||||||||||||||||||||||||||
Db     181 GGACCCGGGCGGGCTTTCCGGCGGTGCGGTGCCTCGGGACGC 240

Qy     241 ACGGGCCGCGCCCCCGCGCCCCTCTTCCGCCAGGTGTCCTGCCCAGGAGCTGGTGGC 300
           |||||||||||||||||||||||||||||||||||||||||||||
Db     241 ACGGGCCGCGCCCCCGCGCCCCTCTTCCGCCAGGTGTCCTGCCCAGGAGCTGGTGGC 300

Qy     301 CCGAGTGCTGCAGAGGCGTGCGGAGCGCGCGGCGGAAGACGTGCTGGCCTTCGGCTTCGC 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCGAGTGCTGCAGAGGCGTGCGGAGCGCGCGGCGGAAGACGTGCTGGCCTTCGGCTTCGC 360

Qy     361 GCTGTGCTGGACAGCGGGCCCCGCGGGGGCCCCCCGGGGGCGTGGGGGCGTCCTGCTGCGG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTGTGCTGGACAGCGGGCCCCGCGGGGGCCCCCCGGGGGCGTGGGGGCGTCCTGCTGCGG 420

Qy     421 CCTGCCCAACACCGTGACCGACCGTGCTGGTGTTCACCTGCCGCACGCGTCTTCCCTGCTGCGG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCTGCCCAACACCGTGACCGACCGTGCTGGTGTTCACCTGCCGCACGCGTCTTCCCTGCTGCGG 480

Qy     481 CCGCGTGGGCGACGACGTGCTGGTCACCTGCCGCACGCGTCTTTGTGCTGT 540
           ||||||||||||||||||||||||||||||||||||||||||||
Db     481 CCGCGTGGGCGACGACGTGCTGGTCACCTGCCGCACGCGTCTTTGTGCTGT 540

Qy     541 GGCTCCCAGCTGCGCCTACCAGTGTGCGCCGCTGTACCAGTCGCGGCTGCCAC 600
           |||||||||||||||||||||||||||||||||||||||||||||
Db     541 GGCTCCCAGCTGCGCCTACCAGTGTGCGCCGCTGTACCAGTCGCGGCTGCCAC 600

Qy     601 TCAGGGCCCCGGGTCCCCACACGCTCAGTGGACCCCGAGGCGTCGGGATGCCGAACGGGC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TCAGGGCCCCGGGTCCCCACACGCTCAGTGGACCCCGAGGCGTCGGGATGCCGAACGGGC 660

Qy     661 CTGAACCATAGCCTCAGGGAGGGCGGCCTCCCCTGGGGCCCCGGGTGCGAG 720
           ||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTGAACCATAGCCTCAGGGAGGGCGGCCTCCCCTGGGGCCCCGGGTGCGAG 720

Qy     721 GAGGGCCGGGGGGGACGCCCGTTGGGGCAGGGGTCCTGGGCAGGGTGCGGGCAGGAGGAC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GAGGGCCGGGGGGGACGCCCGTTGGGGCAGGGGTCCTGGGCAGGGTGCGGGCAGGAGGAC 780

Qy     781 TGCCCCTGAGCCGAGCCGGACGGACGCGCCGTTGGGTCGTGTGGTGTCACCTGCGTCACTG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TGCCCCTGAGCCGAGCCGGACGGACGCGCCGTTGGGTCGTGTGGTGTCACCTGCGTCACTG 840

Qy     841 GCGTGGACCAGTGACCGTGGTTTCGTGTCTGGTGTCGTGTGTCTCACCTGCGTCACTG 900
           ||||||||||||||||||||||||||||||||||||||||||||
Db     841 GCGTGGACCAGTGACCGTGGTTTCGTGTCTGGTGTCGTGTGTCTCACCTGCGTCACTG 900

Qy     901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGGCCACTCCCACCATCCTGGCCGCCGCCA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGGCCACTCCCACCATCCTGGCCGCCGCCA 960

Qy     961 GCACCACGCGGCGCCCCATCACATCGCGCCACCACGTCCCTGGGACACGCCTTGTCC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||
Db     961 GCACCACGCGGCGCCCCATCACATCCACATCGGGCCACCACGTCCCTGGGACACGCCTTGTCC 1020

Qy    1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGGACAAGGAGCAGCTGCG 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGGACAAGGAGCAGCTGCG 1080

Qy    1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGTGGAGGCTCGTGGA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGTGGAGGCTCGTGGA 1140

Qy    1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGAGCCTGCTGCCCCGCCT 1200
           |||||||||||||||||||||||||||||||||||||||||||||
Db    1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGAGCCTGCTGCCCCGCCT 1200

Qy    1201 GCCCCAGCGCTACTGGCAAATGCGGGCCCGTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GCCCCAGCGCTACTGGCAAATGCGGGCCCGTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260

Qy    1261 GTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCCTGCGAGCTCACCCCAGC 1320
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCCTGCGAGCTCACCCCAGC 1320

Qy    1321 AGGGCCGTGTCTGTGCCGCGGAGAAGCTCGTGTGCGGCCCCCAGGAGGAGGA 1380
           ||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 AGGGCCGTGTCTGTGCCGCGGAGAAGCTCGTGTGCGGCCCCCAGGAGGAGGA 1380

Qy    1381 CACAGACCCCGTCGCGCGTGGTGCAGCTCGCCCAGCACAGCAGCCCCCTGGCAGGTGTA 1440
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CACAGACCCCGTCGCGCGTGGTGCAGCTCGCCCAGCACAGCAGCCCCCTGGCAGGTGTA 1440

Qy    1441 CGGCTTCGTGCGGGGCCTGGTGTGCCGCGGCCTTCAACCACCAGCGTGCGCAGCTA 1500
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Db    1441 CGGCTTCGTGCGGGGCCTGGTGTGCCGCGGCCTTCAACCACCAGCGTGCGCAGCTA 1500

Qy    1501 CAACGAACGCCGCTCTCCTCAGGAGAACACCAAGAAGTTCATCTCCCGGGAAGCATGCCAA 1560
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Db    1501 CAACGAACGCCGCTCTCCTCAGGAGAACACCAAGAAGTTCATCTCCCGGGAAGCATGCCAA 1560

Qy    1561 GCTCTCGCTGCAGGAGCTGACGTGCGAAGATGAGCGTGCCGCAGAGATCCTGGC 1620
           ||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GCTCTCGCTGCAGGAGCTGACGTGCGAAGATGAGCGTGCCGCAGAGATCCTGGC 1620

Qy    1621 GAGCCCAGGGGTTGGCTGTGTGTTCCGGCCCCAGAGCGTCTGCGCGGGAGATCCTGGC 1680
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Db    1621 GAGCCCAGGGGTTGGCTGTGTGTTCCGGCCCCAGAGCACCTGCTGCTGCGGGAGATCCTGGC 1680

Qy    1681 CAAGTTCCTGCACTGGCTGATGAGTGTCGTGCGGGC 1740
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Db    1681 CAAGTTCCTGCACTGGCTGATGAGTGTCGTGCGGGC 1740

Qy    1741 TGTCACGGACCACGTTTCAAAAGAACACGGCTCTTTTTCTACCGGAAGAGTGTCGGGAG 1800
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Db    1741 TGTCACGGACCACGTTTCAAAAGAACACGGCTCTTTTTCTACCGGAAGAGTGTCGGGAG 1800

Qy    1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGCGGGAGCTGTC 1860
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGCGGGAGCTGTC 1860

Qy    1861 GGAAGCAGAGGTCAGGAGCATCGGAAGCCAGGCCCGCCCTGCGGAGCTCCGACTCCG 1920
           |||||||||||||||||||||||||||||||||||||||||||||
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Db  1861 GGAAGCAGAGGTCAGGCAGCCATCGGGAACGCCAGGCCCGCCCCTGCTGACGTCCAGACTCCG 1920

Qy  1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980

Qy  1981 CAGAACGTTCCGCAGAGAAAGAGGGCCGAGCGTCTCACCTCGAGGTGAAGGCACTGTT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CAGACGTTCCGCAGAGAAAGAGGGCCGAGCGTCTCACCTCGAGGTGAAGGCACTGTT 2040

Qy  2041 CAGGCTGCTCAACTACGACGAGCGGGCGCCCGGCGGCGCGGCCGGCGGCCGGCCGGCTG 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 CAGGCTGCTCAACTACGACGAGCGGGCGCCCGGCGGCGCGGCCGGCGGCCGGCCGGCTG 2100

Qy  2101 CCTGACGATATCCACAGGGCCTGCGCACCTTCGTGCTGCGGGCCCAGGACCCC 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCTGACGATATCCACAGGGCCTGCGCACCTTCGTGCTGCGGGCCCAGGACCCC 2160

Qy  2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCA 2220

Qy  2221 GGACAGGCTCACGGAGGTCATCGCCAGCAGTCATCAAACCCAGAACACACGTACTGCGTGCG 2280
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Db  2221 GGACAGGCTCACGGAGGTCATCGCCAGCAGTCATCAAACCCAGAACACACGTACTGCGTGCG 2280

Qy  2281 TCGGTATGCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340
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Db  2281 TCGGTATGCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340

Qy  2341 CGTCTCTACCTTGACAGACCTCCAGCCGTTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CGTCTCTACCTTGACAGACCTCCAGCCGTTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400

Qy  2401 GACCAGCCCGCTGAGGGATGCCGGTCGTCATCGCCGAGAGCTCCTCCTGCCTGAATGAGGCCAG 2460
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Db  2401 GACCAGCCCGCTGAGGGATGCCGGTCGTCATCGCCGAGAGCTCCTCCTGCCTGAATGAGGCCAG 2460

Qy  2461 CAGTCCCGCTGCTTCGACGTCTTCATGTGCCACCACGCGCTGCGCATCAGGGG 2520
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Db  2461 CAGTCCCGCTGCTTCGACGTCTTCATGTGCCACCACGCGCTGCGCATCAGGGG 2520

Qy  2521 CAAGTCTACGTCCAGTGACGTCCAGGGTGTTCGGCGGGATTCGGCGGGACGGGCT 2580
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Qy  2641 GCTCCTGCGTTGGTGGATGATTTCTTGTTGGTGACACCTCACCCTCACCACGCGCAGAAAC 2700
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Db  2641 GCTCCTGCGTTGGTGGATGATTTCTTGTTGGTGACACCTCACCCTCACCACGCGCAGAAAC 2700

Qy  2701 CTTCCTCAGGACCCTGTCCGAGTGTCCGAGTGTGCGGTGGCACGGGTGAACTTGCCGGAA 2760
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Qy  2821 GCCGGCCACGCGACTACTCCAGTATTCCCGTGTTGTGCTGCCGGCCACCTGGAGGT 2880
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Db  2941 CGGCTTCAAGGCTGGGAGGAACATGCTGCTCGCCAAACTCTTTGCGGTCTTGCGGCTGAAGTG 3000

Qy  3001 TCAGCAGCCGTGTTTCTGGATTTGCAGGTGAACAGCGCCTCCAGAGCGGTGTGCACCAACATCTA 3060
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Db  3001 TCGCAGCCGTGTTTCTGGATTTGCAGGTGAACAGCGCCTCCAGACGGTGTGCACCAACATCTA 3060

Qy  3061 CAAGATCCTCCTGCTGAGGCCGTACAGTGTTCACGCATGTGTGCTGCAGCTCCATTTCA 3120
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Db  3061 CAAGATCCTCCTGCTGAGGCCGTACAGTGTTCACGCATGTGTGCTGCAGCTCCATTTCA 3120

Qy  3121 TCAGCAAGTTTGGAAGAACCCCACCATTTTCCTGCGCCGTCATCTCTGACACGGCCTCCCT 3180
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Db  3121 TCAGCAAGTTTGGAAGAACCCCACCATTTTCCTGCGCCGTCATCTCTGACACGGCCTCCCT 3180

Qy  3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGTCGGGGGCAAGGGCCGCGC 3240
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Db  3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGTCGGGGGCAAGGGCCGCGC 3240

Qy  3241 CGGCCCCTCTGCCCTCCGAGGCCCGTGAGTGGCGTGTGCAGTGGCCACTCCTGGGGTCA 3300
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Qy  3421 ACTGTCCCTCAGACTTCAAGAGCTTCGTGGCTCACCTGCAGGA 3480
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Db  3421 ACTGTCCCTCAGACTTCAAGAGCTTCGTGGCTCACCTGCAGGA 3480

Qy  3481 GAGCAGACACCAGCAGCCCTGTGTCACGCGGGGTCTACGTCACGCGGGCGCCC 3540
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Qy  3541 CACACCCAGGCCCGCCACCGCCCGGGAGGCCCTGAGTGAGTGTTGGCCGAGGCCTG 3600
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Qy  3601 CATGTCCGGCTGAAGGCTGAGTGTCCGCGGCCTGAGGCGTCAGCGTGCCGAGGGCT 3660
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Qy  3661 GAGTGTCCAGGACACCTGCCGTCTTCACTTCGGCGCTCGGCCTCCACCCCA 3720
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Db  3721 GGGCCAGCTTTTCCTCACCAGGAGCCCACTCCCACTCCCACCATAGGAATAGTCCATCC 3780

Qy  3781 CCAGATTCGCCATTGTTCACCCCCCGCCCTTGCCTTCCACCCCCACCACCATCC 3840
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Qy  3841 AGGTGGAGACCCTGAGAAGGACCCTGGAGGCTCTGGGAATTGGAGTGACCAAAGGTGTG 3900
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Db  3841 AGGTGGAGACCCTGAGAAGGACCCTGGAGGCTCTGGGAATTGGAGTGACCAAAGGTGTG 3900

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Db  3901 CCCTGTACACAGGCGAGGTGCGGCTGCTGATACCCAGCCAGTCTCGGAGGT 3960

Qy  3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAATATATGAGTTTTTCAGTTTGAAAAAA 4015
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Db  3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAATATATGAGTTTTTCAGTTTGGGGG 4015
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RESULT 8
AR265996
LOCUS   AR265996   4015 bp   DNA   linear   PAT 10-APR-2003

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DEFINITION   Sequence 3 from patent US 6492171.
ACCESSION    AR265996
VERSION      AR265996.1   GI:29694842
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 4015)
AUTHORS      Monia,B.P., Gaarde,W.A., Freier,S.M. and Wancewicz,E.
TITLE        Antisense modulation of TERT expression
JOURNAL      Patent: US 6492171-A 3 10-DEC-2002;
FEATURES     Location/Qualifiers
source       1..4015
             /organism="unknown"
BASE COUNT   663 a   1363 c   1275 g    714 t
ORIGIN

Query Match      100.0%;   Score 4015;   DB 6;   Length 4015;
Best Local Similarity  100.0%;   Pred. No. 0;
Matches 4015;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    61 GGCGGCTTCCCCGTGCCGAGCCGTGCGCGCTCCCGTGCGCGCCACTACCGCGGAGGTGCT   120
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Db    61 GGCGGCTTCCCCGTGCCGAGCCGTGCGCGCTCCCGTGCGCGCCACTACCGCGGAGGTGCT   120

Qy   121 GCCGCTGCCAGTTCGTGCGGCCTGGGCGCCCAGGGCTGCGGCTGGTGTCAGCGCCGG     180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCCGCTGCCAGTTCGTGCGGCCTGGGCGCCCAGGGCTGCGGCTGGTGTCAGCGCCGG     180

Qy   181 GGACCCCGGCGGTTTCCGGCGCGCTGGTGGCCCAGTGCGTGCGGCCCTGGGCGTGGCCGG   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACCCCGGCGGTTTCCGGCGCGCTGGTGGCCCAGTGCGTGCGGCCCTGGGCGTGGCCGG   240

Qy   241 ACGGGCGCCCCCCCCGCCGCCCCTCCTTCGGCGTGTCTGCCTGGAAGGAGCTGGTGGC    300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACGGGCGCCCCCCCCGCCGCCCCTCCTTCGGCGTGTCTGCCTGGAAGGAGCTGGTGGC    300

Qy   301 CCGAGTGCTGCGACAGGCCGTGCGGGGGCGGCGGGGCGGCGGCGGGAAGACGTGCTGGCTTCGC   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGAGTGCTGCGACAGGCCGTGCGGGGGCGGCGGGGCGGCGGCGGGAAGACGTGCTGGCTTCGC   360

Qy   361 GCTGCTGACGCGGGGCCCCGGGGGCGCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA   420
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Db   361 GCTGCTGACGCGGGGCCCCGGGGGCGCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA   420

Qy   421 CCTGCCCAACACCGTGACCGACGCCACTGCCCTGCCGGGAGGGCGGCGCTGGGCTGCTGCG   480
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Db   421 CCTGCCCAACACCGTGACCGACGCCACTGCCCTGCCGGGAGGGCGGCGCTGGGCTGCTGCG   480

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Db   481 CCGCTGGGCGACACGTCTGGTTCACCTGCCGGGTTCGCGACCTGCGCGGGCTCTTTGTGCTGGT   540

Qy   541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGCGAAGTCTGCCAGGAGGGCTGTGCCGGCGGCCAC   600
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Db   541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGCGAAGTCTGCCAGGAGGGCTGTGCCGGCGGCCAC   600

Qy   601 TCAGGCCCGGCCCCACACCAGTGACCCGGTCCGGCTGGACGCGGTCTGGACGATGCGAACGGGC   660
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Db   601 TCAGGCCCGGCCCCACACCAGTGACCCGGTCCGGCTGGACGCGGTCTGGACGATGCGAACGGGC   660

Qy   661 CTGGAACCATAGCGTCAGGGAGCGCAGCTGCCAAGTCTGCACGGCTCTTTCTACCGGAACAGGG   720
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Db   661 CTGGAACCATAGCGTCAGGGAGCGCAGCTGCCAAGTCTGCACGGCTCTTTCTACCGGAACAGGG   720

Qy   721 GAGGCGCGGGGGCAGTGCCAAGTCAGGGAGGCGTTGCCGTGCCCCGTTGCCCAAGAGGGCCCAGGCGTGGCGC   780
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Db   721 GAGGCGCGGGGGCAGTGCCAAGTCAGGGAGGCGTTGCCGTGCCCCGTTGCCCAAGAGGGCCCAGGCGTGGCGC   780

Qy   781 TGCCCCTGAGCCGGCGAGCGGAGCGGAGCGCCCGTTGGGCAGGGGTCCTGGGCCAGGAC   840
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Db   781 TGCCCCTGAGCCGGCGAGCGGAGCGGAGCGCCCGTTGGGCAGGGGTCCTGGGCCAGGAC   840

Qy   841 GGCTGGACCGAGTGACCTGGTTCTGTGGTGTCACCGGCCAGACCCGGCCGAGAAGAAGC   900
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Db   841 GGCTGGACCGAGTGACCTGGTTCTGTGGTGTCACCGGCCAGACCCGGCCGAGAAGAAGC   900

Qy   901 CACCTCTTTGGAGGGTGCGCTCTGCACGGCGCCGCCACTCCCACCCATCCGTGGCGCCCCCA   960
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Db   901 CACCTCTTTGGAGGGTGCGCTCTGCACGGCGCCGCCACTCCCACCCATCCGTGGCGCCCCCA   960

Qy   961 GCACCACGCGGCGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC  1020
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Db   961 GCACCACGCGGCGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC  1020

Qy  1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCCAGCGACAAGGAGGAGCAGCTGCG  1080
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Db  1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCCAGCGACAAGGAGGAGCAGCTGCG  1080

Qy  1081 GCCCTCCTTCACTCAGCTCTTCTGAGCCCCAGCCTGACGCTGGCGTCGGCGTCGTGA  1140
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Qy  1141 GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGAGCACTCCCGGTTGCCCGCGCCT  1200
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Db  1141 GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGAGCACTCCCGGTTGCCCGCGCCT  1200

Qy  1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCGTGTTCTGGAGCTGCTTGGAACCACGCGCCA  1260
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Qy  1261 GTGCCCTACGGGGTGCTCCTCAAGACCACTGCCGCGGTCGGGCTGCGCGGCGGTCACCCCAGC  1320
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Qy  1321 AGCCGGTCTGTGCCCGCGGGAGAAGCCCCAGGGCTCTGTGCGGCCCCCCGAGGAGGAGA  1380
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Qy  1441 CGGCTTCGTGCGGCGGCCCCGCGAGGCCTTCACCACCAGCGTCGCGCAGCTA  1500
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Qy  1501 CAACGAAGCGCCGCTTCATCTCCCTGGGAGCATGCCAA  1560
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Qy  1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGCCCGCTGCGACGTCCAGACTCCG  1920
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RESULT 9
AX019310

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LOCUS       AX019310              4015 bp    DNA     linear       PAT 07-SEP-2000
DEFINITION  Sequence 10 from Patent WO9940221.
ACCESSION   AX019310
VERSION     AX019310.1  GI:10043297
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dahm,M.W., Phelps,R.C. and Brockmeyer,C.
  TITLE     Method for quantitatively analyzing tumor cells in a body fluid and
            test kits suited therefor
  JOURNAL   Patent: WO 9940221-A 10 12-AUG-1999;
            DAHM MICHAEL W (DE); PHELPS ROBERT C (DE); BROCKMEYER CARSTEN (DE)
FEATURES             Location/Qualifiers
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BASE COUNT      663 a   1363 c   1275 g    714 t
ORIGIN
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Query Match   100.0%; Score 4015; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db         1 GCAGGCGCTGGTCCTGCTGCCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCCGATGCC 60

Qy        61 GCGGCTCCCCGCTGCCGAGCCGTGCGCCCTGGGCGCCTGGCCCTGGCGCCAGCCGAGGTGCT 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GCGGCTCCCCGCTGCCGAGCCGTGCGCCCTGGGCGCCTGGCCCTGGCGCCAGCCGAGGTGCT 120

Qy       121 GCCGCTGGCCACGTTCGTGCGCGCCCTGGGGCGCCCAGGGCTGGCTGGTGCAGCGCGG 180
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Db       121 GCCGCTGGCCACGTTCGTGCGCGCCCTGGGGCGCCCAGGGCTGGCTGGTGCAGCGCGG 180

Qy       181 GGACCCGGCGGCTTTCCGCGCGCTGTGGTCCCAGTGCCTGGTGTGCGCCCTGGGACGC 240
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Db       181 GGACCCGGCGGCTTTCCGCGCGCTGTGGTCCCAGTGCCTGGTGTGCGCCCTGGGACGC 240

Qy       241 ACGGGCCCCCCGCCGCGCCCCCTCCTTCGCGCCACGTTCCTGCCTGAAGGAGCTGGTGGC 300
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Qy       301 CCGAGTGCTGCAGAGGGCGTGCGAGAGCCGGCGGCCGAAGAACGTGCTGCGCCTTCGC 360
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Qy       361 GCTGCTGGACGCGGGCGGCCCCGCGGGGGCCCCCGCGGGGGCCGCCTTCACCCACCAGTGC 420
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Qy  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAGAGAGGTGCAGCTGCGGGAGCTGTC  1860
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Qy  1921  CTTCATCCCCAAGCCTGACGGCTGCCGCCATTGTGAACATGGACTACGTCGTGGGAGC  1980
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Qy  2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCCGTACGACACCATCCCCCA  2220
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Qy  2221  GGACAGGCCCGCTGAGGGATGCCGTCATCGGCGAGCATCATCAAACCCCAGAACACGTACTGCGCG  2280
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Db  2281  TCGGTATGCCGTGGTCCAGAGAGGCCGCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA  2340

Qy  2341  CGTCTCTACCTTGACAGACTTCCAGCCGTACATGGCGACAGTTCGTTGCTCACCTGCAGGA  2400
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Qy  2401  GACCGTTGTACGGCACGACATGGAGAACAAGCTGTTTCGGCGGATTCGGCGAATGAGGCCAG  2460
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Qy  2461  CAGTGCCTTCGACGTCTTCTCCTACGCTTCATGTGCCACCACGCCGCGCCACCACGGGG  2520
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Qy  2521  CAAGTCCTCAGGACCCTGCTCCCAGGATCCCGGCCAGGGGATCCCATCCTCTCCCACGCTGCTCTG  2580
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RESULT 10
AX133979
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DEFINITION Sequence 1 from Patent EP1108789.
ACCESSION   AX133979
VERSION   AX133979.1 GI:14139919
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1
  AUTHORS   Chang,S.Y. and Santini,C.D.
  TITLE   Quantitation of htert mrna expression
  JOURNAL   Patent: EP 1108789-A 1 20-JUN-2001;
            F. HOFFMANN-LA ROCHE AG (CH)
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BASE COUNT   663 a   1363 c   1275 g   714 t
ORIGIN

Query Match   100.0%; Score 4015; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GCAGCGCTGCGTCCTGCGTCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC 60
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Db   1 GCAGCGCTGCGTCCTGCGTCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC 60

Qy   61 GCGCGCTCCCGTGCCCAGCCGTGCCGCGCTCCCTGCTCGCGCCAGCCACTACCGCGAGGTGCT 120
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Qy   1081 GCCCTCCTTCCTACTCAGCTCTCTGGAGGCCCAGCCTGACTGGGGCTCGGAGGCTCGTGGA 1140
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Qy   1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCGTGTTTCTGGAGCTGTGGAACCACGCGCA 1260
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Db   1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCGTGTTTCTGGAGCTGTTGGAACCACGCGCA 1260

Qy   1261 GTGCCCTACGGGTGCTCCTCAAGACGCACTGCGCGTGCGAGCTGCCGTCACCCAGC 1320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGCCCTACGGGTGCTCCTCAAGACGCACTGCGCGTGCGAGCTGCCGTCACCCCAGC 1320

Qy   1321 AGCCGGTGTCGTGCCCGTCGCGGCGGCTCTCGCCGCCGGCTCTGTGGCGGCCCCCGAGGAGGA 1380
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Db   1321 AGCCGGTGTCGTGCCCGTCGCGGCGGCTCTCGCCGCCGGCTCTGTGGCGGCCCCCGAGGAGGA 1380

Qy   1381 CACAGACCCCCGTCTGCTGCCGCTGCCTGGTGCCCCAGCCAGCAGCCGCCTGGCAGGTGTA 1440
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Qy   1441 CGGCTTCGTTGCGGCGGCTGCCGCGGTGGTGCCCCAGCCTGCGCCAGCTA 1500
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Db   1441 CGGCTTCGTTGCGGCGGCTGCCGCGGTGGTGCCCCAGCCTGCGCCAGCTA 1500

Qy   1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
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Qy  2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGTACGACACCATCCCCCA 2220
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Db  2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGTACGACACCATCCCCCA 2220

Qy  2221 GGACAGGCTCACGAGGTCATCGGCCAGCATCATCAAACCCAGAACACGTACTGCCTGCG 2280
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Qy  2281 TCGGTATGCCGTGGTCCAGAGACCTCGGACACGTCGTTGGCTCACCTCAGGACGCCA 2340
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Db  2281 TCGGTATGCCGTGGTCCAGAGACCTCGGACACGTCGTTGGCTCACCTCAGGAGCCA 2340

Qy  2341 CGTCTCTACCTTGACAGACCTTCCAGCCGTACACGTCGTTGGCTCACCTGCTGCAGGA 2400
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Qy  2461 CAGTTGGCCTCTTCGACGTCTTCATGTGCCACCACGCGCGGGGACCTCACCACCAGGGG 2520
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Qy    3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG  3960
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Db    3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG  3960

Qy    3961  GAGGTGCTGTGGGAGGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA  4015
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RESULT 11
AX552695
LOCUS   AX552695   4015 bp   DNA   linear   PAT 27-NOV-2002
DEFINITION   Sequence 1 from Patent WO02074948.
ACCESSION   AX552695
VERSION   AX552695.1 GI:25896697
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Denning,C., Clark,A.J. and Schiff,J.M.
  TITLE   Animal tissue with carbohydrate antigens compatible for human
                transplantation
  JOURNAL   Patent: WO 02074948-A 1 26-SEP-2002;
                Geron Corporation (US)
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT   663 a   1363 c   1275 g   714 t
ORIGIN

Query Match   100.0%;   Score 4015;   DB 6;   Length 4015;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1  GCAGGCTGCGTCCTGCTGCCGCACGTGGGAAGCCCTGGCCCACCCCCGGCACCCCGGATGCC   60
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Db       1  GCAGGCTGCGTCCTGCTGCCGCACGTGGGAAGCCCTGGCCCACCCCCGGCACCCCGGATGCC   60

Qy      61  GGGCGGCTGCCCTGCCCCGAGCCGTGCGCCGTCCCTGCTGCGCGAGGTTGCCCCGGAGGTGCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  GGGCGGCTGCCCTGCCCCGAGCCGTGCGCCGTCCCTGCTGCGCGAGGTTGCCCCGGAGGTGCT  120

Qy     121  GGGCGGCTGCCACGTTCGTGCGGGGCGGCGCCGTCCGGGCGGGCCGTCGGGCTGGTGGTGGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  GGGCGGCTGCCACGTTCGTGCGGGGCGGCGCCGTCCGGGCGGGCCGTCGGGCTGGTGGTGGC  180

Qy     181  GGACCCGGCGGCTTCCGGGGCGGGGCGCTGTGCGGGGAACGCTGCTGGTGCGTGCCCTGGGACGC  240
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Db     181  GGACCCGGCGGCTTCCGGGGCGGGGCGCTGTGCGGGGAACGCTGCTGGTGCGTGCCCTGGGACGC  240

Qy     241  ACGGGCCGGCCGCCCCCGCCCCCTCCTTCGCGGACCGTGTCCTGCCAGGTGTCCTGCCTGAAGGAGCTGGTTGGC  300
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Db     241  ACGGGCCGGCCGCCCCCGCCCCCTCCTTCGCGGACCGTGTCCTGCCAGGTGTCCTGCCTGAAGGAGCTGGTTGGC  300

Qy     301  CCGAGTGCTGCAGAGCTGTGCGGGGCGGGCCGAGAACGTGCTGCCCTTCGGCCTTCGC  360
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Qy     361  GCTGCTGGACGGGGCGGGCCGGGCGGGGCGCTGCACCCGCAGGCCTTCACCACCACGTGCGCAGCTA  420
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Db     361  GCTGCTGGACGGGGCGGGCCGGGCGGGGCGCTGCACCCGCAGGCCTTCACCACCACGTGCGCAGCTA  420

Qy     421  CCTGCCCAACACGGTGACCGACGACTGCGTGGTTCACCTGGCCGTTGCCGGGGCTGCGGGGCTGCGCG  480
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Qy     481  CCGCGTGGGCGACGACGTGCTGTGTTCACCTGCTGCGCGCACGCGCTGGCACGCGCTGCTTGTCTTTGTGCTGGT  540
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Qy     601  TCAGGCCCGGCCCCCGGCCACGCGCTAGTGGCAGGCGTCTGGGATGCGAACGGGGC  660
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Db     601  TCAGGCCCGGCCCCCGGCCACGCGCTAGTGGCAGGCGTCTGGGATGCGAACGGGGC  660

Qy     661  CTGGAACCATAGCGTCAGGAGGCGGGGTCCCCTGGCCTGCCAGCCCGGTGCGAG  720
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Qy     721  GAGGCGCGGGGCAGTGCCAGCCGGAGTCTGCCGTTGCCGGTGCTCAGGCGTGGCGC  780
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Qy     781  TGCCCCTGAGCGGAGCGACGCCCTCTGCACGCGCACGCACTCCCACCATCCGTGGGCCGCCA  840
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Qy     841  GCGTGGACCGAGTGACCTGGTTTCTGTGGTGTCACTGCCAGACCCGCCGAAGAAGC  900
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Db     841  GCGTGGACCGAGTGACCTGGTTTCTGTGGTGTCACTGCCAGACCCGCCGAAGAAGC  900

Qy     901  CACCTCTTTGGAGGGTGCGCTCTGCGCACGCGCCACTCCCACCATCCGTGGGCCGCCA  960
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Db     901  CACCTCTTTGGAGGGTGCGCTCTGCGCACGCGCCACTCCCACCATCCGTGGGCCGCCA  960

Qy     961  GCACCACGCGGGCGCGGGCCCCCATCCACATCCACATCGCGCGCCCACCAGTGCCCTGGGACACGCCCTTGTCC  1020
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Qy    1021  CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCGACTGGCGCTCGAGGAGCAGCTGCG  1080
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Qy    1141  GACCATCTTTTCTGGGTTCCAGGCCCTGGATGCCAGCCACTACCGCGAGGTGCT  1200
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Qy    1201  GCCCCAGCGCTACTGGCAAATGCGCGCCCCTGCTGTTTCGGAGCTGTTGGAACCACGCGCA  1260
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Db    1201  GCCCCAGCGCTACTGGCAAATGCGCGCCCCTGCTGTTTCGGAGCTGTTGGAACCACGCGCA  1260

Qy    1261  GTGCCCTACGGGCGGCTTCGTGCTCCTCAAGACGCACTGCCGTCGGTCACCCCAGC  1320
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Db    1261  GTGCCCTACGGGCGGCTTCGTGCTCCTCAAGACGCACTGCCGTCGGTCACCCCAGC  1320

Qy    1321  AGCCGGTGTCTGTGCGCCGGAGAAGCCCTGCCTGAAGGAGCTGGTGGC  1380
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Qy    1381  CACAGACCCCGTGCCGCCTGGTGCTGGCGGAGAACGTGCTGCCCTTCGGCCTTCGC  1440
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Qy    1501  CAACGAACGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560
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Db    1501  CAACGAACGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560

Qy    1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCCTTGGCTGCGCAG  1620
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Qy 1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCCCAGAGCACCGTCTGCGTGAGAGATCCTGGC 1680
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Db 1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCCCAGAGCACCGTCTGCGTGAGAGATCCTGGC 1680

Qy 1681 CAAGTTCCTGCCACTGGCTGCTGAGTGAGTGTGTACGTCGTCGAGCTGCTCAGTCTTTCTTTTA 1740
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Qy 1741 TGTCACGGAGGAGACCACGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1800
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Qy 1981 CAGAACGTTCCGCAGAGAAAAGAGGGCGAGCGTCTCACCTCGAGGTGAAGGCACTGTT 2040
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Qy 2641 GCTCCTGCGTTGGTGATGATTCTTTGTTGGTGACACCTCACCTCACCGCGAAAAC 2700
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Qy 2701 CTTCCTCAGGACCCTGGTCCGGAGGTGTCCCTGAGTATGGCTGCGTTGGTGAACTTGCGGAA 2760
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Db 2701 CTTCCTCAGGACCCTGGTCCGGAGGTGTCCCTGAGTATGGCTGCGTTGGTGAACTTGCGGAA 2760

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Qy 3661 GAGTGTCCAGCACACTGCCCGTTCGGGGATTCGGCGGCTGGCGCTGGCGCTCCCGCCGGCC 3720
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Db 3661 GAGTGTCCAGCACACTGCCCGTTCGGGGATTCGGCGGCTGGCGCTGGCGCTCCCGCCGGCC 3720

Qy 3721 GGGGCCAGTCTTTTCCTCACCAGAGCCCGGCTTCCACTCCCCACCAGGAATAGTCCATCC 3780
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Qy 3781 CCAGATTCGCCATTGTTCACCCCGCCCTCGCCCTGCCTTCCACCCACCATCC 3840
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RESULT 12
BD011044
LOCUS   BD011044   4015 bp   DNA   linear   PAT 31-JAN-2002
DEFINITION Human telomerase catalytic subunit.
ACCESSION   BD011044
VERSION   BD011044.1 GI:18639417
KEYWORDS   JP 2001081042-A/1.
SOURCE   unidentified
  ORGANISM unidentified
            unclassified.
REFERENCE   1 (bases 1 to 4015)
  AUTHORS   Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
            Harley,C.B. and Andrews,W.H.
  TITLE   Human telomerase catalytic subunit
  JOURNAL   Patent: JP 2001081042-A 1 27-MAR-2001;
            GERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT   OS   Unidentified
            PN   JP 2001081042-A/1
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            MORIN,
            PI   CALVIN B HARLEY,WILLIAM H ANDREWS
            PC   A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
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            CC   Topology: Linear;
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     FH   Key   Location/Qualifiers
     FT   CDS   56..3454.
BASE COUNT   663 a   1363 c   1275 g   714 t
ORIGIN

Query Match   100.0%; Score 4015; DB 6; Length 4015;
Best Local Similarity   100.0%;
Matches 4015; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db     1 GCAGGCGCTGGCTCCTGCTGCGCGAGCCGTGCCACGTGGGAAGCCCTGGCCCCCGCCCGCCGATGCC 60

Qy    61 GCGGCGCTCCCCGCCTGCGAGCCGCGTGCGCGGAGCCCTGGCCCCTCCGGTGGTGCT 120
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Qy              1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCGTCGCTGCGAGCTGCTCAGGTCTCTTCTTTA 1740
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Qy              1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTCTTTTCTCACCGGAAGAGTGTCTGGAG 1800
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Qy              1921 CTTCATCCCCAAGCCTGCGCGGGCTGCCGCCCGATTGTGAACATGTGAACATGGACTACGTCGTGGGAGC 1980
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Qy              1981 CAGAACGTTCCGACAGAGAAAAGAGGGCCGAGCGTCTCACCTGCAGGGTGAAGGCACTGTT 2040
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Qy              2041 CAGCGGCTCAACTGCGAGCGGGGGCCGCGCCCGGGGCTGCCGCCCTGTGCGGGAGC 2100
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Qy              2101 CCTGGACGATATCCCACAGGGCCTGCGGCGCACCTTCGTGTGCGGCCCCAGGACCC 2160
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Qy              2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCCGCCCTACGACACACCATCCCCCCA 2220
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Qy              2221 GGACAACGGTCACGGAGGTCATCGCCAGCAATCATCAAAACACGTACTGCTGCGG 2280
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Qy              2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGCAGAGCTCCTCCCTGAATAGAGGCCAG 2460
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Qy              2461 CAGTGGCCTCTTCGACGTCTTCCTGACGCTTCATGTGCCATCAGGGG 2520
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Qy              2521 CAAGTCCTACGTCCAGTGCGACATGGGAGAACAAGCTGTTTCGGGGATTCGGCGGGACGGGGCT 2580
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Qy              2641 GCTCCTCGGTTTGGTGTCCGAGTGTCCCGAGTATGCGCCGAGTGGTGGTGAACTTGCGGAA 2700
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Qy              3061 CAAGATCCTCCTGCTGCAGGCGTACCTCACCTGCAGTGTGCTGCACTGT TCA 3120
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Qy              3121 TCAGCAAGTTGGAAGAACCCCACATTTTCCTGCGCGTCATCCTGACACGGCCTCCCT 3180
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Qy              3301 GACTCGACACCGTGTCACCTACGGTGCCACTCCTGGGGTCACTCAGGACGCCAGACCCCAGAGGGCG 3360
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Qy              3361 GCTGAGTCGGAAGCTCCGGGGACGTCCCGGGGAGGCCGCCAACCCGGC 3420
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ORIGIN                  /db_xref="taxon:9606"

Query Match          100.0%;  Score 4015;  DB 6;  Length 4015;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 4015;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy    3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTTGATGGCCACCCGCCCACAGCCAGGCCGA  3480
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RESULT 13
BD015832
LOCUS       BD015832          4015 bp    DNA       linear      PAT 27-AUG-2002
DEFINITION  Quantitation of expression of hTERTmRNA.
ACCESSION   BD015832
VERSION     BD015832.1  GI:22556969
KEYWORDS    JP 200120483-A/1.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 4015)
AUTHORS     Chang,S.Y.P. and Santini,C.D.
TITLE       Quantitation of expression of hTERTmRNA
JOURNAL     Patent: JP 200120483-A 1 31-JUL-2001;
            F HOFFMANN LA ROCHE AG
OS          Homo sapiens (human)
PN          JP 200120483-A/1
PD          31-JUL-2001
PF          18-DEC-2000 JP 200384268
PR          16-DEC-1999 US 09/465491
PI          SHEN YUN PAI CHANG,CHRISTOPHER DAVID SANTINI
PC          C12N15/09,C12Q1/48,C12Q1/68,C12N15/00
CC          Quantitation of expression of hTERTmRNA
FH          Key             Location/Qualifiers
FT          source          1..4015
FT                          Location/Qualifiers
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Qy         1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080
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                OS   Homo sapiens (human)
                PN   JP 2001309791-A/1
                PD   06-NOV-2001
                PF   02-MAY-2000 JP 2000138250
                PI   HAJIME KANEUCHI,MAKOTO KAMIMORI
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FEATURES        Location/Qualifiers
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BASE COUNT      663 a     1363 c     1275 g      714 t
ORIGIN

Query Match            100.0%;  Score 4015;  DB 6;  Length 4015;
  Best Local Similarity 100.0%;  Pred. No. 0;
  Matches 4015;  Conservative 0;  Mismatches 0;  Indels. 0;  Gaps 0;

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Qy   61 GCGGCTCCCCGCGTGCCGAGCCGTGCGCTCCTCGCTGCGAGCCACTACCCGCGAGGTGCT   120
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DEFINITION    Method for distinguishing cancer cell.
ACCESSION     BD082985
VERSION       BD082985.1  GI:22628595
KEYWORDS      JP 2001309791-A/1.
SOURCE        Homo sapiens (human)
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1  (bases 1 to 4015)
  AUTHORS     Kaneuchi,H. and Kamimori,M.
  TITLE       Method for distinguishing cancer cell
  JOURNAL     Patent: JP 2001309791-A 1 06-NOV-2001;
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Wed Oct 15 09:29:26 2003

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Db 1381 CACAGAACCCCCGTCGCTGGTGCAGTCTCCGCCACAGCAGCCCCTGGCCAGTGTA 1440

Qy 1441 CGGCTTCGTGCGGGGCCTGCGCCGGCCTGGTGCCCCGGCCTCGGGGCTCCAGGCA 1500
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Qy 1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
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Db 1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

Qy 1561 GCTCTGCTGCAGGAGCTGACGTGGTGTCCGGCCGAGATGAGCGTGCGCTTGCGCTTGCGGAGGAGATCCTGGC 1620
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Qy 1681 CAAGTTCCTGCACTGGCTGCGATGAGTGTACGTCGTCGAGCTGTCTCAGGTCTTCTTTA 1740
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Qy 1741 TGTCACGGAGACCACCACGTTTCAAAAGAACAGCTCTCTTTTCTACCGGAAGAGTGTCTGGAG 1800
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Qy 1801 CAAGTTGCAAAGCATTGGAATGCAGCACTTGAAGAGGTGCAGCTGCCGGAGCGTGTC 1860
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Db 1801 CAAGTTGCAAAGCATTGGAATGCAGCACTTGAAGAGGTGCAGCTGCCGGAGCGTGTC 1860

Qy 1861 GGAAGCAGAGGTCAGGCAGCATCGGGAGGAAGCCAGGCCCGCCCTGCTGACGTCCGAGACTCCG 1920
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DEFINITION    Method for quantitating tumor cells in body fluid and exmination
              kit suitable therefor.
ACCESSION     BD131727
VERSION       BD131727.1  GI:23226672
KEYWORDS      JP 2002503454-A/10.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 4015)
AUTHORS       Dahm,M.W., Phelps,R.C. and Brockmeyer,C.
TITLE         Method for quantitating tumor cells in body fluid and exmination
              kit suitable therefor
JOURNAL       Patent: JP 2002503454-A 10 05-FEB-2002;
              MICHAEL W DAHM
COMMENT       OS  Homo sapiens (human)
              PN  JP 2002503454-A/10
              PD  05-FEB-2002
              PF  03-FEB-1999 JP 2000530631
              PR  04-FEB-1998 DE 198 04 372.4
              PI  MICHAEL W DAHM,ROBERT C PHELPS,CARSTEN BROCKMEYER PC
              C12N15/09,C12Q1/68,C12N15/00
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FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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BASE COUNT      663 a    1363 c    1275 g    714 t
ORIGIN
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Query Match          100.0%;  Score 4015;  DB 6;  Length 4015;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 4015;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy    1  GCAGCGCTGCGTCCTGCCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCCGCCGATGCC  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  GCAGCGCTGCGTCCTGCCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCCGCCGATGCC  60

Qy   61  GCGGCCTCCCCGTCCGAGCCGTGCGCTCCCTGCGCCAGCCACTACCGCGAGGTGCT  120
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Db   61  GCGGCCTCCCCGTCCGAGCCGTGCGCTCCCTGCGCCAGCCACTACCGCGAGGTGCT  120

Qy  121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCGCTGGTGCAGCGCGG  180
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Db  121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCGCTGGTGCAGCGCGG  180

Qy  181  GGACCCGGCGGCTTTCCGGCGCGTGTCGCCGCCGGACGC  240
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Db  181  GGACCCGGCGGCTTTCCGGCGCGTGTCGCCGCCGGACGC  240

Qy  241  ACGGCCGCGCTGTGCGAGCGCGGGCCCCCCGAGGCCTTCGGCTTCGC  300
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Db  241  ACGGCCGCGCTGTGCGAGCGCGGGCCCCCCGAGGCCTTCGGCTTCGC  300

Qy  301  CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGGCGGAAGAACGTGCTGGCCTTCGC  360
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Db  301  CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGGCGGAAGAACGTGCTGGCCTTCGC  360

Qy  361  GCTGCTGGACGGGGCCCCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA  420
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Qy  421  CCTGCCCAACACGTGACCGACGCACTGCGGGGGCGTGGGGGCCGTGGGGGTGCTGCGCG  480
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Qy  481  CCGGCGTGGGGCGACGACGTGCTGGTTCACCTGGTCTCTTTGTGCTGGT  540
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Db  3001  TCACAGCCGTGTTTCTGGATTTGCAGGTGAACAGCGCCTCCAGACGGGTGTGCACCAACATCTA  3060

Qy  3061  CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCGCATGTGTGCTGCAGCTCCCATTTCA  3120
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Db  3061  CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCGCATGTGTGCTGCAGCTCCCATTTCA  3120

Qy  3121  TCAGCAAGTTGGAAGAACCCACATTTTCCTGCGCGGTCATCTCTGACACGGCCTCCCT  3180
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Db  3121  TCAGCAAGTTGGAAGAACCCACATTTTCCTGCGCGGTCATCTCTGACACGGCCTCCCT  3180

Qy  3181  CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGC  3240
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Db  3181  CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGC  3240

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Qy  3301  GACTCGACACCGTGTCACCTAGCTGCCACTCCTGGGTCACTCAGGACAGCCCAGACGCA  3360
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Db  3301  GACTCGACACCGTGTCACCTAGCTGCCACTCCTGGGTCACTCAGGACAGCCCAGACGCA  3360

Qy  3361  GCTGAGTCGGAAGCTCCCGGGACGACGACGCCTGACTCGCCTGGAGGCCGCAGCCGCAACCGGC  3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  GCTGAGTCGGAAGCTCCCGGGACGACGACGCCTGACTCGCCTGGAGGCCGCAGCCGCAACCGGC  3420

Qy  3421  ACTGCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCCACAGCCAGGCCGA  3480
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Db  3421  ACTGCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCCACAGCCAGGCCGA  3480

Qy  3481  GAGCAGACACCAGCAGCAGCCCTGTCACGCCGGGCTCTACGCTCACGCCCGGCTCTACGCGGGC  3540
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Db  3481  GAGCAGACACCAGCAGCAGCCCTGTCACGCCGGGCTCTACGCTCACGCCCGGCTCTACGCGGGC  3540

Qy  3541  CACACCCCAGGCCCGCCACCGCACCCGCACCCGCTGGGAGTCTGGGAGTCTGAGGCGCTGAGTGAGTGTTTGGCCGGCCTG  3600
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Qy  3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCCTGAGGCGTCCAGCCAAGGGCT  3660
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Db  3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCCTGAGGCGTCCAGCCAAGGGCT  3660

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Db  3661  GAGTGTCCAGCACACCTGCGTCTTCACTTCCCCACAGCCTGCGCTGCGCTCCACCCCA  3720

Qy  3721  GGGCCAGCGTTTCCTCACCAGGAGCCCGCTTCACTCCCACATAGGAATAGTCCATCC  3780
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Db  3721  GGGCCAGCGTTTTCTCACCAGGAGCCCGCTTCACTCCCACATAGGAATAGTCCATCC  3780

Qy  3781  CCAGATTCGCCATTGTTCACCCCCTCCTTGCCTTCCACCCCCATCC  3840
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Qy  3841  AGGTGGAGACCCTGAGAAGGCTCTGGGAATTTGGAGTGACCAAAGGTGTG  3900
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Qy  3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG  3960
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Db  3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG  3960

Qy  3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA  4015
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BD131727
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Qy          CACCTCTTTGGAGGGTGCGCTGCTCTGCGCAGCGCCACCCCACCGTGGGCCGCCA  960
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Qy          GCCCTCCTTCTACTCCAGCTCTTCTGAGGCCCAGCCTGACTGCGGCTCGGAGGCTCGTGGA  1140
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Qy          GTGCCCCTACGGGGTGCTCTCCTCAAGACGCACTGCCGGTGCGGTTGCGGCTCGGTGTA  1320
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Qy          CGGCTTCTACGTGCTACGGGCGACATGGAAGCACTTCCTTCATGTGCGGCATCAGGGG  1500
Db          CGGCTTGTCTACGGGCGACATGGAAGCACTTCCTTCATGTGCGGCATCAGGGG  1500

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Db          GCTCCTGCGGTTTGGTGGATGAGCGTGCGGGACTGCCTGCCGCAG  1620
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Qy          CAAGTTCCTGCACTGGCTGTGATGAGTGTGTACGTCGTGAGCGTGCTGCTCAGGTCTCTTTA  1740
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Qy          CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC  1860
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Qy          CCTGGACGATATCCACAGCCTTCGTGCTGCTGCGTGCGCTGCGGACCC  2160
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Qy          GGACAGGCCGCGAGGTCACCGAGGTCATCGAGACGTCGTCATCAAACCCAGCTACTGCGTGCG  2280
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Qy          CGTCTCTACCTTGACAGACCTCCAGCGTTCGTGGCTCACCTGCAGGA  2400
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Qy          GACCAGCCCGCTGAGGGGATGCCCGTCGTCATCGAGCAGCAGCTCCTCCCTGAATGAGGCCAG  2460
Db          GACCAGCCCGCTGAGGGGATGCCCGTCGTCATCGAGCAGCAGCTCCTCCCTGAATGAGGCCAG  2460

Qy          CAGTGGCCTCTTCATGTGCCCATCAGGGGG  2520
Db          CAGTGGCCTCTTCATGTGCCCATCAGGGGG  2520

Qy          CAAGCCTCTACGTGCTACGGGCGGATCCCGGCTGCTCCATCCTCTCACGGCGTGCTCTG  2580
Db          CAAGCCTCTACGTGCTACGGGCGGATCCCGGCTGCTCCATCCTCTCACGGCGTGCTCTG  2580

Qy          CAGCCTGTGTCTACGGGCGACATGGAACAAGCTGTTTCGGGGATTCGGCGGACGGGCT  2640
Db          CAGCCTGTGTCTACGGGCGACATGGAACAAGCTGTTTCGGGGATTCGGCGGACGGGCT  2640

Qy          GCTCCTGCGTTTGGTGGATGATTCTTGTTGGTGACACCTCACCTCACCCCACCCAG  2700
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Qy  3781 CCAGATTCGCCATTGTTCACCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCC 3840
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Qy  3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAA 4015
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Search completed: October 15, 2003, 02:25:11
Job time : 14244 secs
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Qy 2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820
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Db 2881 GCAGAGGCACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTTCACCTTCAACCG 2940

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Db 3001 TCACAGCCTGTTCTGGATTTGCAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060

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Qy 3241 CGGCCCTCTGCCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3241 CGGCCCTCTGCCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300

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Db 3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360

Qy 3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCGTGACCGCTGACTGCCCTGGAGGCCGCAGCCAACCCGC 3420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCGTGACCGCTGACTGCCCTGGAGGCCGCAGCCAACCCGC 3420

Qy 3421 ACTGCCCCTCAGACTTCAAGACCATCCTGACTGACTTCAGAGACCTCCAGGCCACCCCAGCCAGGCCGA 3480
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Db 3421 ACTGCCCCTCAGACTTCAAGACCATCCTGACTGACTTCAGAGACCTCCAGGCCACCCCAGCCAGGCCGA 3480

Qy 3481 GAGCAGACACCAGCAGCCCGTCCCGGGCCTCTACGTCCCAGGGAGGGAGGGCGGCC 3540
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Qy 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCCTGAGCGTGTCCAGCCAAGGGCT 3660
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Qy 3661 GAGTGTCCAGCACACTTGCCGTCTTCACTTCCCGCTCGGCGCTCGGCCTCCACCCCA 3720
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Qy 3721 GGGCCAGCTTTTCCTCACCAGGAGCCCCGCTTCCACTCCCCATAGGAATAGTCCATCC 3780
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Db 3721 GGGCCAGCTTTTCCTCACCAGGAGCCCCGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
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            GenCore version 5.1.6
   Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October 14, 2003, 20:23:54 ; Search time 988 Seconds
                                          (without alignments)
                                          10969.882 Million cell updates/sec

Title:     US-10-054-295-224
Perfect score: 4015
Sequence:  1 GCAGGCCTGGCTCCTGCTGC.........TTTTTCAGTTTTGAAAAAAA 4015

Scoring table: IDENTITY_NUC
           Gapop 10.0 , Gapext 1.0

Searched:  2252756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:     5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : N_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4015	100.0	4015	20	AAZ30154	cDNA encoding a hu
2	4015	100.0	4015	20	AAZ20279	Human telomerase r
3	4015	100.0	4015	20	AAZ00724	Human telomerase c
4	4015	100.0	4015	22	AAH45901	Human hTERT gene.
5	4015	100.0	4015	24	AAD46821	Human telomerase r
6	4015	100.0	4015	24	ABA97534	Cancer cell discri
7	4015	100.0	4015	25	ABZ22474	Human telomerase r
8	4015	100.0	4042	20	AAV72117	Human catalytic te
9	4015	100.0	4070	24	ABL53711	Human telomerase c
10	4013.4	100.0	4015	20	AAZ08150	Human telomerase r
11	4013.4	100.0	4015	25	ABZ18391	Group III cDNA can
12	4011.8	99.9	4023	19	AAV60320	Human telomerase g
13	4007	99.8	4037	19	AAV22428	Human telomerase r
14	4002	99.7	4027	20	AAX89424	Human EST2 coding
15	4002	99.7	4027	21	AAA29388	hEST2, a human tel
16	3956.8	98.6	3964	20	AAX18254	Human telomerase c
17	3885	96.8	3955	19	AAV22379	Human telomerase r
18	3872	96.4	3918	20	AAX18269	Telomerase coding
19	3872	96.4	3918	20	AAX18278	Telomerase coding
20	3782.8	94.2	3798	19	AAV27876	Human telomerase p
21	3641	90.7	3855	19	AAV22382	Human telomerase r
22	3400	84.7	3453	25	ABZ76217	Human TERT coding
23	3400	84.7	13766	24	AAD46790	pGRN145 plasmid DN
24	3399	84.7	3399	24	ABZ35720	Human elomerase re
25	3399	84.7	3399	24	ABX09963	Human telomerase r
26	3399	84.7	3399	24	ABV78144	Human telomerase r
27	3399	84.7	3399	22	ABL91685	Human polynucleoti
28	3396	84.6	3396	22	AAH44366	Human telomerase n
29	3396	84.6	3396	22	AAH48235	Heart muscle cell
30	3396	84.6	3396	22	AAH49601	Human coding seque
31	3392.8	84.5	3396	20	AAX18266	Telomerase coding
32	3388 c	84.4	8742	24	AAD46793	pWGB5a plasmid DNA
33	3278.8	81.7	3500	20	AAX18275	Telomerase (ver. 2
34	3201.4	79.7	3203	20	AAX18268	Altered C-terminus
35	3121	77.7	3167	20	AAX18271	Altered C-terminus
36	3121	77.7	3167	20	AAX18280	Altered C-terminus
37	3077.4	76.6	7688	20	AAX18351	Altered C-terminus
38	3073	76.5	3323	20	AAX18277	Telomerase coding
39	2889.2	72.0	7797	20	AAX18350	Telomerase coding
40	2843	70.8	3069	20	AAX18276	Truncated telomera
41	2843	70.8	3069	20	AAX18267	Truncated telomera
42	2837	70.7	2848	19	AAV27872	Human telomerase p
43	2762.6	68.8	3033	20	AAX18270	Truncated telomera
44	2762.6	68.8	3033	20	AAX18279	Truncated telomera
45	2513.6	62.6	7615	20	AAX18349	Telomerase coding

ALIGNMENTS

```
RESULT 1
AAZ30154
ID   AAZ30154 standard; cDNA; 4015 BP.
XX
AC   AAZ30154;
XX
DT   26-JAN-2000 (first entry)
XX
DE   cDNA encoding a human telomerase reverse transcriptase (TRT).
XX
KW   Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
KW   dendritic cell; telomerase activity; cancer cell; proliferating cell;
KW   immunological destruction; telomerase; cancer; proliferation disease;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             56..3454
FT                   /*tag= a
FT                   /product= "telomerase reverse transcriptase"
XX
PN   WO9950392-A1.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;  99WO-US06898.
XX
PR   31-MAR-1998;  98US-0112006.
XX
PA   (GERO-) GERON CORP.
```

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XX
PI   Gaeta FCA;
XX
DR   WPI; 1999-610845/52.
DR   P-PSDB; AAY43621.
XX
PT   Eliciting an in vivo immune response for prevention and treatment of
PT   cancers -
XX
PS   Disclosure; Fig 2; 26pp; English.
XX
CC   The present sequence encodes a human telomerase reverse transcriptase
CC   (TRT) polypeptide. The protein is used in the method of the invention.
CC   The specification describes a method for activating a T lymphocyte,
CC   comprising contacting the T lymphocyte with a dendritic cell that
CC   expresses a TRT peptide in the context of a MHC class I or MHC class
CC   II molecule. The protein causes induction of an in vivo immunological
CC   response to telomerase activity. Cancer cells are characterized by
CC   expression of endogenous TRT gene and the presence of detectable
CC   telomerase activity. Therefore, by eliciting a specific immune response
CC   to TRT or to TRT-expressing cells, it is possible to selectively target
CC   proliferating cells for immunological destruction. The method is used
CC   for eliciting an in vivo immune response to telomerase by activating
CC   a T lymphocyte, and is useful for prevention and treatment of cancers and
CC   other proliferation diseases/conditions.
XX
SQ   Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;

Query Match       100.0%;   Score 4015;   DB 20;   Length 4015;
Best Local Similarity    100.0%;
Matches 4015;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;
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Qy      1 GCAGCGCTGCGCTCCTGCTCGCGCACGTGGAAGCCCTGGCCCCGGCCACCCCCGGCGATGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAGCGCTGCGCTCCTGCTCGCGCACGTGGAAGCCCTGGCCCCGGCCACCCCCGGCGATGCC 60

Qy     61 GCGCGGCCTCCCCGCCGCCGAGCCGGTGCGCTCCCGCTGCTCGCTGCTCGCCGCCGAGGTGCT 120
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Qy    121 GCGCTGCGCCAGTTCGTGCGGCGGGCCCTGGGCCCCAGGGCTGGTGCAGCGCGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCGCTGCGCCAGTTCGTGCGGCGGGCCCTGGGCCCCAGGGCTGGTGCAGCGCGG 180

Qy    181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCGGCTGCCCAGTGCCGGTGTGCGGTCCCGGACGC 240
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Qy    241 ACGGCCGCCCCCCCCCCGCGCGCCCCCCCTCCGCCCTTCCGGCAGGTGTCCTGCCAGGTGTCGGTGGC 300
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Db    241 ACGGCCGCCCCCCCCCCGCGCGCCCCCCCTCCGCCCTTCCGGCAGGTGTCCTGCCAGGTGTCGGTGGC 300

Qy    301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGGCGGGAAGAACGTGCTGGCCTTCGGC 360
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Qy    361 GCTGCTGGACGGGGCGGCCCCGGGGCCCGGGGCCCCCCCGGGGAAGCCGTGCGCAGCTA 420
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Qy    421 CCTGCCCAACACCGGTGACGACCACTGCCTGGGGCGGGGCCTGGGGGCTGCGTGCTGCGG 480
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Qy    481 CCGGAGTGGGCGACGACGTGCTGTTCACCTGCTGGGGCGACGTGCTCTTTTGTGCTGGT 540
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Qy    721 GAGGCGCGGGGCAGTGCCAGTGCCGCCGAAGTCTGCGGTGCCGTGCCGTGGGCGTGGCGC 780
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Qy    781 TGCCCCTGAGCCGAGGCGACGCCCCGTTGGCCAGGGTCTGGGCCCACCGGCCAGGAC 840
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Qy    841 GCGTGGACCGAGTGACCGTGTTTCGTGGTGTGGTGTCGCGCCACGCGCACCCGCGAGAAGC 900
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Db    841 GCGTGGACCGAGTGACCGTGGTTCTGTGGTGTGGTGTCGCGCCAGCCGCCGCGAGAAGC 900

Qy    901 CACCTCTTTGGAGGTGCGCTCTGTGACCGCGCACTCCCACTCCCATCCGTGGGCCCCCA 960
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Qy    961 GCACCACGCGGGCGCCCCCCATCCACATCGCGGCCCACACGTCCCTGGACACGCCCTGTCC 1020
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Qy   1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080
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Qy   1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCCACCTGCAGGGTGAAGGCACTGTT 2040
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Qy   2161 GCCGGCTGAGCTGTACTTGTCAAGTGGATGTGACGGGCGTACGACACCCATCTGCGTGCGG 2220
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Qy   2221 GGACAGGCGTCACGGACGGAGGTCATCGCCAGCATCAATCAAAACCCAGAACACGTACTGCG 2280
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Qy   2461 CAGTGGCCTTCGACGTCTTCATGTGCCACCAGCGCGTGCCATCAGGGG 2520
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Db   2581 CAGCGTTGGTACGCGACATGGAGAACAAGCTGTTTGCGGGATTCGGCGGACGGGCT 2640

Qy   2641 GCTCCTGCGTTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACGCGGAAAAC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCTCCTGCGTTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACGCGGAAAAC 2700

Qy   2701 CTTCCTCAGGACCCTGGTCCGGAGTGTGCCCTGAGTATGGCCCTGAGTTGCCGGAA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTTCCTCAGGACCCTGGTCCGGAGTGTGCCCTGAGTATGGCCCTGAGTTGCCGGAA 2760

Qy   2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGAGGCGGCACGGGTTGTTCAGAT 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGAGGCGGCACGGGTTGTTCAGAT 2820


Qy   2821 GCCGGCCACGGCCTATTCCCCTGGTGCGGCCGCCTGCTGTGCGATACCCGGACCCTGGAGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GCCGGCCACGGCCTATTCCCCTGGTGCGGCCGCCTGCTGTGCGATACCCGGACCCTGGAGT 2880

Qy   2881 GCAGAGCCACTACTCCAGCTATGCCCGGACCTCTGCGTGGGAGCTGTCTCACCTTCAACCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCAGAGCCACTACTCCAGCTATGCCCGGACCTCTGCGTGGGAGCTGTCTCACCTTCAACCG 2940

Qy   2941 CGGCTTCAAGGTGGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CGGCTTCAAGGTGGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000

Qy   3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCCTCCAGCGTGTGCACACGCTGTGCTCCA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCCTCCAGCGTGTGCACACGCTGTGCTCCA 3060

Qy   3061 CAAGATCCTCCTGCTGCAGGCGTTCACGGCGTTACAGGTTTGCAGTGTCGCTGCTCCCT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CAAGATCCTCCTGCTGCAGGCGTTCACGGCGTTACAGGTTTGCAGTGTCGCTGCTCCCT 3120

Qy   3121 TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTTGCGCGTCATCTCTGACACGGCGCCGCG 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTTGCGCGTCATCTCTGACACGGCGCCCT 3180

Qy   3181 CTGCTACTCCATCCTGAAAACGCAGGATGTCGCTGGCGTGCCAACGCAATTCCTGCTCAAGCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CTGCTACTCCATCCTGAAAACGCAGGATGTCGCTGGCGTGCCAACGCAATTCCTGCTCAAGCT 3240

Qy   3241 CGGCCCTCGCCCTCCGAGGCGTCCGAGGGCGTGCAGTGGCGTGCCAACTCCTGGGGTCACTCGC 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CGGCCCTCGCCCTCCGAGGCGTCCGAGGGCGTGCAGTGGCGTGCCAACTCCTGGGGTCACTCGC 3300

Qy   3301 GACTCGACACCGTGTCACTAGTGCCAACTCTGGGGTCACTCCTGGGGTCACTCGAGCGCA 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GACTCGACACCGTGTCACTAGTGCCAACTCTGGGGTCACTCCTGGGGTCACTCGAGCGCA 3360

Qy   3361 GCTGAGTCGGAAGCTTCCCGGGACGACCCTGAGCCGGCCGCCAACCCGGC 3420
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GCTGAGTCGGAAGCTTCCCGGGACGACCCTGAGCCGGCCGCCAACCCGGC 3420

Qy   3421 ACTGCCCTCAGACTTCAAGACCATCCTGATGCCTGATGCCCCGCCACCCCAGGCCGA 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 ACTGCCCTCAGACTTCAAGACCATCCTGATGCCTGATGCCCCGCCACCCCAGGCCCA 3480

Qy   3481 GAGCAGACCAGCAGCCCTACGGCTCTACGCTCCAGGAGGGCGGCCTC 3540
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GAGCAGACCAGCAGCCCTACGGCTCTACGCTCCAGGAGGGCGGCCTC 3540

Qy   3541 CACACCCAGGGCCCACCCGGGTCGAGTGTTGGCCGGCCCTG 3600
          |||||||||||||||||||||||||||||||||||||||||
Db   3541 CACACCCAGGGCCCACCCGGGTCGAGTGTTGGCCGGCCCTG 3600

Qy   3601 CATGTCCGGCTGAAGGGTCAGTGTCCGGCGTCGAGGCCTGGGCCAAGGGCT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CATGTCCGGCTGAAGGGTCAGTGTCCGGCGTCGAGGCCTGGGCCAAGGGCT 3660

Qy   3661 GAGTGTCCAGCAACCTGCCACTTCACTTCACCCGGCTCGGCTCCACCCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGTGTCCAGCAACCTGCCACTTCACTTCACCCGGCTCGGCTCCACCCCA 3720

Qy   3721 GGGCCCAGCTTTTCCTCCACTCCCCACTCCCCATAGGAATAGTCCATCC 3780
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GGGCCCAGCTTTTCCTCCACTCCCCACTCCCCATAGGAATAGTCCATCC 3780

Qy   3781 CCAGATTCGCACATTGTTCACCCCGCCTTCCTTCCGCCCTCCACCATCC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CCAGATTCGCACATTGTTCACCCCGCCTTCCTTCCGCCCTCCACCATCC 3840

Qy   3841 AGGTGGAGACCCCTGAGAAGGACCCTGGGAATTCGGAGTGACCAAAGGTGTG 3900
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 AGGTGGAGACCCCTGAGAAGGACCCTGGGAATTCGGAGTGACCAAAGGTGTG 3900
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Qy      3901 CCCTGTACACAGGCGAGGACCCTGCCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 CCCTGTACACAGGCGAGGACCCTGCCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960

Qy      3961 GAGGTGCTGTGGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA 4015
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 GAGGTGCTGTGGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA 4015
```

RESULT 2

AAZ20279
ID   AAZ20279 standard; cDNA; 4015 BP.
XX
AC   AAZ20279;
XX
DT   17-JAN-2000 (first entry)
XX
DE   Human telomerase reverse transcriptase (hTRT) cDNA.
XX
KW   Telomerase reverse transcriptase; human; hTRT; cell proliferation;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   56..3454
FT   /*tag= a
XX
PN   WO9950386-A2.
XX
PD   07-OCT-1999.
XX
PF   31-MAR-1999;   99WO-US07097.
XX
PR   31-MAR-1998;   98US-0052864.
PR   03-AUG-1998;   98US-0128354.
XX
PA   (GERO-) GERON CORP.
XX
PI   Morin GB;
XX
DR   WPI; 1999-610842/52.
DR   P-PSDB; AAY32090.
XX
PT   New catalytic polypeptide and polynucleotide, useful for increasing
PT   catalytic activity in a cell -
XX
PS   Disclosure; Fig 2; 24pp; English.
XX
CC   This is the nucleotide sequence of cDNA encoding human telomerase
CC   reverse transcriptase (hTRT, see AAY32090). Human telomerase is a
CC   target for diagnosing and treating diseases relating to cell
CC   proliferation and senescence, such as cancer, or for increasing
CC   the proliferative capacity of a cell. A claimed method for
CC   increasing the proliferative capacity of a vertebrate cell,
CC   especially a human or other mammalian cell, involves introducing
CC   into the cell a recombinant hTRT polynucleotide encoding an hTRT
CC   variant in which residues 192-323, 200-323, 192-271, 200-271,
CC   222-240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are
CC   deleted. A claimed method for reducing telomerase activity in a
CC   cell involves introducing a recombinant polynucleotide encoding
CC   an hTRT variant having a deletion of amino acids 192-450, 560-565,
CC   637-660, 638-660, 748-764 or 1055-1071. The polynucleotides are
CC   obtained by mutagenesis of the hTRT coding sequence.
XX
SQ   Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;

Query Match   100.0%;   Score 4015; DB 20; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy         1 GCAGCGCTGCGTCCTGCGCCACGTGGGAAGCCCCTGGCCCCCGGCCACCCCCGCGATGCC 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GCAGCGCTGCGTCCTGCGCCACGTGGGAAGCCCCTGGCCCCCGGCCACCCCCGCGATGCC 60
```

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Qy        1 GCAGCGCTGCGTCCTGCGCCACGTGGGAAGCCCCTGGCCCCCGGCCACCCCCGCGATGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GCGGCGCTCCCGCGCTGCGCCACCGTGGGCGCTCCCGCTGCCGCCAGCCACTACCGGAGGTGCT 120

Qy       61 GCGGCGCTGCCACGTTCGTGCGGCGGCCTGGGGGGCGCTGGGGGGGCTGGTCAGCGCGG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCCCTGGCCACGTTCGTGCGGCGGCCTGGGGGGCGCTGGGGGGGCTGGTCAGCGCGG 180

Qy      121 GACCCGGCGGCTTTCCGCGCTGCCCAGTGCCGCCGTGTGCGTGCCTGGGACGC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGACCCGGCGGCTTTCCGCGCTGCCCAGTGCCGCCGTGTGCGTGCCTGGGACGC 240

Qy      181 GACCCGGCGGCTTTCCGCGCTGCCCAGTGCCGCCGTGTGCGTGCCTGGGACGC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGACCCGGCGGCTTTCCGCGCTGCCCAGTGCCGCCGTGTGCCCTGGGACGC 240

Qy      241 ACGGCGCCCGCCCCCTCCTTCCGCGCGCCCGAGCCCGCCCGCCCCGCGCCCGCCCCGCGC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACGGCGCCCGCCCCCTCCTTCCGCGCGCCCGAGCCCGCCCGCCCCGCGCCCGCCCCGCGC 300

Qy      301 CCGAGTGCTGCAGAGGCGTGCGAGCCGCGCGGCGGGGAAGACGTGCTGGCCTTGGCTTCGC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGAGTGCTGCAGAGGCGTGCGAGCCGCGCGGCGGGGAAGACGTGCTGGCCTTCGGCTTCGC 360

Qy      361 GCTGCTGACGGGCCCCGGCCCCGGGGGGGGGCCCCCCCCGAGGCCTTCACCACCAGCGTGC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCTGCTGACGGGCCCCGGCCCCGGGGGGGGGCCCCCCCCGAGGCCTTCACCACCAGCGTGC 420

Qy      421 CCTGCCAACACGTGACCGACACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 CCTGCCAACACGTGACCGACACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG 480

Qy      481 CCGCGTGGCGACGAGTGCTGGTTCACCTGCGCACGCGCTGGTCTTTTGTCTGGT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CCGCGTGGCGACGAGTGCTGGTTCACCTGCGCACGCGCTGGTCTTTTGTCTGGT 540

Qy      541 GGCTCCCAGCTGCCTACCAGTGTGCGGGCCCCGTGTGCGGCGGCCAC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GGCTCCCAGCTGCCTACCAGTGTGCGGGCCCCGTGTGCGGCGGCCAC 600

Qy      601 TCAGGCCCGCCCACACGTCAGTGGACCCGAAGGCGTCTGGGATGCGAACGGGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TCAGGCCCGCCCACACGTCAGTGGACCCGAAGGCGTCTGGGATGCGAACGGGC 660

Qy      661 CTGGAACCATAGCGTCAGGGAGCCCGGGGTCCCCTGGGCCCGCAGCCCGGGGTGCGAG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CTGGAACCATAGCGTCAGGGAGCCCGGGGTCCCCTGGGCCCGCAGCCCGGGGTGCGAG 720

Qy      721 GAGGCGCGGGGCAGTGCCAGCGCAGTGCTCCGTTGGCAGGGTCTGGGGCCCACCCGGGCAGGAC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GAGGCGCGGGGCAGTGCCAGCGCAGTGCTCCGTTGCCCGTTGCCCAGGAGGCCCAGGCCGGGCGC 780

Qy      781 TGCCCCTGAGCGGACCGGACGCCCGTTGGGCAGGGGTCCTGGGTGTGGGTGTTTCTGTGGTG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 TGCCCCTGAGCGGACCGGACGCCCGTTGGGCAGGGGTCCTGGGTGTGGGTGTTTCTGTGGTG 840

Qy      841 GCGTGGACCAGTGACCGTGTTTCTGTGGTGTCACCTGCCAGACCCCGAAGAAGC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GCGTGGACCAGTGACCGTGGTTTCGTGTGTGTCACCTGCCAGACCCCGAAGAAGC 900

Qy      901 CACCTCTTTGGAGGGTGCGCTCTCGGACACGCGCCACTCCACCCATCCGTGGGGCGCCCA 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 CACCTCTTTGGAGGGTGCGCTCTCGGACACGCGCCACTCCACCCATCCGTGGGGCGCCCA 960

Qy      961 GCACCACGCGGGCCCCCATCCACATGCGGCCCACCACGTCCCTGGACACGCGCCTTGTCC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 GCACCACGCGGGCCCCCATCCACATGCGGCCCACCACGTCCCTGGACACGCGCCTTGTCC 1020

Qy     1021 CCGGTGTACGCCGAGACCCGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 CCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080

Qy     1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCGACGGCCTCGGAGGGCTCGGTGGA 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCGACGGCCTCGGAGGGCTCGGTGGA 1140
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Qy  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGCCAGGTTGCCCCGCCT  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGCCAGGTTGCCCCGCCT  1200

Qy  1201  GCCCCAGCGCTACTGCAAATGCGGCCCCTGTTTCTGGGAGCTGCTTGGGAACCACGCGCA  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  GCCCCAGCGCTACTGCAAATGCGGCCCCTGTTTCTGGGAGCTGCTTGGGAACCACGCGCA  1260

Qy  1261  GTGCCCCTACGGGGTGCTCCTCAGACGCACTGCCCGGCCTGCGAGCTGCGGTCACCCCAGC  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  GTGCCCCTACGGGGTGCTCCTCAGACGCACTGCCCGGCCTGCGAGCTGCGGTCACCCCAGC  1320

Qy  1321  AGCCGGTGTGTGCCCGGGAGAAGCCCAGGGGCTCGTGTCGTGGCGCCCCGAGGAGGAGGA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  AGCCGGTGTGTGCCCGGGAGAAGCCCAGGGGCTCGTGTCGTGGCGCCCCGAGGAGGAGGA  1380

Qy  1381  CACAGACCCCGTCGCCGTGGTGCAGCTGCTCCGCGACAGCAGCCCTCTGGGGCCTGCAGTGTA  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CACAGACCCCGTCGCCGTGGTGCAGCTGCTCCGCGACAGCAGCCCTCTGGGGCCTGCAGTGTA  1440

Qy  1441  CGGCTTCGTGTCGCGGCCTGCCTGGCGGCCTGGTGCCCCAGGGCTCTCGGGGCTCCAGGCA  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  CGGCTTCGTGTCGCGGCCTGCCTGGCGGCCTGGTGCCCCAGGGCTCTCGGGGCTCCAGGCA  1500

Qy  1501  CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCGGGGAAGCATGCCAA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCGGGGAAGCATGCCAA  1560

Qy  1561  GCTCTCGCTCGAGGAGCTGACGTGCGGCCTGCGCTCTTTCTACCGGAGAGTGCTGCGCAG  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  GCTCTCGCTCGAGGAGCTGACGTGCGGCCTGCGCTCTTTCTACCGGAGAGTGCTGCGCAG  1620

Qy  1621  GAGCCCAGGGGTTGGCTGTGTTCCGCGCCGAGAGCACCGGCTGGCGTGAGATCCTGGC  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  GAGCCCAGGGGTTGGCTGTGTTCCGCGCCGAGAGCACCGGCTGGCGTGAGATCCTGGC  1680

Qy  1681  CAAGTTCCTGCACTGGCTGCGATGAGTGTACGTCGTCGAGCGTCGTTCAGGTCTTCTTTTA  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CAAGTTCCTGCACTGGCTGCGATGAGTGTACGTCGTCGAGCGTCGTTCAGGTCTTCTTTTA  1740

Qy  1741  TGTCACGGAGACCACGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  TGTCACGGAGACCACGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG  1800

Qy  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC  1860

Qy  1861  GGAAGCAGAGGTCAGGCAGCACTACGACGCGGGGGCGCGGCCCCGCGGGGCTCGTGCCGG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  GGAAGCAGAGGTCAGGCAGCACTACGACGCGGGGGCGCGGCCCCGCGGGGCTCGTGCCGG  1920

Qy  1921  CTTCATCCCATCCTGGACGATCCCCAAGCCTCGCGGGCTCGGGGCCACTTGAACATGTGAAC  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CTTCATCCCATCCTGGACGATCCCCAAGCCTCGCGGGCTCGGGGCCACTTGAACATGTGAAC  1980

Qy  1981  CAGAACGTTCCGACGAGAAAAGAGGGCCGAGCGTTCACCTGAGGGTGAAGGCACTGTT  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAGAACGTTCCGACGAGAAAAGAGGGCCGAGCGTTCACCTGAGGGTGAAGGCACTGTT  2040

Qy  2041  CAGCCGTGCTCAACTACGAGCCGGGAGCCACCAGCAGAGGCCTCGTGCTGCTGGG  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CAGCCGTGCTCAACTACGAGCCGGGAGCCACCAGCAGAGGCCTCGTGCTGCTGGG  2100

Qy  2101  CCTGGACGATATCCACAGGGCCACTTCGTGCTGCTTCGTGCTGCTCGGGCGCACCAGGACCC  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTGGACGATATCCACAGGGCCACTTCGTGCTGCTTCGTGCTGCTCGGGCGCACCAGGACCC  2160

Qy  2161  GCGGCCCTGAGCTGTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACCACCATCCCCCA  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCGGCCCTGAGCTGTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACCACCATCCCCCA  2220
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Qy  2221  GGACAGGCTCACGGAGTCATGCCAGCACATCATCAAACCCAGAACACGTACTGCGTCG  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGACAGGCTCACGGAGTCATGCCAGCACATCATCAAACCCAGAACACGTACTGCGTCG  2280

Qy  2281  TCGGTATGCCGGTGGTCCAGAGCACGTCCGCAAGGCACGTTCCAAGAGCCA  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCGGTATGCCGGTGGTCCAGAGCACGTCCGCAAGGCACGTTCCAAGAGCCA  2340

Qy  2341  CGTCTCTACCTTGACAGACCTCCAGCGTCGGCGACAGTTCGTGGCGTCACCTGCAGGA  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGTCTCTACCTTGACAGACCTCCAGCGTCGGCGACAGTTCGTGGCGTCACCTGCAGGA  2400

Qy  2401  GACCAGCCGCGTGAGGGATGCCGTCGTCATCGAGCAGCAGAGCGCTCCTCCCTGAATGAGGCCAG  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GACCAGCCGCGTGAGGGATGCCGTCGTCATCGAGCAGCAGAGCGCTCCTCCCTGAATGAGGCCAG  2460

Qy  2461  CAGTGGGCGTCTTCGACGTCTTCTTCGCTCTCTACGCTTCATGTGCCACACGCCGTGCGCATCAGGGG  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CAGTGGGCGTCTTCGACGTCTTCTTCGCTCTCTACGCTTCATGTGCCACACGCCGTGCGCATCAGGGG  2520

Qy  2521  CAAGTCCTACGTCCAGTGCAGGGGATCCCGCAGGGCCTCCCATCCTCTCCACGCTGCTCTG  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CAAGTCCTACGTCCAGTGCAGGGGATCCCGCAGGGCCTCCCATCCTCTCCACGCTGCTCTG  2580

Qy  2581  CAGCCTGCTCACGGCGACACATGGAGAACAAGTGTTTGCGGGGGATTCGGCGGGACGGGGCT  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CAGCCTGCTCACGGCGACACATGGAGAACAAGTGTTTGCGGGGGATTCGGCGGGACGGGGCT  2640

Qy  2641  GCTCCTGCGTTTGGTGGATGATGATTCTTGTTGGTGACACCTCACCCACGCGGAAAAC  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCTCCTGCGTTTGGTGGATGATGATTCTTGTTGGTGACACCTCACCCACGCGGAAAAC  2700

Qy  2701  CTTCCTCAGGACCCTGGTTCCGAGTGTCCCGAGTATGGCGTGCGGTGAACTTGCGGAA  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CTTCCTCAGGACCCTGGTTCCGAGTGTCCCGAGTATGGCGTGCGGTGAACTTGCGGAA  2760

Qy  2761  GACAGTGTGAACTTCCCTGTAGAAGACGAGCGCCCTGGGTGGCACGCGTTTTGTTCAGAT  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  GACAGTGTGAACTTCCCTGTAGAAGACGAGCGCCCTGGGTGGCACGCGTTTTGTTCAGAT  2820

Qy  2821  GCCGGCCACGGCCTATTCCCTGCGTGTCGCTGCTGGACCCTGGAGT  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  GCCGGCCACGGCCTATTCCCTGCGTGTCGCTGCTGGACCCTGGAGT  2880

Qy  2881  GCAGAGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTTCACCTTCAACCG  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  GCAGAGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTTCACCTTCAACCG  2940

Qy  2941  CGGCTTCAAGGGTGGGAGGAACATGCGTCGCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  CGGCTTCAAGGGTGGGAGGAACATGCGTCGCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG  3000

Qy  3001  TCACAGCCTGTGTTTCTGGATTTGCAGTTGAACACGCCTCGAACGGTGCACCAACATCTA  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  TCACAGCCTGTGTTTCTGGATTTGCAGTTGAACACGCCTCGAACGGTGCACCAACATCTA  3060

Qy  3061  CAAGATCCTCCTGCTCAGGCGTGCGAGCGTTTCACGCAGTGTCGTGCGCAGCTCCATTCA  3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  CAAGATCCTCCTGCTCAGGCGTGCGAGCGTTTCACGCAGTGTCGTGCGCAGCTCCATTCA  3120

Qy  3121  TCAGCAAGTTTGGAAGAACCCCACCATTTTCCTGCGCGTCATCTCGACACGGCCCTCCCT  3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  TCAGCAAGTTTGGAAGAACCCCACCATTTTCCTGCGCGTCATCTCGACACGGCCCTCCCT  3180

Qy  3181  CTGCTACTCCATCCTGAAAACGCAGGGATGTCGCTGGGCTGCACCAACAACATCGGCCGC  3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  CTGCTACTCCATCCTGAAAACGCAGGGATGTCGCTGGGCTGCACCAACAACATCGGCCGC  3240

Qy  3241  CGGCCCTCGCCCCGAGGCCCGTACGACGTGGCTGTGCGCAAGCAATTCCTGCTCAAGCT  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  CGGCCCTCGCCCCGAGGCCCGTACGACGTGGCTGTGCGCAAGCAATTCCTGCTCAAGCT  3300

Qy  3301  GACTCGCACCGTGTCACCTCGGGGTCACTCAGGCAGCAGCCCAGAGCCA  3360
```

PA   (DAHM/) DAHM M W.
XX
PI   Dahm MW;
XX
DR   WPI; 1999-431408/37.
XX
PT   Quantifying tumor cells by amplifying mRNA encoding the catalytic
PT   subunit of telomerase
XX
PS   Example: Fig 1A-B; 26pp; German.
XX
CC   This invention describes a novel method for the quantitation of tumour
CC   cells in a body fluid which comprises (1) enrichment or isolation of
CC   tumour cells in the sample, (2) amplification of mRNA from these cells
CC   that encodes the catalytic subunit of telomerase and (3) quantifying
CC   the amount of amplified mRNA. The method is applied to tumour cells
CC   derived from (micro)metastases, e.g. associated with a wide range of
CC   tumours such as T-cell lymphoblastoma, chronic myeloid or acute
CC   lymphatic leukemia, melanoma, pulmonary carcinoma, cancer of colon or
CC   breast etc. This sequence encodes a human telomerase protein catalytic
CC   domain.
XX
SQ   Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;

Query Match   100.0%; Score 4015; DB 20; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GCAGCGCGTGCGTCGCGACCACGTTGCTGCTGCTGCGGAAGCCCTGGCCCCGGCGATGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCAGCGCGTGCGTCGCGACCACGTTGCTGCTGCTGCGGAAGCCCTGGCCCCGGCGATGCC 60

Qy   61 GCGCGCTCCCGCGTGCGCGAGCCGTGCGCGCTGCGCCCTGGGCGGCCCCAGGGCGAGGTGCT 120
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Db   61 GCGCGCTCCCGCGTGCGCGAGCCGTGCGCGCTGCGCCCTGGGCGGCCCCAGGGCGAGGTGCT 120

Qy   121 GCGGCTGGCCACGTTCGTGCGGCCGCTGGGCCTGGGGCCGGCCTGGTGCGCAGCGCGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCGGCTGGCCACGTTCGTGCGGCCGCTGGGCCTGGGGCCGGCCTGGTGCGCAGCGCGG 180

Qy   181 GGACCCGGCGGCGTTTCCGGCGCGCCCCTCCTCGCCCAGGTGCGCCCTGGGACGCCTGGTGGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACCCGGCGGCGTTTCCGGCGCGCCCCTCCTCGCCCAGGTGCGCCCTGGGACGCCTGGTGGC 240

Qy   241 ACGGCGCGCTGCTGCAGAGGCGGCGCGGCGCCGAAGAACGTGCTGGCCTTCGCGCTTCGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACGGCGCGCTGCTGCAGAGGCGGCGCGGCGCCGAAGAACGTGCTGGCCTTCGCGCTTCGC 300

Qy   301 CCGAGTGCTGCAGAGGCGTGCGAGCGGCGCCCCCCGAGCGGCTTCACCACCAGCGTGCCAGCTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGAGTGCTGCAGAGGCGTGCGAGCGGCGCCCCCCGAGCGGCTTCACCACCAGCGTGCCAGCTA 360

Qy   361 GCTGCTGACGAGGGGCCGGGGGCGCCCCCCGAGGCGGGCTGTGGGGGCTGCTCTTTGTGCTGGT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCTGCTGACGAGGGGCCGGGGGCGCCCCCCGAGGCGGGCTGTGGGGGCTGCTCTTTGTGCTGGT 420

Qy   421 CCTGCCCAACACGTGACCGACGTGCTGCGTACCAGCGTGGGGGCTGCTGCTGCG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTGCCCAACACGTGACCGACGTGCTGCGTACCAGCGTGGGGGCTGCTGCTGCG 480

Qy   481 CCCGTGGCGACGACGTGCTGGTTCACCTGCTGGCACGGCTGCGGCGCTCTTTGTGCTGGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCCGTGGCGACGACGTGCTGGTTCACCTGCTGGCACGGCTGCGGCGCTCTTTGTGCTGGT 540

Qy   541 GGCTCCCAGCTGCGGCCTACCAGTGTGGGGGCCCCGTACCAGCTGGGGCTGCTGCCAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCTCCCAGCTGCGGCCTACCAGTGTGGGGGCCCCGTACCAGCTGGGGCTGCTGCCAC 600

Qy   601 TCAGGCCCGGCCACACGGCTGGGATGCCTCGGGATGCCCGAAGGCGTCGGAACGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCAGGCCCGGCCACACGGCTGGGATGCCTCGGGATGCCCGAAGGCGTCGGAACGGGC 660

Qy   661 CTGAACCATAGCGTCAGGAGGCCGGGGTCCCCTGGCGCTGCCAGCCCGGGTGCGAG 720

Db   3301 GACTCGACACCGTCACTACGTGCCACTCCTGGGGTCACTCAGGGACACCCGGCA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3361 GCTGAGTCGGAAGCTCCGGGACGACGCTGCTGAGGCCCTGACTGCCTGGGGACGACCCGGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GCTGAGTCGGAAGCTCCGGGACGACGCTGCTGAGGCCCTGACTGCCTGCCCAACCCGGC 3420

Qy   3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA 3480

Qy   3481 GAGCAGACACCAGCAGCCCTGTCACGGCCTCTACGTCCCACGGCTCCCAGGAGGGAGGGGCGGCC 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GAGCAGACACCAGCAGCCCTGTCACGGCCTCTACGTCCCACGGCTCCCAGGAGGGAGGGGCGGCC 3540

Qy   3541 CACACCCAGGCCCGCCACCGCTGGGAGTCTGAGCGCTGAGTGAGTGTTTGGCGAGGCCTG 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CACACCCAGGCCCGCCACCGCTGGGAGTCTGAGCGCTGAGTGAGTGTTTGGCGAGGCCTG 3600

Qy   3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCCGAGTGTCCAGCCAAGGGCT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCCGAGTGTCCAGCCAAGGGCT 3660

Qy   3661 GAGTGTCCAGACACACCTGCCCGTCTTCACTTCCCACAGGCTGGCGCTGGCGCTCGGCTCCACCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGTGTCCAGACACACCTGCCCGTCTTCACTTCCCACAGGCTGGCGCTGGCGCTCGGCTCCACCCA 3720

Qy   3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780

Qy   3781 CCAGATTCGCCATTGTTCACCCCTGCCCTCCTTGCCTTCACCCCCACCATCC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CCAGATTCGCCATTGTTCACCCCTGCCCTCCTTGCCTTCACCCCCACCATCC 3840

Qy   3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGTCTGGAGTGACCAAAGGTGTG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGTCTGGAGTGACCAAAGGTGTG 3900

Qy   3901 CCCTGTACACAGGCGAGGACCCCTGCACCTGACTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CCCTGTACACAGGCGAGGACCCCTGCACCTGACTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960

Qy   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA 4015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA 4015

RESULT 3
AAZ00724
ID   AAZ00724 standard; DNA; 4015 BP.
XX
AC   AAZ00724;
XX
DT   06-OCT-1999 (first entry)
XX
DE   Human telomerase catalytic domain DNA.
XX
KW   Telomerase; catalytic domain; human; quantitation; tumour cell; melanoma;
KW   body fluid; metastases; T-cell lymphoblastoma; chronic myeloid leukemia;
KW   acute lymphatic leukemia; melanoma; pulmonary carcinoma; colon cancer;
KW   breast cancer; ss.
XX
OS   Homo sapiens.
XX
PN   DE19804372-A1.
XX
PD   05-AUG-1999.
XX
PF   04-FEB-1998; 98DE-1004372.
XX
PR   04-FEB-1998; 98DE-1004372.
XX

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Db  1741 TGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTTCTACCGGAAGAGTGCTCTGGAG 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1801 CAAGTTGCAAAGCATTGGAATCAGCATCAGACAGCACTTGAAGAGGGTCAGCTGCGGAGCTGTC 1860
Db  1801 CAAGTTGCAAAGCATTGGAATCAGCATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTC 1860

Qy  1861 GGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCCGCCCCTGCTGACGTCCAGACTCCG 1920
Db  1861 GGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCCGCCCCTGCTGACGTCCAGACTCCG 1920

Qy  1921 CTTCATCCCCAAGCCTCCAGACCCGCCGATTGTGAACATGGACTACTACGTCGTGGGAGC 1980
Db  1921 CTTCATCCCCAAGCCTCCAGACCCGCCGATTGTGAACATGGACTACTACGTCGTGGGAGC 1980

Qy  1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCCAGCGTCTCACCTCACCTCGAGGGTGAAGGCACTGTT 2040
Db  1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCCAGCGTCTCACCTCACCTCGAGGGTGAAGGCACTGTT 2040

Qy  2041 CAGCGTGCTCAACTACGAGCGGGCGGCGGCGGCCTGGCACCTTCGTGCGTGCCAGGACCC 2100
Db  2041 CAGCGTGCTCAACTACGAGCGGGCGGCGGCGGCCTGGCACCTTCGTGCGTGCCAGGACCC 2100

Qy  2101 CCTGGACGATATCCACAGGGCCTGATGTGTTGTCAAGGTGCGTGACGGGCGCGTACGACACCATCCCCCA 2160
Db  2101 CCTGGACGATATCCACAGGGCCTGATGTGTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCA 2160

Qy  2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCGTGCG 2220
Db  2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCGTGCG 2220

Qy  2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCAAACCCGACACGTACTGCGTGCG 2280
Db  2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCAAACCCGACACGTACTGCGTGCG 2280

Qy  2281 TCGGTATGCCGTGGTCGTGACAGACCTCGACAGTTCGTGCGTCACCTGCAGGA 2340
Db  2281 TCGGTATGCCGTGGTCGTGACAGACCTCGACAGTTCGTGCGTCACCTGCAGGA 2340

Qy  2341 CGTCTCTACCTTGACAGGGATGCCGTCGTCGTGAGGAGCTCATCATGTGCGCCTGGGGG 2400
Db  2341 CGTCTCTTACCTTGACAGGGATGCCGTCGTCGTGAGGAGCTCATCATGTGCGCCTGGGGG 2400

Qy  2401 GACCAGCCCGCTGAGGATGCCGTCGTCGTCGTGAGGAGCTCCTGCTTCATGTGCGCCTGCAGGGG 2460
Db  2401 GACCAGCCCGCTGAGGATGCCGTCGTCGTCGTGAGGAGCTCCTGCTTCATGTGCGCCTGCAGGGG 2460

Qy  2461 CAGTGGCCTCTTCGACGCTCTTCTTCATGTGGTAGTCTTCTTGTTGGTGTACACCTCACCTCACCACGCGAAAAC 2520
Db  2461 CAGTGGCCTCTTCGACGCTCTTCTTCATGTGGTAGTCTTCTTGTTGGTGTACACCTCACCTCACCACGCGAAAAC 2520

Qy  2521 CAAGTCCTACGTCCAGTGCACGGGATCCCGCAGGGCTCCCAGTGTCCCTGAGTATGCGCTCTG 2580
Db  2521 CAAGTCCTACGTCCAGTGCACGGGATCCCGCAGGGCTCCCAGTGTCCCTGAGTATGCGCTCTG 2580

Qy  2581 CAGCCTGTGTCTACGGCGACATGGCAGACATGGAGAACAAGCTGTTTCGGGGGATTCGGCGGGACGGGGCT 2640
Db  2581 CAGCCTGTGTCTACGGCGACATGGCAGACATGGAGAACAAGCTGTTTCGGGGGATTCGGCGGGGCT 2640

Qy  2641 GCTCTCCTGCGTTTGGTGATGATTTCTTGTTGGTGTACACCTCACCTCACCACGCGAAAAC 2700
Db  2641 GCTCTCCTGCGTTTGGTGATGATTTCTTGTTGGTGTACACCTCACCTCACCACGCGAAAAC 2700

Qy  2701 CTTCCTCAGGACCCTGGTCTCCAGTGTCCTGAGTATGCGCTCTGGCTGTGGTGGGAACTTGCGGAA 2760
Db  2701 CTTCCTCAGGACCCTGGTCTCCAGTGTCCTGAGTATGCGCTCTGGCTGTGGTGGGAACTTGCGGAA 2760

Qy  2761 GACAGTGGTGAACTTCCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820
Db  2761 GACAGTGGTGAACTTCCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820

Qy  2821 GCCGGCCACGCGCCTATTCCCCTTGGTCGCTGCTGGTGCGCTCGTGGATACCCGGACCCTGGAGGT 2880
Db  2821 GCCGGCCACGCGCCTATTCCCCTTGGTCGCTGCTGGTGCGCTCGTGGATACCCGGACCCTGGAGGT 2880
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             |||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGGAACCATAGCGTCGAGGGAGGGGGCCGGGGTCCCCCTGGGCCTGCCCCAGGCGTGGCGC 720
Qy   721 GAGGGCGGGGGCCGGGGTCCCCCTGGGCCTGCCCCAGGCGTGGCGC 780
Db   721 GAGGGCGGGGGCCGGGGTCCCCCTGGGCCTGCCCCAGGCGTGGCGC 780

Qy   781 TGCCCCTGAGCGGAGCGGACGCCCGTTGGGCAGGGTCCTGGGCGCAGGGGCCAGGAC 840
Db   781 TGCCCCTGAGCGGAGCGGACGCCCGTTGGGCAGGGTCCTGGGCGCAGGGGCCAGGAC 840

Qy   841 GCGTGGACCGGAGTGTGTTTCTGTCACCTCCGCGTCCCAGACCCGCCGAAGAAGC 900
Db   841 GCGTGGACCGGAGTGTGTTTCTGTCACCTCGTCCCAGACCCGCCGAAGAAGC 900

Qy   901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCA 960
Db   901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCA 960

Qy   961 GCAACACGCGGGCCCCCATCCACATCGCGGCCACCACGCCCTTGTCTCCTGGACACGCCCTTGTCTCC 1020
Db   961 GCAACACGCGGGCCCCCATCCACATCGCGGCCACCACGCCCTTGTCTCCTGGACACGCCCTTGTCTCC 1020

Qy  1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTGAGGCCCTGACTGGCGCTCGTGGA 1080
Db  1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTGAGGCCCTGACTGGCGCTCGTGGA 1080

Qy  1081 GCCCTCCTTCTACTCAGCTCTCGAGGGCCCTGACTGGCGCTCGTGGA 1140
Db  1081 GCCCTCCTTCTACTCAGCTCTCGAGGGCCCTGACTGGCGCTCGTGGA 1140

Qy  1141 GACCATCTTTCTGGGTTCCAGGCCCTGGAATGCGGAGACTGCCCCGCCT 1200
Db  1141 GACCATCTTTCTGGGTTCCAGGCCCTGGAATGCGGAGACTGCCCCGCCT 1200

Qy  1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260
Db  1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260

Qy  1261 GTGCCCCTAGGGTCTGTGCCCCGGAGAAGCGCACTGCCCCAGGGAGGCTGTCGGTGCCGAGCTGGGCCAGC 1320
Db  1261 GTGCCCCTAGGGTCTGTGCCCCGGAGAAGCGCACTGCCCCAGGGAGGCTGTCGGTGCCGAGCTGGGCCAGC 1320

Qy  1321 AGCCGGTGTCGTGTGCCCCGGAGAAGCGCACTGCCCCAGGGAGGCTCTGTGTGCCCGGAGGA 1380
Db  1321 AGCCGGTGTCGTGTGCCCCGGAGAAGCGCACTGCCCCAGGGAGGCTCTGTGTGCCCGGAGGA 1380

Qy  1381 CACAGAACGGCCGCTTCGCAGCTGCAGCTGCGGGGACTGCGCTCCGGCAGCATGCCAA 1440
Db  1381 CACAGAACGGCCGCTTCGCAGCTGCAGCTGCGGGGACTGCGCTCCGGCAGCATGCCAA 1440

Qy  1441 CGGCTTCGGCTTCGCCTGCGGGCCTGTGTGCCCCAGGGCTCTCAGGCA 1500
Db  1441 CGGCTTCGGCTTCGCCTGCGGGCCTGTGTGCCCCAGGGCTCTCAGGCA 1500

Qy  1501 CAACGAACGGCCGCTTCGCCTGCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
Db  1501 CAACGAACGGCCGCTTCGCCTGCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

Qy  1561 GCTCTCGCTGCAGGAGCTGACGTGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCTTGGC 1620
Db  1561 GCTCTCGCTGCAGGAGCTGACGTGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCTTGGC 1620

Qy  1621 GAGCCCAGGGGTTGGCTGTGTTCCGCCGCAGAGACCACCGGCAGCGTGAGATCCTGGC 1680
Db  1621 GAGCCCAGGGGTTGGCTGTGTTCCGCCGCAGAGACCACCGGCAGCGTGAGATCCTGGC 1680

Qy  1681 CAAGTTCCTGCACTGGCTGATGAGTTGTGTACGTCGTCGAGCTGCTCAGGTCTTTTTTTA 1740
Db  1681 CAAGTTCCTGCACTGGCTGATGAGTTGTGTACGTCGTCGAGCTGCTCAGGTCTTTTTTTA 1740

Qy  1741 TGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTTCTACCGGAAGAGTGCTGGAG 1800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3961 GAGGTGCTGTGGGAGTAAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA 4015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GAGGTGCTGTGGGAGTAAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA 4015


RESULT 4
AAH45901
ID   AAH45901 standard; DNA; 4015 BP.
XX
AC   AAH45901;
XX
DT   06-SEP-2001 (first entry)
XX
DE   Human hTERT gene.
XX
KW   Human; hTERT; telomerase; catalytic subunit; mRNA quantitation;
KW   detection; beta-region; diagnosis; cancer; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            1..274
FT                   /*tag= a
FT                   /number= 1
FT   exon            275..1628
FT                   /*tag= b
FT                   /number= 2
FT   exon            1629..1824
FT                   /*tag= c
FT                   /number= 3
FT   exon            1825..2005
FT                   /*tag= d
FT                   /number= 4
FT   exon            2006..2185
FT                   /*tag= e
FT                   /number= 5
FT   exon            2186..2341
FT                   /*tag= f
FT                   /number= 6
FT   primer_bind     complement (2309..2325)
FT                   /*tag= g
FT                   /note= "primer SYC1076 (AAH45902) binding site"
FT   primer_bind     complement (2311..2325)
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FT                   /note= "primer SYC1118 (AAH45905) binding site"
FT   exon            2342..2437
FT                   /*tag= i
FT                   /number= 7
FT   misc_binding    complement (2345..2374)
FT                   /*tag= j
FT                   /bound_moiety= "hybridisation probe CS3"
FT                   /note= "AAH45908"
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FT                   /bound_moiety= "hybridisation probe CS12"
FT                   /note= "AAH45906"
FT   exon            2438..2523
FT                   /*tag= l
FT                   /number= 8
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FT                   /bound_moiety= "hybridisation probe CS1"
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FT   exon            2524..2637
FT                   /*tag= o
FT                   /number= 9
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FT                   /*tag= p
FT                   /note= "primer SYC1078 (AAH45903) binding site"
FT   exon            2638..2709
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Qy 2881 GCAGAGGCGACTACTCCAGCTATGCCCGACCTTCCATCAGAGCCAGTCTTCACCTTCAACCG 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2881 GCAGAGGCGACTACTCCAGCTATGCCCGACCTTCCATCAGAGCCAGTCTTCACCTTCAACCG 2940

Qy 2941 CGGCTTCAAGGCTGGGAGGAACATGCCGCAAACTCTTTGGGGTCTTGCGCGTGAAGTG 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCCGCAAACTCTTTGGGGTCTTGCGCGTGAAGTG 3000

Qy 3001 TCACAGCCGTGTTTCTGGATTTGCAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3001 TCACAGCCGTGTTTCTGGATTTGCAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060

Qy 3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120

Qy 3121 TCAGCAAGTTTGGAAGAACCCCACCATTTTCCTGCGGCCGTCATCTGACACCGGCCTCCCT 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3121 TCAGCAAGTTTGGAAGAACCCCACCATTTTCCTGCGGCCGTCATCTGACACCGGCCTCCCT 3180

Qy 3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCCAAGGGCGCCGC 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCCAAGGGCGCCGC 3240

Qy 3241 CGGCCCCTGCCCTCCGCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3241 CGGCCCCTGCCCTCCGCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy 3301 GACTCGACACCGTGTCACTCCACTCCTGGGTCACTCAGGACGCCCAGAGCCA 3360
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3301 GACTCGACACCGTGTCACTCCACTCCTGGGTCACTCAGGACGCCCAGAGCCCA 3360

Qy 3361 GCTGAGTCGGAAGCTCCCGGGACGAGCTCCTGCCCTGGAGGCCGCAGCCAACCCGGC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3361 GCTGAGTCGGAAGCTCCCGGGACGAGCTCCTGCCCTGGAGGCCGCAGCCAACCCGGC 3420

Qy 3421 ACTGCCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCATCCTGGAGGCCAGAGGGCCGA 3480
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Db 3421 ACTGCCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCATCCTGGAGGCCAGAGGGCCGA 3480

Qy 3481 GAGCAGACACCAGCACCAGCCCTGTCACGCCGGCTCTACGTCCCAGGGAGGGAGGGGCGGCC 3540
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Db 3481 GAGCAGACACCAGCACCAGCCCTGTCACGCCGGCTCTACGTCCCAGGGAGGGAGGGGCGGCC 3540

Qy 3541 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTG 3600
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Db 3541 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTG 3600

Qy 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCGTCCAGCCAAGGGCT 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCGTCCAGCCAAGGGCT 3660

Qy 3661 GAGTGTCCAGCACCACCTGCCGTCTTCACTTCCCCACAGGCTGCGCCTCGGCCTCCACCCA 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3661 GAGTGTCCAGCACCACCTGCCGTCTTCACTTCCCCACAGGCTGCGCCTCGGCCTCCACCCA 3720

Qy 3721 GGGCCCAGCTTTTCCTCACCAGGAGCCCGCTTCCACTCCCACATAGGAGAATAGTCCATCC 3780
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Db 3721 GGGCCCAGCTTTTCCTCACCAGGAGCCCGCTTCCACTCCCACATAGGAGAATAGTCCATCC 3780

Qy 3781 CCAGATTGCCGCATTGTTCACCCCTGCCTCCTTGCCTTCCACCCACCATCC 3840
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Db 3781 CCAGATTGCCGCATTGTTCACCCCTGCCTCCTTGCCTTCCACCCACCATCC 3840

Qy 3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTTGACCAAAGGTGTG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTTGACCAAAGGTGTG 3900

Qy 3901 CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960
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Db 3901 CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960
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XX
PD   20-JUN-2001.
XX
PF   15-DEC-2000; 2000EP-0127228.
XX
PR   16-DEC-1999; 99US-0465491.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Chang SP, Santini CD;
XX
DR   WPI; 2001-376930/40.
XX
PT   Quantitating expression of mRNA encoding hTERT, the catalytic subunit
PT   of telomerase, as an indicator of cancer, by amplifying RNA using
PT   primers complementary to hTERT gene sequence and quantitating amplified
PT   products -
XX
PS   Claim 1; Page 5-7; 29pp; English.
XX
CC   The present sequence is that of the hTERT gene encoding the catalytic
CC   subunit of the human telomerase, comprising 16 exons, which is useful in
CC   a method for quantitating hTERT mRNA. The method is useful for detecting
CC   the presence of beta-region (a 182 nucleotide region consisting of exons
CC   7 and 8) of the hTERT-mRNA in a human sample for diagnosis and prognosis
CC   of cancer. The method provides an accurate measure of telomerase activity
CC   by selectively measuring mRNA that encodes an active hTERT protein.
XX
SQ   Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;

Query Match          100.0%;  Score 4015;  DB 22;  Length 4015;
Best Local Similarity 100.0%;
Matches 4015;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy        1 GCAGCGCTGCGTCCCCGCTCCCGCTGCCGAGCCGTGCGCACGTGGGAAGCCCGGCCCCGGCCACCCCGGCCGATGCC     60
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Db        1 GCAGCGCTGCGTCCCCGCTCCCGCTGCCGAGCCGTGCGCACGTGGGAAGCCCGGCCCCGGCCACCCCGGCCGATGCC     60

Qy       61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCACGTGGGCCGGCCCCCCAGGGGCGGGCCTGGCCGTGCGCGGG     120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      121 GCCGCTGGCCACGTCGTGCGGGCACCGTCGGGCGGGCCCCAGGGGCGGGCCTGGTCGCAGGGTGCGCGG     180

Qy      181 GGACCCGGCGGCTTTCCGCGCGCTGGGCCCAGTGCCTGGTGTGCGGCTGCCTGCTGTGCCGTGGGACGC     240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGACCCGGCGGCTTTCCGCGCGCTGGGCCCAGTGCCTGGTGTGCGGCTGCCTGCTGTGCCGTGGGACGC     240

Qy      241 ACGGCGCCGCCCCCGCGCGCGCCCCTCCTTCCGCGCCGGGCTGTCCTGCCCCAGTGCGGGCCTGCTGGGC     300
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Db      241 ACGGCGCCGCCCCCGCGCGCGCCCCTCCTTCCGCGCCGGGCTGTCCTGCCCCAGTGCGGGCCTGCTGGGC     300

Qy      301 CCGAGTGCTGCGAGAGGCGTGCGAGCCGGCGGCCGGGGCCCCGGGGCCGCCCTTCGGCCTTCGC     360
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Db      301 CCGAGTGCTGCGAGAGGCGTGCGAGCCGGCGGCCGGGGCCCCGGGGCCGCCCTTCGGCCTTCGC     360

Qy      361 GCTGCTGCGACGGGCGCCCGGGGAGGCGGGCCACTCGGGCCGGCGGGAGGCCGTGGGGCGTCTGCTGTCG     420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCTGCTGCGACGGGCGCCCGGGGAGGCGGGCCACTCGGGCCGGCGGGAGGCCGTGGGGCGTCTGCTGTCG     420

Qy      421 CCTGCCCAACACGGTGACCGACACTGCGGGGGAGCCGGGCCTGGGGGCGTCTCTGCTGTCG     480
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Db      421 CCTGCCCAACACGGTGACCGACACTGCGGGGGAGCCGGGCCTGGGGGCGTCTCTGCTGTCG     480

Qy      481 CCGGTGGGCGACGACTGCTGTTCACCTGCGTGTTCACCTGCTCTTTGTCGTGT     540
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Qy      541 GGCTCCCAGTCGCGCTACCAGTGTGCGGGCCGCGCCTACCAGTCGGGCGGCTGCCAC     600
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Db      541 GGCTCCCAGTCGCGCTACCAGTGTGCGGGCCGCGCCTACCAGTCGGGCGGCTGCCAC     600

Qy      601 TCAGGCCCGCCCCACACGGCGTCTGGCAGGGTCTGGGCAGGGG     660
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TCAGGCCCGCCCCACACGGCGTCTGGCAGGGTCTGGGCAGGGG     660

Qy      661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGCCTTGGGCCTGGCCTGCCCGGGGTGCGAG     720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGCCTTGGGCCTGGCCTGCCCGGGGTGCGAG     720

Qy      721 GAGGCGGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCGTGGCGC     780
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Db      721 GAGGCGGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCGTGGCGC     780

Qy      781 TGCCCCTGAGCCGGACGGCGGCCGTGTGGCAGGGGTCTGGGCAGGGGCCCACCCGGGCAGGAC     840
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Db      781 TGCCCCTGAGCCGGACGGCGGCCGTGTGGCAGGGGTCTGGGCAGGGGCCCACCCGGGCAGGAC     840

Qy      841 GGGTGGACCGAGTGACCGTGGTTTCTGGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC     900
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Db      841 GCGTGGACCGAGTGACCGTGGTTTCTGGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC     900

Qy      901 CACCTCTTTGGAGGGTGCGCTCTCGCACGGGCCACTCCCACCGTGGGCCGCCA     960
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Db      901 CACCTCTTTGGAGGGTGCGCTCTCGCACGGGCCACTCCCACCGTGGGCCGCCA     960

Qy      961 GCACCACGCGGGCCCCCATCCACATCCGGGACTCCCTGGGACACGCCTTGTCC     1020
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Db      961 GCACCACGCGGGCCCCCATCCACATCCGGGACTCCCTGGGACACGCCTTGTCC     1020

Qy     1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGCAAGGAGCAGCTGCG     1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGG     1080

Qy     1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCGACTGGCCTCGGAGGCTCGTTGCCCGGCCT     1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCGACTGGCCTCGGAGGCTCGTTGCCCGGCCT     1140

Qy     1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCCTGCTGCGCAGCCACTACCGCCGGAGGTGCT     1200
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Db     1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCCTGCTGCGCAGCCACTACCGCCGGAGGTGCT     1200

Qy     1201 GCCCCAGCGCTACTGGCAAATGCGCGCCCCGTGTTCTGGAACTGCCTGGTGCTGTCAGCCGCA     1260
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Db     1201 GCCCCAGCGCTACTGGCAAATGCGCGCCCCGTGTTTCTGGAACTGCCTGGTGCTGTCAGCCGCA     1260

Qy     1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGTGCGCTCACCCCAGC     1320
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Db     1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGTGCGCTCACCCCAGC     1320

Qy     1321 AGCCGGTGTCTGTGCCCGGCGGAGCCCCTCCTTCCGCGCCCCGCCCCCAGGAGCAGAGGAGGA     1380
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Db   1321 AGCCGGTGTCTGTGCCCGGAGAGCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAGGA 1380

Qy   1381 CACAGACCCCGTGCGTCGGCTTGGTGCAGCTGCTCCGCCAGCACAGCACGCCCTGGCCAGGTGTA 1440
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Db   1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

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Db   1561 GCTCTCGCTGCACGAGCGTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCCAG 1620

Qy   1621 GAGCCCAGGGGTTGGCTTGTGTTCCGCGAGCACCGTCTGCGTGAGGAGGAGATCCTGCC 1680
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Db   1621 GAGCCCAGGGGTTGGCTGTGTTCCGCGAGCACCGTCTGCGTGAGGAGGAGATCCTGCC 1680

Qy   1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCAGTCTGCTCAGTCTTTTCTTTTA 1740
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Db   1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCAGTCTGCTCAGTCTTTTCTTTTA 1740

Qy   1741 TGTCACGGAGACCACAGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800
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Db   1741 TGTCACGGAGACCACAGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800

Qy   1801 CAAGTTGCAAAGCATTGGAATCAGAACATCAGACACTTGAAGAGGGTCAGCTGCGGGAGCTGTC 1860
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Db   1801 CAAGTTGCAAAGCATTGGAATCAGAACATCAGACACTTGAAGAGGGTCAGCTGCGGGAGCTGTC 1860

Qy   1861 GGAAGCAGGAGTCAGGCAGCATCGGGAAGCCCAGGCCCCGCCCTGCTGACGTCCAGACTCCG 1920
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Db   1861 GGAAGCAGGAGTCAGGCAGCATCGGGAAGCCCAGGCCCCGCCCTGCTGACGTCCAGACTCCG 1920

Qy   1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGTGGGAGC 1980
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Db   1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGTGGGAGC 1980

Qy   1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTGAGGGTGAAGGCACTGTT 2040
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Db   1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTGAGGGTGAAGGCACTGTT 2040

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Db   2101 CCTGGACGATATCCACAGGGCTGTACTTGTCAAGGTGGATGGTGACGGACGGCGTACGCGCG 2160

Qy   2161 GCGCCGTCACGGAGCTCATCGGCAGCATCATCAAACCCCAGAAACCCCAGAACACCATCCCCA 2220
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Db   2161 GCGCCGTCACGGAGCTCATCGGCAGCATCATCAAACCCCAGAACACCATCCCCA 2220

Qy   2221 GGACAGGCTCACGGAGTCCCGGGAGGCCCGCCCATGGGCACGTCCCGCAAGGCCTTCAAGAGCA 2280
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Db   2221 GGACAGGCTCACGGAGTCATGGGCACGTCCCGCAAGGCCTTCAAGAGCCA 2280

Qy   2281 TCGGTATGCCGTGGTCCAGAAGGCCACGTCCGGACGCTCCCGGACGCTGCCTTCAAGAGCCA 2340
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Db   2281 TCGGTATGCCGTGGTCCAGAAGGCCACGTCCGGACGCTCCCGGACGCTGCCTTCAAGAGCCA 2340

Qy   2341 CGTCTCTACCTTGACAGACTTCGTGGCTCACCTGCTCACCTGCTCTGGAGGA 2400
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Db   2341 CGTCTCTACCTTGACAGACTTCGTGGCTCACCTGCTCACCTGCTCTGCGAGGA 2400

Qy   2401 GACCAGCACCAGCCCGCTGCGTCCTCGCTCCCGGGCTCTCAGCCAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460
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Db   2401 GACCAGCACCAGCCCGCTGCGTCCTCGCTCCCGGGCTCTCAGCCAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460
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Qy   2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCATCCACCACGCCGTGCCGCCGTTCCACGCTGCTCTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCATCCACCACGCCGTGCCGCCGTTCCACGCTGCTCTG 2520

Qy   2521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCCAGGGGCTCCATCCTCCTCCACGCTGCTCTG 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCCAGGGGCTCCATCCTCCTCCACGCTGCTCTG 2580

Qy   2581 CAGCCTGTGCTCACGGCGACATGAGAACAAGCTGTTTGCGGGGATTCGGCGGGGACCGGGCT 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 CAGCCTGTGCTCACGGCGACATGAGAACAAGCTGTTTGCGGGGATTCGGCGGGGACCGGGCT 2640

Qy   2641 GCTCCTGCGTTGGTGGATGATTCTGTGTTGGTGACACCTCACCTCACCTCACCCACGCGAAAAC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCTCCTGCGTTGGTGGATGATTCTGTGTTGGTGACACCTCACCTCACCCACGCGAAAAC 2700

Qy   2701 CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCGTGCGTGGTGACTTGCGGAA 2760
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Db   2701 CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCGTGCGTGGTGACTTGCGGAA 2760

Qy   2761 GACAGTGGTGAACTTCCCTGAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820
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Db   2761 GACAGTGGTGAACTTCCCTGAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820

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Db   2821 GCCGGCCCACGGCCTATTCCCCTGGTGCGCGGCCTGCTGCTCGGATACCCTGGAGGT 2880

Qy   2881 GCAGAGCGACTACTCCAGTCTCCATCAGAGCCAGTCGTCGCGACTTCAACCG 2940
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Db   2881 GCAGAGCGACTACTCCAGTCTCCATCAGAGCCAGTCGTCGCGACTTCAACCG 2940

Qy   2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000
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Db   2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000

Qy   3001 TCACAGCGTGTTTCTGGATTGCAGTGAACATGGACTACGTCGTGACCAACCATCTA 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TCACAGCGTGTTTCTGGATTGCAGTGAACATGGACTACGTCGTGACCAACCATCTA 3060

Qy   3061 CAAGATCCTCCGCTGCAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCATTTCA 3120
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Db   3061 CAAGATCCTCCGCTGCAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCATTTCA 3120

Qy   3121 TCAGCAAGTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180
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Db   3121 TCAGCAAGTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180

Qy   3181 CTGCTACTCCATCCTGAAAGCCAGAGGGATGTCGCTGTGCCACCAGGAGGCGGCCGC 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CTGCTACTCCATCCTGAAAGCCAGAGGGATGTCGCTGTGCCACCAGGAGGCGGCCGC 3240

Qy   3241 CGGGCCCTGCGACACCGTGCACTCCTGGGGTGCTGCTGCCACCAGATTCTGCTCAAGCT 3300
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Db   3241 CGGGCCCTGCGACACCGTGCACTCCTGGGGTGCTGCTGCCACCAGATTCTGCTCAAGCT 3300

Qy   3301 GACTCGGAAGCTCCCGGTCACCTGGGGTCACTCTGGAGGCCGCAGCCCAGACGCCA 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GACTCGGAAGCTCCCGGTCACCTGGGGTCACTCTGGAGGCCGCAGCCCAGACGCA 3360

Qy   3361 GCTGAGTCGGAAGCTCCCGGGGACGCTGCCCTGGAGGCTGACTGCTCCAACCCGGC 3420
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Db   3361 GCTGAGTCGGAAGCTCCCGGGGACGCTGCCCTGGAGGCTGACTGCTCCAACCCGGC 3420

Qy   3421 ACTGCCCTCAGACTTCAAGACCATCCTGCTGATGGCGACCATCCTGACTGACTTCGTGGCTCACCAGGA 3480
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Db   3421 ACTGCCCTCAGACTTCAAGACCATCCTGCTGATGGCGACCATCCTGACTGACTTCGTGGCTCACCAGGA 3480

Qy   3481 GAGCAGACCAGCAGCCTCACGCGGCCTCTACGTCCAGGGGCGGCGGC 3540
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GAGCAGACCAGCAGCCTCACGCGGCCTCTACGTCCACGGGGGCGGC 3540
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XX
CC    The invention relates to animal tissues with carbohydrate antigens that
CC    are compatible for transplantation into human patients. The mammalian
CC    cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
CC    transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
CC    fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
CC    with carbohydrate antigens that are compatible for transplantation into
CC    human patients. The present sequence is human telomerase reverse
CC    transcriptase (TERT) cDNA used in the invention.
XX
SQ    Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;

Query Match             100.0%;   Score 4015;  DB 24;  Length 4015;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 4015;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1 GCAGCGCTCGCTGCTGCGCACGTGGGAAGCCCTGCCCCGGCCACCCCCGCCCACCCCGCCGATGCC 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCAGCGCTCGCTGCTGCGCACGTGGGAAGCCCTGCCCCGGCCACCCCCGCCCACCCCGCCGATGCC 60

Qy      61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120

Qy     121 GCGCGCTGGCCACGTTCGTGCGCGCCGCCTGGGCGCGCCCAGGGCTGCGCGGTCGTCAGCGACGCCGCGG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCGCGCTGGCCACGTTCGTGCGCGCCGCCTGGGCGCGCCCAGGGCTGCGCGGTCGTCAGCGACGCCGCGG 180

Qy     181 GGACCCGGCGGCTTCCGGCGCGCCCGCCCCCGTGGTGCGCCCAGTGCGCTGGTGTGCGTGTGCGTGCTGGGACGC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GGACCCGGCGGCTTCCGGCGCGCCCGCCCCCGTGGTGCGCCCAGTGCGCTGGTGTGCGTGTGCGTGCTGGGACGC 240

Qy     241 ACGGCCGCGCCCCCCCTTCCTCCGCCTCCTCCGCCGCGCCGGTGCTGCTGGACACGCTGCTTGTCTTGGTGGT 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ACGGCCGCGCCCCCCCTTCCTCCGCCTCCTCCGCCGCGCCGGTGCTGCTGGACACGCTGCTTGTCTTGGTGGT 300

Qy     301 CCGAGTGCTGCGAGAGGCTGTGGGAGCCGCGCCGAAGAACGTGCTGCGCTTCGGCTTCGC 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCGAGTGCTGCGAGAGGCTGTGGGAGCCGCGCCGAAGAACGTGCTGCGCTTCGGCTTCGC 360

Qy     361 GCTGCTGGACGCGGGCCCGGCGCCCCCCGGGGCCTTCACCACCAGCGTGCGCAGCTA 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTGCTGGACGCGGGCCCGGCGCCCCCCGGGGCCTTCACCACCAGCGTGCGCAGCTA 420

Qy     421 CCTGCCCAACACGGTGACCGACGCCACTCGGGGGGAGCGGGGTGTGGGGCTGCTGTCGCGG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCTGCCCAACACGGTGACCGACGCCACTCGGGGGGAGCGGGGTGTGGGGCTGCTGTCGCGG 480

Qy     481 CCGGTGGGGCGACGACTGCTGTTCACCGTGCCCGGCACGCCTGGCACGCCTCTTGTGCTTGGT 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CCGGTGGGGCGACGACTGCTGTTCACCGTGCCCGGCACGCCTGGCACGCCTCTTTGTGCTTGGT 540

Qy     541 GGCTCCCAGTCGTGCGGGGCCGGCGCCCTGCCCCGCCCGCTGTACCAGTCTCGGCCTGCCAC 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GGCTCCCAGTCGTGCGGGGCCGGCGCCCTGCCCCGCCCGCTGTACCAGTCTCGGCCTGCCAC 600

Qy     601 TCAGGGCCCGCACCCCGCCAGTGCAGTCTCGGGATGCGAACGGGC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TCAGGGCCCGCACCCCGCCAGTGCAGTCTCGGGATGCGAACGGGC 660

Qy     661 CTGGAACCATAGCGTCAGGGAGCTGCGTCCCCTGGGCCTGCCCCTGGGCCTGCCCAGGGGTGCCAG 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTGGAACCATAGCGTCAGGGAGCTGCGTCCCCTGGGCCTGCCCCTGGGCCTGCCCAGGGGTGCCAG 720

Qy     721 GAGGGGCGGGGCAGTCCAGCCGAAGTCGCCGTTGCCGAAGGCCTGGCGTGCGC 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GAGGGGCGGGGCAGTCCAGCCGAAGTCGCCGTTGCCGAAGGCCTGGCGTGCGC 780

Qy     781 TGCCCCTGAGCCGAGGCGGACGCCCGTTGGGCAGGGGTCCTGGGGGTCACCCGGGCAGCAGAC 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TGCCCCTGAGCCGAGGCGGACGCCCGTTGGGCAGGGGTCCTGGGGGTCACCCGGGCAGCAGAC 840

Qy     841 GCCTGGACCGAGTGACCGTGGTTTCTGTGTGCTCACTGCACGACCCGCCGCCAAGAAGC 900
```

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Qy    3541 CACACCCAGGCCCGCCACCCCTGGGAGTCTGAGTGAGTGTTTGGCCGAGGCCTG 3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541 CACACCCAGGCCCGCCACCCCTGGGAGTCTGAGTGAGTGTTTGGCCGAGGCCTG 3600

Qy    3601 CATGTCCGGCTGAAGGCTGAGGGTCCGGCTGAGCCGTGCGAGCCGAGTGTCCAGCCAAGGGGCT 3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 CATGTCCGGCTGAAGGCTGAGGGTCCGGCTGAGCCGTGCGAGCCGAGTGTCCAGCCAAGGGCT 3660

Qy    3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCCGCTCGGCTCCACCCCA 3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCCGCTCGGCTCCACCCCA 3720

Qy    3721 GGGCCAGCTTTTCCTCACCAGGACCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 GGGCCAGCTTTTCCTCACCAGGACCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780

Qy    3781 CCAGATTCGCCATTGTTCACCCCTGCCCTCCTTGTCGCCCTCCTTTGCCTTCCACCCCCTTCCTTGCCTTCCACCCCACCATCC 3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 CCAGATTCGCCATTGTTCACCCCTGCCCTCCTTGTCGCCCTCCTTTGCCTTCCACCCCCTTCCTTGCCTTCCACCCCACCATCC 3840

Qy    3841 AGGTGGAGACCCTGAGAAGGACTCTGGGAATTGGAGTGACGTGTG 3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 AGGTGGAGACCCTGAGAAGGACTCTGGGAATTGGAGTGACGTGTG 3900

Qy    3901 CCCTGTACACAGGGCGAGGACCCTGCACCTGGATGGGGTCCCTGGGTCAAATTGGGGG 3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 CCCTGTACACAGGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960

Qy    3961 GAGGTGCTGTGGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 GAGGTGCTGTGGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015
```

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RESULT 5
AAD46821
ID   AAD46821 standard; cDNA; 4015 BP.
XX
AC   AAD46821;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Human telomerase reverse transcriptase (TERT) cDNA.
XX
KW   Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
KW   transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
KW   telomerase reverse transcriptase; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key               Location/Qualifiers
FT   CDS               56..3454
FT                     /tag= a
FT                     /product= "Human telomerase reverse transcriptase"
XX
PN   WO200274948-A2.
XX
PD   26-SEP-2002.
XX
PF   21-MAR-2002; 2002WO-CA00378.
XX
PR   21-MAR-2001; 2001US-277811P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Denning C,  Clark AJ,  Schiff JM;
XX
DR   WPI; 2002-759895/82.
DR   P-PSDB; AAE29226.
XX
PT   Mammalian cells, useful for producing animal tissues with carbohydrate
PT   antigens that are compatible for transplantation into human patients -
XX
PS   Disclosure; Page 33-34; 71pp; English.
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Db  1921 CTTCATCCCAAGCCTGACGGCTGCGGCGCGATTGTGAACATGACTACGTCGTGGGAGC 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCTGTCACCTCGAAGGGTGAAGGCACTGTT 2040
         |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  1981 CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCTGTCACCTCGAAGGGTGAAGGCACTGTT 2040

Qy  2041 CAGCGTGCTCAACTACGAGCGGGCGGCGGCGCCCGGCCTCCTGTGCGTCTGTGCTGGG 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 CAGCGTGCTCAACTACGAGCGGGCGGCGGCGCCCGGCCTCCTGTGCGTCTGTGCTGGG 2100

Qy  2101 CCTGGACGATATCCACAGGGCCTGGCGTGCGTGCCGGCACCT TCGTCGTCCTGGGCGTGTGCGGCCCCAGGACCC 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCTGGACGATATCCACAGGGCCTGGCGTGCGTGCCGGCACCTTCGTCGTCCTGGGCGTGTGCGGCCCCAGGACCC 2160

Qy  2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGCGTACGACACCATCCCCA 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGCGTACGACACCATCCCCA 2220

Qy  2221 GGACAGGGTCACGGAGGTCATCGAGCATCAAACCCCAGAACACAGTACTGCGTGCG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GGACAGGGTCACGGAGGTCATCGAGCATCAAACCCCAGAACACAGTACTGCGTGCG 2280

Qy  2281 TCGGTATGCCGTGGTCCAGAAGGCCACGTCCGCAAGGCCTTCAAGAGCCA 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TCGGTATGCCGTGGTCCAGAAGGCCACGTCCGCAAGGCCTTCAAGAGCCA 2340

Qy  2341 CGTCTCTACCTTGACAGACCTCCAGCCGTCGTCATCGACAGTTCGTGGCTCACCTGCAGGA 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CGTCTCTACCTTGACAGACCTCCAGCCGTCGTCATCGACAGTTCGTGGCTCACCTGCAGGA 2400

Qy  2401 GACCAGCCCGCTGAGGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GACCAGCCCGCTGAGGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460

Qy  2461 CAGTGCCGCTCTTCCTCGACGTCTTCGACGTCTTCATGTGCCACCAGGCTCCATCCGCTGCTCTG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGTGCCGCTCTTCCTCGACGTCTTCGACGTCTTCATGTGCCACCAGGCTCCATCCGCTGCTCTG 2520

Qy  2521 CAAGTCCTACGTCCAGTCCAGTCCCGAGTGTCCCGAGTATGCGGGGATTCGGCGGGGACGGGCT 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CAAGTCCTACGTCCAGTCCAGTCCCGAGTGTCCCGAGTATGCGGGGATTCGGCGGGGACGGGCT 2580

Qy  2581 CAGCCTGTGCTACGGCGCACATGGAGAACAAGCTGTTTGCGGGACACCTCACCTCACCCACGCGAAAAC 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CAGCCTGTGCTACGGCGCACATGGAGAACAAGCTGTTTGCGGGACACCTCACCTCACCCACGCGAAAAC 2640

Qy  2641 GCTCCTGCGTTGGTGGATGATTTCTTGGTGCAGCACCTTCACCTCACCCACCGCAGCAGTTCGGAA 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 GCTCCTGCGTTGGTGGATGATTTCTTGGTGCAGCACCTTCACCTCACCCACCGCAGCAGTTCGGAA 2700

Qy  2701 CTTCCTCAGGACCCTGGTCTCCGAGTGTCCCGAGTGTCGCGTGGGTGAACTTGCGGAA 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CTTCCTCAGGACCCTGGTCTCCGAGTGTCCCGAGTGTCGCGTGGGTGAACTTGCGGAA 2760

Qy  2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGCGGGTGGCACGGCTTTGTTCAGAT 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGCGGGTGGCACGGCTTTGTTCAGAT 2820

Qy  2821 GCCGGGCCCACGGCCTATTCCCGTCGGCCTGCTCGCTGCGGATACCGGACCCTGGAGGT 2880
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  2821 GCCGGGCCCACGGCCTATTCCCGTCGGCCTGCTCGCTGCGGATACCGGACCCTGGAGGT 2880

Qy  2881 GCAGAGCGACTACTCCAGCTATGCCGGCGACCTCCAGTCTCATCAGAGCGTCTTCAACCG 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 GCAGAGCGACTACTCCAGCTATGCCGGCGACCTCCAGTCTCATCAGAGCGTCTTCAACCG 2940

Qy  2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGCGTCTTGGGCGTGAAGTG 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGCGTCTTGGGCGTGAAGTG 3000

Qy  3001 TCACAGCCGTGTTTCTGGATTTGCAGGTGAACGGTGTGCACCAACATCTA 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 TCACAGCCGTGTTTCTGGATTTGCAGGTGAACGGTGTGCACCAACATCTA 3060
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Db   841 GGGTGGACCGAGTGACCGTGGTTCTGTGTGGTCACCTGGCACCGCCGGAAGAGC 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   901 CACCTCTTTGGAGGGTGCGCTCTCGCGCCACTCCACCACCATCCGTGGGCCGCCA 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   901 CACCTCTTCCTACTCCAGCTCTCTGAGGCCCACTCCACCATCCGTGGCCGCCCA 960

Qy   961 GCACCACGCGGGGCCCCCATCCACATCGCGGCCCACGTCGGCGGCCACGCGTTGTCC 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GCACCACGCGGGGCCCCCATCCACATCGCGGCCCACGTCGGCGGCCACGCGTTGTCC 1020

Qy  1021 CCCGGTGTACGGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGACAGCTGCG 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 CCCGGTGTACGGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGACAGCTGCG 1080

Qy  1081 GCCCTCCTTCCTACTCAGCTCTGAGGCCCAGCTGACTGGCGCGCTCGGAGGCTCGTGGA 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 GCCCTCCTTCCTACTCAGCTCTGAGGCCCAGCTGACTGGCGCGCTCGGAGGCTCGTGGA 1140

Qy  1141 GACCATCTTCTGGTTCCAGGCCTGGATGCAGGAGGACTCCCGGCAGGTTGCCCCGCCT 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GACCATCTTCTGGTTCCAGGCCTGGATGCAGGAGGACTCCCGGCAGGTTGCCCCGCCT 1200

Qy  1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCGTGCTTGGGAACCACGCGGCA 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCGTGCTTGGGAACCACGCGGCA 1260

Qy  1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGCGTCACCCCAGC 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGCGTCACCCCAGC 1320

Qy  1321 AGCCGGTGTCTGTGCCCGGAGAAGCACCAGCCCCAGGGCTCTGTGGGCGGCCCCGAGGAGGA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 AGCCGGTGTCTGTGCCCGGAGAAGCACCAGCCCCAGGGCTCTGTGGGCGGCCCCGAGGAGGA 1380

Qy  1381 CACAGACCCCCGTGCCTGAGCTGCGCGCCGCTGTGCCCCAGCACAGCAGCAGCCCTGGCAGGTGTA 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CACAGACCCCCGTGCCTGAGCTGCGCGCCGCTGTGCCCCAGCACAGCAGCAGCCCTGGCAGGTGTA 1440

Qy  1441 CGGCTTCGTGCGCCTGCTCCGCGCCGCTGTGGGCGCCTCTGGGGCTCTGGGGCTCCAGGCA 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CGGCTTCGTGCGCCTGCTCCGCGCCGCTGTGGGCGCCTCTGGGGCTCTGGGGCTCCAGGCA 1500

Qy  1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

Qy  1561 GCTCTCGCGCGCAGGAGCTGACGTGGAAGATGAGCGTGCGGCGTTGGGACTGCGCTTGGCCGCAG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 GCTCTCGCGCGCAGGAGCTGACGTGGAAGATGAGCGTGCGGCGTTGGGACTGCGCTTGGCCGCAG 1620

Qy  1621 GAGCCCAGGGGTTGGCGTGTGTTCCGGCGCCGCAGAGCCACCGTTGCGGTGAGGGATCCTGGC 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 GAGCCCAGGGGTTGGCGTGTGTTCCGGCGCCGCAGAGCCACCGTTGCGGTGAGGGATCCTGGC 1680

Qy  1681 CAAGTTCCTGCACTGGCTGATGAGTGTACGCGTCGTGCTGCTCAGGTCTCTTTGTTCTTTTA 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CAAGTTCCTGCACTGGCTGATGAGTGTACGCGTCGTGCTGCTCAGGTCTCTTTGTTCTTTTA 1740

Qy  1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1800

Qy  1801 CAAGTTGCAAAGCACATTGGAATCAGAACAGACAGGGGTGCAGCTGTGCGGGGAGTGTC 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 CAAGTTGCAAAGCACATTGGAATCAGAACAGACAGGGGTGCAGCTGTGCGGGGAGTGTC 1860

Qy  1861 GGAAGCAGAGAGGTCAGGCAGCATCGGGGAAGCCCAGGCCCGCCGCCGCTGCTCGACTCCG 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GGAAGCAGAGAGGTCAGGCAGCATCGGGGAAGCCCAGGCCCGCCGCCGCTGCTCGACTCCG 1920

Qy  1921 CTTCATCCCAAGCCTGACGGCTGCGGCGCGATTGTGAACATGACTACGTCGTGGGAGC 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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XX
DE   Cancer cell discrimination method related human DNA.
XX
KW   Human; telomerase; enzyme; cancer cell discrimination; gene;
KW   reverse transcriptase; ds.
XX
OS   Homo sapiens.
XX
PN   JP2001309791-A.
XX
PD   06-NOV-2001.
XX
PF   02-MAY-2000; 2000JP-0138250.
XX
PR   02-MAY-2000; 2000JP-0138250.
XX
PA   (KANE/) KANEUCHI H.
PA   (KAMI/) KAMIMORI M.
XX
DR   WPI; 2002-134853/18.
XX
PT   Discrimination of a cancer cell in a sample tissue, comprises
PT   determining the expression level of a reverse transcriptase component
PT   of telomerase using a hybridization assay -
XX
PS   Claim 2; Page 9-10; 16pp; Japanese.
XX
CC   The present invention relates to a method for the discrimination of a
CC   cancer cell in a sample tissue, which involves determining the expression
CC   level of a reverse transcriptase component of telomerase in a cell
CC   constituting the sample tissue by an in situ hybridization of the mRNA of
CC   the enzyme, and judging a cell showing a higher expression level than
CC   that of the reverse transcriptase component of telomerase in a normal
CC   cell to be a cancer cell. The present sequence is a human DNA used in the
CC   exemplification of the invention.
XX
SQ   Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;
```

Query Match   100.0%; Score 4015; DB 24; Length 4015;
Best Local Similarity   100.0%;
Matches 4015; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 GCAGCGCTGCGGTCCTGCTGCCACGTGGGAAGCCCTGCCCCCGGCCACCCCCGCGATGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCAGCGCTGCGGTCCTGCTGCCACGTGGGAAGCCCTGCCCCCGGCCACCCCCGCGATGCC 60

Qy         61 GCGCGCTCCCCGGCTGCGAGCCGTCCCTGCTCGCGCTCCCTGCGCGTCCCTGCGAGGTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGCGCTCCCCGGCTGCGAGCCGTCCCTGCTCGCGCTCCCTGCGCGTCCCTGCGAGGTGCT 120

Qy        121 GCCGCTGCCACGTTCGTGCGTGGCGGCCCTCGGCGCCCAGGCTGCGGCTGGTCAGCGCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCGCTGCCACGTTCGTGCGTGGCGGCCCTCGGCGCCCAGGCTGCGGCTGGTCAGCGCGG 180

Qy        181 GGACCCGGCGGCTTTCCGGCCGCTGGCGCTCCAGTGACGTGGCCCTGGGACGCGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGACCCGGCGGCTTTCCGGCCGCTGGCGCTCCAGTGACGTGGCCCTGGGACGCGC 240

Qy        241 ACGGCGCCCCGGCCGCCCCCCTCCTTCCGCGCGCCAGGCGCGCCGAAGACGTGCTGGTGGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGGCGCCCCGGCCGCCCCCCTCCTTCCGCGCGCCAGGCGCGCCGAAGACGTGCTGGTGGC 300

Qy        301 CCGAGTGCTGCAGAGGCGTGTGCCAGCGCGGCCGAAGAACGTGCTGGCCTTCGGCTTCGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGAGTGCTGCAGAGGCGTGTGCCAGCGCGGCCGAAGAACGTGCTGGCCTTCGGCTTCGC 360

Qy        361 GCTGCTGACGGGGCCCGGGGGGGCGGGGGAGCCGGGGGCTGCTGCTCGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCTGCTGACGGGGCCCGGGGGGGCGGGGGAGCCGGGGGCTGCTGCTCGG 420

Qy        421 CCTGCCCAACACGGTGACCGACACCTGCGGGGCGGGGCGGGGGGCTGCTGCTGCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCCCAACACGGTGACCGACACCTGCGGGGCGGGGCGGGGGGCTGCTGCTGCG 480
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Qy       3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACCGCATGTGTGCGCAGCTCCCATTTCA 3120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACCGCATGTGTGCGCAGCTCCCATTTCA 3120

Qy       3121 TCAGCAAGTTGGAAGAACCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 TCAGCAAGTTGGAAGAACCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180

Qy       3181 CTGCTACTCCATCTCTGAAAGCCAGGATGTCGCTGGGCCTGGGGGCCAAGGGGCCCGC 3240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTGCTACTCCATCTCTGAAAGCCAGGATGTCGCTGGGCCTGGGGGCCAAGGGGCCCGC 3240

Qy       3241 CGGCCCTCGCTGCCCTCCGAGGCCGTGCAGTGCGTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CGGCCCTCGCTGCCCTCCGAGGCCGTGCAGTGCGTGTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy       3301 GACTCGACACGGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GACTCGACACGGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360

Qy       3361 GCTGAGTCGGAAGCTCCCGGGACGCGCTGACTGCCCTGGAGCCGCAGCCAACCCGGC 3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GCTGAGTCGGAAGCTCCCGGGACGCGCTGACTGCCCTGGAGCCGCAGCCAACCCGGC 3420

Qy       3421 ACTGCCCTCCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA 3480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 ACTGCCCTCCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA 3480

Qy       3481 GAGCAGACACCAGCAGCCCTGTCACGCGGCTCTACGTCCCAGGAGGGAGGGGGCGGC 3540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GAGCAGACACCAGCAGCCCTGTCACGCGGCTCTACGTCCCAGGAGGGAGGGGGCGGC 3540

Qy       3541 CACACCCAGGCCCGCACCCGCACCCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGGAGGCCTG 3600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 CACACCCAGGCCCGCACCCGCACCCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGGAGGCCTG 3600

Qy       3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGCGCTGAGAGGCCTGAGCGGTCCAGCCAAGGGCT 3660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGCGCTGAGAGGCCTGAGCGGTCCAGCCAAGGGCT 3660

Qy       3661 GAGTGTCCAGCACACTGCCGCTCTTCACTTCCCCACAGCCTGGCGCTCGGCTCCACCCCA 3720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GAGTGTCCAGCACACTGCCGCTCTTCACTTCCCCACAGCCTGGCGCTCGGCTCCACCCCA 3720

Qy       3721 GGGCCAGCTTTTCCTTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GGGCCAGCTTTTCCTTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780

Qy       3781 CCAGATTCGGCCATTGTTCACCCCTTGCCTTCCACCCCACCATCC 3840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 CCAGATTCGGCCATTGTTCACCCCTTGCCTTCCACCCCACCATCC 3840

Qy       3841 AGGTCGGAGACCCTGAGAAGGACCCTGGGAATTTGGACTGACCAAAGGTGTG 3900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 AGGTGGAGACCCTGAGAAGGACCCTGGGAATTTGGACTGACCAAAGGTGTG 3900

Qy       3901 CCCTTGTACACAGGGCGAGGACCTGGATGGGGGTCCCTGTTGGGTCAAATTTGGGGG 3960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 CCCTGTACACAGGGCGAGGACCTGGATGGGGGTCCCTGTGTGGGTCAAATTTGGGGG 3960

Qy       3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015
```

```
RESULT 6
ABA97534
ID   ABA97534 standard; DNA; 4015 BP.
XX
AC   ABA97534;
XX
DT   05-APR-2002  (first entry)
```

Right column section (positions 1561–2700):

```
Qy 1561 GCTCTGCTGCTGAGGACTGACGTGGAAGATGAGCGTGCGGGACTGGCTTGGCTGCGCAG 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1561 GCTCTGCTGCTGAGGACTGACGTGGAAGATGAGCGTGCGGGACTGGCTTGGCTGCGCAG 1620

Qy 1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTA 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||| | |||||
Db 1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTA 1680

Qy 1681 CAAGTTCCTGCACTGGCTGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTA 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681 CAAGTTCCTGCACTGGCTGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTA 1740

Qy 1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTCTCAAAGAGTGTCTGGAG 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTCTCAAAGAGTGTCTGGAG 1800

Qy 1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860

Qy 1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCCCTGCTCCGACGTCCGACTCCG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCCCTGCTCCGACGTCCGACTCCG 1920

Qy 1921 CTTCATCCCCAAGCCTGACGGCTGCGCGGCGATTGTGAACATGGACTACGTCTGGGAGC 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921 CTTCATCCCCAAGCCTGACGGCTGCGCGGCGATTGTGAACATGGACTACGTCTGGGAGC 1980

Qy 1981 CAGAACGTTCCCAGAGAAAAGAGGGGCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1981 CAGAACGTTCCCAGAGAAAAGAGGGGCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040

Qy 2041 CAGCGTGCTCAACTACGACGGGGGCCTGGGCGCCTCTCGTGCGTGGG 2100
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 2041 CAGCGTGCTCAACTACGACGGGGGCCTGGGCGCCTCTCGTGCGTGGG 2100

Qy 2101 CCTGGACGATATCCACAGGGCCTGGCGTGCTGGTGTGCGGGCCCAGGACCC 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2101 CCTGGACGATATCCACAGGGCCTGGCGTGCTGGTGTGCGGGCCCAGGACCC 2160

Qy 2161 GCGGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2161 GCGGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA 2220

Qy 2221 GGACAGGCTCACGGAGTTCATCCCAGCATCATCAAACCCCAGAACACTACTTGCGTGCG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2221 GGACAGGCTCACGGAGTTCATCCCAGCATCATCAAACCCCAGAACACTACTTGCGTGCG 2280

Qy 2281 TCGGTATGCCGTGCTTCCAGAAGGCCACGTCGTGTGCGGCAAGGCCTTCAAGAGCCA 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2281 TCGGTATGCCGTGCTTCCAGAAGGCCACGTCGTGTGCGGCAAGGCCTTCAAGAGCCA 2340

Qy 2341 CGTCTCTACCTTGACAGACCTCCAGCTGGCTTCGTGGCTCACCTGCAGA 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2341 CGTCTCTACCTTGACAGACCTCCAGCTGGCTTCGTGGCTCACCTGCAGA 2400

Qy 2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2401 GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAG 2460

Qy 2461 CAGTGGCCTCTTCTTCGAGCGTCTTCCTACGCTTCATGTGCCACCACGCCTCAGGGG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2461 CAGTGGCCTCTTCTTCGAGCGTCTTCCTACGCTTCATGTGCCACCACGCCTCAGGGG 2520

Qy 2521 CAAGTCCTACGTCCAGTGCCAGTGCGGATCCCGCAGGGCTCCCATCCTCCTGCGCTCTG 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2521 CAAGTCCTACGTCCAGTGCCAGTGCGGATCCCGCAGGGCTCCCATCCTCCTGCGCTCTG 2580

Qy 2581 CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2581 CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGGCT 2640

Qy 2641 GCTCCTGCGTTGGTGGATGATTCTTGTTGGTGACACCACGGCGAAAAC 2700
```

Main body section (positions 481–1560):

```
Qy 481 CCGCGTGGGCGACGACGTGCTGGTTCACCTGGTGTCTGGCACGCGTCTTTGTGCTGGT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 CCGCGTGGGCGACGACGTGCTGGTTCACCTGGTGTCTGGCACGCGTCTTTGTGCTGGT 540

Qy 541 GGCTCCCAGCTGCGCTACCAGTGTGCGGGCCGCGTGTACCAGCTCGGCGCTGCCAC 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 GGCTCCCAGCTGCGCTACCAGTGTGCGGGCCGCGTGTACCAGCTCGGCGCTGCCAC 600

Qy 601 TCAGGCCCGGCCCCGCCACACGCTAGTGGACCCCGCCACACGCTAGTGGACCCCGCCACACGCGGGC 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 TCAGGCCCGGCCCCGCCACACGCTAGTGGACCGCCACACGCTAGTGGACCGCCACACGGGGC 660

Qy 661 CTGGAACCATAGCGTCAGGGAGGAGGCCGGGGTCCCTGGGCTGCCAGCCAGCCCGGTGTGCGAG 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 CTGGAACCATAGCGTCAGGGAGGAGGCCGGGGTCCCTGGGCTGCCAGCCAGCCCGGTGTGCGAG 720

Qy 721 GAGGCCGGGGGCAGTGCCAGCGAAGTCTGCCGTTGCCCAAGAGGCCCAGCCGTGGCGC 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 GAGGCGCGGGGGCAGTGCCAGCGAAGTCTGCCGTTGCCCAAGAGGCCCAGCCGTGGCGC 780

Qy 781 TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCCCACCCGGCAGGAC 840
        ||||||||||||||||||||||||||||||||||||||||||||||
Db 781 TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCCCACCCGGCAGGAC 840

Qy 841 GGCGTGGACGAGTGAGCCTGGTTTCTGTGTGTCACCTGCCAGACCTGCCGAGAAGC 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 GCGTGGACGAGTGAGCCTGGTTTCTGTGTGTCACCTGCCAGACCCGCCGAGAAGC 900

Qy 901 CACCTCTTTGGAGGGTGCGCTCTGCGCACGCCCACTCCCACCACCTCCGTGGGCGCCCCA 960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 CACCTCTTTGGAGGGTGCGCTCTGCGCACGCCCCATCCCACCACCTCCGTGGGCGCCCCA 960

Qy 961 GCACCACGGCGGGCCCCCATCCACACGTCGGCACACGTCCTGTCC 1020
        |||||||||||||||||||||||||||||||||||||||||||||
Db 961 GCACCACGGCGGGCCCCCATCCACACGTCGGCACACGTCCTGTCC 1020

Qy 1021 CCCGGTGTACGGCGAGACCAAGAACACTTCCTCTACTCCTCAGGCGCAGGAGCAGCTGCG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 CCCGGTGTACGGCGAGACCAAGAACACTTCCTCTACTCCTCAGGCGCAGGAGCAGCTGCG 1080

Qy 1081 GCCCTCCTTCTAGTCAGCTCTGAGGCCCTGGCGCTCGGAGGCTCGTGGA 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 GCCCTCCTTCTAGTCAGCTCTGAGGCCCTGGCGCTCGGAGGCTGTGGA 1140

Qy 1141 GACCATCTTTCTGGGTTCCAGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCCT 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 GACCATCTTTCTGGGTTCCAGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGTTGCGCCCT 1200

Qy 1201 GCCCCAGCGTACTGGCAAATGCGGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 GCCCCAGCGTACTGGCAAATGCGGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260

Qy 1261 GTGCCCCTACGGGTGTCTGCCCCGGCTTGCGCGCGGGCTGTCTGGGAGCTGCGGTCACCCAGC 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 GTGCCCCTACGGGTGTCTGCCCCGGCTTGCGCGCGGGCTGTCTGGGAGCTGCGGTCACCCAGC 1320

Qy 1321 AGCCGGGTGTCTGCCCCGGAGAAGCCCAGGGCTCTGTGCGGCCCCCGAGGAGGA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 AGCCGGGTGTCTGCCCCGGAGAAGCCCAGGGCTCTGTGCGGCCCCCGAGGAGGA 1380

Qy 1381 CACAGAGACCCGTCGGCTACGGGGTCTCGCCTCGGCTGTGCTGCCTCCGCAGCAGCAGCCCCTGGCAGGTGTA 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 CACAGAGACGCGTCGGCTACGGGGTCTCGCCTCGGCTGTGCTGCCTCCGCAGCAGCAGCCCCTGGCAGGTGTA 1440

Qy 1441 CGGCTCGGTGCCCTGCCTGCGGGGCTTCGTGCCCCCGAGGCTCTGGGGCTCCACGCGGAGCTCCAGGCA 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 CGGCTCGGTGCCCTGCCTGCGGGGCTTCGTGCCCCCGAGGCTCTGGGGCTCCACGCGGAGCTCCAGGCA 1500

Qy 1501 CAACGAACGCCGTCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCCATGCATGCCAA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501 CAACGAACGCCGTCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCCATGCATGCCAA 1560
```

Left column (Db/Qy sequence alignment):

```
2641  Db  ||||||||||||||||||||||||||
          GCTCCTGGCGTTGGTGGATGATTCTTGTTGGTGGTGACACCTCACCTCACCCACGCGCGAAAAC  2700
2701  Qy  CTTCCTCAGAGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGGTGACTTGCGGAA  2760
      Db  CTTCCTCAGAGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGGTGACTTGCGGAA  2760
2761  Qy  GACAGTGGTGAACTTCCCTGTAGAGAGGAGAGGCCCTGGGTGGCACGGCTTTTGTTGTTCAGAT 2820
      Db  GACAGTGGTGAACTTCCCTGTAGAGAGGAGAGGCCCTGGGTGGCACGGCTTTTGTTGTTCAGAT 2820
2821  Qy  GCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGACCCTGGAGGT              2880
      Db  GCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGACCCTGGAGGT              2880
2881  Qy  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG      2940
      Db  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG      2940
2941  Qy  CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGGCTGAAGTG    3000
      Db  CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGGCTGAAGTG    3000
3001  Qy  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA     3060
      Db  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA     3060
3061  Qy  CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGCTGCTGCAGGTCCCATTTCA   3120
      Db  CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGCTGCTGCAGGTCCCATTTCA   3120
3121  Qy  TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGGCGTCATCTCTGACACGGCCTCCCT    3180
      Db  TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGGCGTCATCTCTGACACGGCCTCCCT    3180
3181  Qy  CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCCAAGGGGCCGCGC 3240
      Db  CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCCAAGGGGCCGCGC 3240
3241  Qy  CGGCCCCTCTGCCCTCCGCCCTCCGGCCGTGTGCCACCAAGCATTCCTGCTCAAGCT       3300
      Db  CGGCCCCTCTGCCCTCCGCCCTCCGGCCGTGTGCCACCAAGCATTCCTGCTCAAGCT       3300
3301  Qy  GACTCGACACCGTGCACCTACGTGCCCACTCCCTGGGGTCACTCAGGACCAGCGACGCGCA   3360
      Db  GACTCGACACCGTGCACCTACGTGCCCACTCCCTGGGGTCACTCAGGACCAGCGACGCGCA   3360
3361  Qy  GCTGAGTCGGAAGTCCCGGGGACGTCCCGGGAGGCCTGACTGCCCTGAGGCCCAACCCGGC  3420
      Db  GCTGAGTCGGAAGTCCCGGGGACGTCCCGGGAGGCCTGACTGCCCTGAGGCCCAACCCGGC  3420
3421  Qy  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCCGCCCACAGCCAGGCCGA   3480
      Db  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCCGCCCACAGCCAGGCCGA   3480
3481  Qy  GAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCACGGCGGAGGGGGCGGGGCC   3540
      Db  GAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCACGGCGGAGGGGGCGGGGCC   3540
3541  Qy  CACACCCAGGCCCGCACCGCCGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTG    3600
      Db  CACACCCAGGCCCGCACCGCCGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTG    3600
3601  Qy  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT   3660
      Db  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT   3660
3661  Qy  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA   3720
      Db  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACCAGGCTGGCGCTCGGCTCCACCCCA  3720
3721  Qy  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGGAATAGTCCATCC  
```

Right column:

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3721  Db  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC  3780
3781  Qy  CCAGATTCGCCATTGTTCACCCCCTCCCTTGCCTCCACCATCC                     3840
      Db  CCAGATTCGCCATTGTTCACCCCCTCCCTTGCCTCCACCCCCACCATCC                3840
3841  Qy  AGTGGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG   3900
      Db  AGGTGGGAGACCCTGGGGAATTTGGAGTGACCAAAGGTGTG                        3900
3901  Qy  CCCTGTACACAGGCGGCGAGCACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960
      Db  CCCTGTACACAGGCGGCGAGCACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960
3961  Qy  GAGGTGCTGTGGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAA          4015
      Db  GAGGTGCTGTGGGGAGTAAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAA          4015

RESULT 7
ABZ22474
ID   ABZ22474 standard; cDNA; 4015 BP.
XX
AC   ABZ22474;
XX
DT   25-MAR-2003  (first entry)
XX
DE   Human telomerase reverse transcriptase encoding cDNA SEQ ID NO:1.
XX
KW   Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;
KW   vulnerary; antiulcer; epithelial cell migration promoter; wound;
KW   epithelisation; skin wound; lesion; burn; surgical incision; ulcer;
KW   epithelial cell; keratinocyte; epidermal; mucosal; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             56..3454
FT                   /*tag= a
FT                   /product= "human telomerase reverse transcriptase"
XX
PN   WO200291999-A2.
XX
PD   21-NOV-2002.
XX
PF   09-MAY-2002; 2002WO-US14867.
XX
PR   09-MAY-2001; 2001US-289903P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Jiang X,  Chiu C,  Harley CB;
XX
DR   WPI; 2003-120591/11.
DR   P-PSDB; ABP56676.
XX
PT   Composition for treating wounds and enhancing epithelization of a skin
PT   surface, comprises vector encoding telomerase reverse transcriptase or
PT   telomerized epithelial cells on a microparticle or a matrix -
XX
PS   Disclosure; Page 31-32; 68pp; English.
XX
CC   The present invention describes a pharmaceutical composition (I)
CC   comprising a vector encoding telomerase reverse transcriptase (TERT) in
CC   an excipient or device, or comprises telomerised epithelial cells on a
CC   microparticle or a matrix suitable for topical administration or
CC   administration to a wound site. (I) has vulnerary and antiulcer
CC   activities and can be used to promote epithelial cell migration. (I) is
CC   useful for treating a wound and enhancing epithelisation of a skin
CC   surface. The wound is especially skin wound including acute lesion such
CC   as traumatic lesion, burn, or surgical incision, chronic lesion such as
CC   chronic venous ulcer, diabetic ulcer or compression ulcer and the wound
CC   is further monitored for closure. The telomerase activity or TERT
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CC   expression is increased in epithelial cells at the site of treatment and
CC   also in fibroblasts or endothelial cells at the site of treatment. The
CC   epithelial cells are especially keratinocytes. A polynucleotide encoding
CC   TERT is useful for the preparation of a medicament for treatment of a
CC   wound or an epithelial surface in a human or animal. An epithelial cell
CC   with increased telomerase activity or increased expression of TERT is
CC   useful for preparation of a medicament for the treatment of a wound in a
CC   human or animal. (I) is also useful for treating wounds of other
CC   epidermal surfaces including mucosal surfaces such as bronchus, mouth,
CC   nose, oesophagus, stomach, or intestine. The present sequence encodes
CC   human TERT (hTERT), which is given in the exemplification of the present
CC   invention. hTERT is located to chromosome 5.
XX
SQ   Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;

Query Match             100.0%;  Score 4015;  DB 25;  Length 4015;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches   4015;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GCAGCGGCTGGCTCCTGCTGCGTGGAACGCGTGGGAAGCCCTGGCCCCCGGCCACCCCGGCGATGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GCAGCGGCTGGCTCCTGCTGCGTGGAACGCGTGGGAAGCCCTGGCCCCCGGCCACCCCGGCGATGCC 60

Qy       61 GCGGCTGGCCACGTTCGTGCGGCCTGGCGGCCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GCGGCTGGCCACGTTCGTGCGGCCTGGCGGCCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120

Qy      121 GCCGCTGGCCACGTTCGTGCGGCGGCCTGGGCGCCCCAGGGCCTGGCGTGCAGCGCGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCCGCTGGCCACGTTCGTGCGGCGGCCTGGGCGCCCCAGGGCCTGGCGTGCAGCGCGG 180

Qy      181 GGACCCGGCGGCTTTCCGGGCGCGCGCTGGTGCCGCGCTGGTGTGCCCTGGGACGC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGACCCGGCGGCTTTCCGGGCGCGCGCTGGTGCCGCGCTGGTGTGCCCTGGGACGC 240

Qy      241 ACGGGCCGCGCCCCCGCGCGCCCCCCGCGCCCCCCCAGTGCCTGGCTCTGAAGGAGGC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACGGGCCGCGCCCCCGCGCGCCCCCCGCGCCCCCCCAGTGCCTGGCTCTGAAGGAGGC 300

Qy      301 CCGAGTGCTGCAGAGGCGCGGCGGCGCGGCGGAAGCAGCGTGCCGCCTTCGC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGAGTGCTGCAGAGGCGCGGCGGCGCGGCGGAAGCAGCGTGCCGCCTTCGC 360

Qy      361 GCTGCTGACGGGGCCCCGGGGGGCCCCCCGCGGGGGCGCCCCAGGCCTTCACCAGCGTGCGCAGCTA 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GCTGCTGACGGGGCCCCGGGGGGCCCCCCGCGGGGGCGCCCCAGGCCTTCACCAGCGTGCGCAGCTA 420

Qy      421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGCGGGCGCGGGGCCGTGGGGCCTGCTGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGCGGGCGCGGGGCCGTGGGGCCTGCTGCGG 480

Qy      481 CCGGTGGGCGGCGACGTGCTGGTTCACCTGGCGCGGCTGTCTTTGTGCTGGT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CCGGTGGGCGGCGACGTGCTGGTTCACCTGGCGCGGCTGTCTTTGTGCTGGT 540

Qy      541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGCCTGGCCCGTGTGCGGCGGCTGCCAC 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGCCTGGCCCGTGTGCGGCGGCTGCCAC 600

Qy      601 TCAGGCCCGGCCCCCGCCACACGGCTAGTGACGCTGGGATGCGGAACGGGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TCAGGCCCGGCCCCCGCCACACGGCTAGTGACGCTGGGATGCGGAACGGGC 660

Qy      661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGCCCAGCCCGGGTGCCAG 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGCCCAGCCCGGGTGCCAG 720

Qy      721 GAGGGCGGGGGCAGTGCCAGCCGAGTCTGCCCGTTGCCCAAGAGGGCCCAGGCGTGGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GAGGGCGGGGGCAGTGCCAGCCGAGTCTGCCCGTTGCCCAAGAGGGCCCAGGCGTGGCGC 780

Qy      781 TGCCCCTGAGCCGAGCCGACGCGCCCGTTGGCAGGGGTCTCGGGCCCACCCCGGCCAGGAC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 TGCCCCTGAGCCGAGCCGACGCGCCCGTTGGCAGGGGTCTCGGGCCCACCCCGGCCAGGAC 840

Qy      841 GCGTGGACCGAGTGACCGTGGTTTCGTGTGGTGTCACCTGCCAGACCCGCGAAGAAGC 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GCGTGGACCGAGTGACCGTGGTTTCGTGTGGTGTCACCTGCCAGACCCGCGAAGAAGC 900

Qy      901 CACCTCTTTGGAGGGTGCGGCTCTCTGGCACGCGCCACTCCCACCATCCGTGGGCGCCCA 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 CACCTCTTTGGAGGGTGCGGCTCTCTGGCACGCGCCACTCCCACCATCCGTGGGCGCCCA 960

Qy      961 GCACCACGGCGGGCCCCCATCCACATGCGCCACCAGTCCTGGCACGCGTGGGACACGCGTGTCC 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 GCACCACGGCGGGCCCCCATCCACATGCGCCACCAGTCCTGGCACGCGTGGGACACGCGTGTCC 1020

Qy     1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080

Qy     1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGTCGGCTCGTGA 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGTCGGCTCGTGA 1140

Qy     1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGCACTACCGCGAGGTGCT 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGCACTACCGCGAGGTGCT 1200

Qy     1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTGGGAACCACGCCA 1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTGGGAACCACGCCA 1260

Qy     1261 GTGCCCTACGGGGTGCTCCTCAAGACCCACTGCCCGCTGCGCGCTGCCCGCCCAGC 1320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 GTGCCCTACGGGGTGCTCCTCAAGACCCACTGCCCGCTGCGCGCTGCCCGCCCAGC 1320

Qy     1321 AGCCGGTGTCGTGCCCGGCTGCCTGCGCCAGCAGCACAGCAGGAGGA 1380
            |||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 AGCCGGTGTCGTGCCCGGCTGCCTGCGCCAGCAGCACAGCAGGAGGA 1380

Qy     1381 CACAGACCCCGCGCTGCCGTGGTGCAGCTGCTCGCCTTCGGCTTCGC 1440
            |||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 CACAGACCCCGCGCTGCCGTGGTGCAGCTGCTCGCCTTCGGCTTCGC 1440

Qy     1441 CGGCTTCGTGCGCGGCCTGCTGGGCGGCCTGCCGCCGGTGCCCCAGGCTA 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 CGGCTTCGTGCGCGGCCTGCTGGGCGGCCTGCCGCCGGTGCCCCAGGCTA 1500

Qy     1501 CAACGAAGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGGAAGCATGCCAA 1560
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 CAACGAAGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGGAAGCATGCCAA 1560

Qy     1561 GCTCTCGCTGCAGAGCTGACGTGCGGCGGCCTTGGCGCTTGGCGCTGTGCGCAG 1620
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 GCTCTCGCTGCAGAGCTGACGTGCGGCGGCCTTGGCGCTTGGCGCTGTGCGCAG 1620

Qy     1621 GAGCCCAGGGTTGGCTGTGTTCCGGCGGCCGCAGAGCACCGCGTCTCGCGGC 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 GAGCCCAGGGTTGGCTGTGTTCCGGCGGCCGCAGAGCACCGCGTCTCGCGGC 1680

Qy     1681 CAAGTTCCTGCACTGGCTGATGAGTGTGCGGGCCGATGCGAACGGGC 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 CAAGTTCCTGCACTGGCTGATGAGTGTGCGGGCCGATGCGAACGGGC 1740

Qy     1741 TGTTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 TGTTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800

Qy     1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCGGGAGCGTC 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCGGGAGCGTC 1860

Qy     1861 GGAAGCAGGAGGTCAGGCAGCATCGGGAAGCCCGGCCCCCTGCTGCAGCTCCAGACTCCG 1920
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 GGAAGCAGGAGGTCAGGCAGCATCGGGAAGCCCGGCCCCCTGCTGCAGCTCCAGACTCCG 1920
```

The page contains a two-sequence nucleotide alignment (labeled "Qy" and "Db") presented in two columns. Each aligned block shows a query sequence line (Qy), a match line of vertical bars (|), and a database sequence line (Db), with numeric position markers at the left and right of each line.

Left column (positions 1921–3000):

```
Qy  1921  CTTCATCCCCAAGCCTGACGGGCTGGCGCCCATTGTGAACATGGACTACGTCGTGGGAGC  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CTTCATCCCCAAGCCTGACGGGCTGGCGCCCATTGTGAACATGGACTACGTCGTGGGAGC  1980

Qy  1981  CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCGAGGTGAAGGCACTGTT         2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAGAACGTTCCCGCTGCGCCGAGCGTCTCGAGGTGAAGGCACTGTT               2040

Qy  2041  CAGCGTGCTCAACTACGAGCGGCGGCCGGCGGCGGCCCGCCTGGGCGCCCTGTGTGCTGGG  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CAGCGTGCTCAACTACGAGCGGCGGCCGGCGGCGGCCCGCCTGGGCGCCCTGTGTGCTGGG  2100

Qy  2101  CCTGACGCGATATCCAGACCTGGCCACCTTCGTGCTGCGCGTGTGCCCAGGACCCC       2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTGACGCGATATCCACAGACCTGGCCACCTTCGTGCTGCGCGTGTGCCCAGGACCCC     2160

Qy  2161  GCCGCCTGAGCTGTACTTTGTGACGGCCGTACGACACCATCCCCCA                2220
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCCGCCTGAGCTGTACTTTGTGACGGCCGTACGACACCATCCCCCA                2220

Qy  2221  GGACAGGCTCACGGAGGTCATCGCCCAGACATCATCAAACCCCAGAACACGTACTGCGTGCG  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGACAGGCTCACGGAGGTCATCGCCCAGACATCATCAAACCCCAGAACACGTACTGCGTGCG  2280

Qy  2281  TCGGTATGCCGTGGTCCAGAAGGCACGTCCGCAAGGCCTTCAAGAGCCA              2340
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCGGTATGCCGTGGTCCAGAAGGCACGTCCGCAAGGCCTTCAAGAGCCA              2340

Qy  2341  CGTCTCTTGACAGACCGTACAGTTCGTGGCTCACCTGCAGGA                    2400
          ||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGTCTCTTGACAGACCGTACAGTTCGTGGCTCACCTGCAGGA                    2400

Qy  2401  GACCAGCCCGCTGAGGGGATGCCGTCATCGAGACAGAGCTCCTCCCTGAATGAGGCCAG    2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GACCAGCCCGCTGAGGGGATGCCGTCATCGAGACAGAGCTCCTCCCTGAATGAGGCCAG    2460

Qy  2461  CAGTGGCCTTCGACTTCTCCGACCGCTCTTCCTACGCGTGTCCACCACGCGTGCGCATCC  2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CAGTGGCCTTCGACTTCTCCGACCGCTCTTCCTACGCGTGTCCACCACGCGTGCGCATCC  2520

Qy  2521  CAAGTCCTACGGTCCCAGTGCCAGGGATCCCGCAGGGCTCTG                    2580
          ||||||||||||||||||||||||||||||||||||||||||
Db  2521  CAAGTCCTACGGTCCCAGTGCCAGGGATCCCGCAGGGCTCTG                    2580

Qy  2581  CAGCCTGTGTACGGCGACACTGTTTGCGGGATTCGGCGGACGGGGCT               2640
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CAGCCTGTGTACGGCGACACTGTTTGCGGGATTCGGCGGACGGGGCT               2640

Qy  2641  GCTCCTCCGTCGGTTGGTGATGATTTCTTGTTGGTGACACCTCACCTGCCCGGGCGAAAAC  2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCTCCTCCGTCGGTTGGTGATGATTTCTTGTTGGTGACACCTCACCTGCCCGGGCGAAAAC  2700

Qy  2701  CTTCCTCAGGACCCTGCCGAGGTGTCCCGAGTGCGTGGTGTGAACTTGCCGGAA        2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CTTCCTCAGGACCCTGCCGAGGTGTCCCGAGTGCGTGGTGTGAACTTGCCGGAA        2760

Qy  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTGTTCCAGAT  2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  CAGCCGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTTGTTGTTCCAGAT  2820

Qy  2821  GCCGGCCCACGGCCTATTCCCGGTTGCGGTGCGGCCTGCTGCTGCTGCTGCCGAGGT     2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  GCCGGCCCACGGCCTATTCCCGGTTGCGGTGCGGCCTGCTGCTGCTGCTGCCGAGGT     2880

Qy  2881  GCAGAGCGACTACTCCAGCTATGCCCCGGACCTTCACAGAGCGCAGTCTCAACCCG      2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  GCAGAGCGACTACTCCAGCTATGCCCCGGACCTTCACAGAGCCAGTCTCAACCCG       2940

Qy  2941  CGGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGCGGCTGAAGTG  3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  CGGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGCGGCTGAAGTG  3000
```

Right column (positions 3001–4015):

```
Qy  3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGCACCAACATCTA    3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGCACCAACATCTA    3060

Qy  3061  CAAGATCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA   3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA   3120

Qy  3121  TCAGCAAGTTTGGAAGAACCCCACATTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT   3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  TCAGCAAGTTTGGAAGAACCCCACATTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT   3180

Qy  3181  CTGCTACTCCATCCTGAAAAGCCAAGAACGCAGGATGTCGCTGGGGCGCCAAGGGCGCCGC  3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  CTGCTACTCCATCCTGAAAAGCCAAGAACGCAGGATGTCGCTGGGGCGCCAAGGGCGCCGC  3240

Qy  3241  CGGCCCTCTGCCCTCCGAGGCCGTGCGCAGTGGCTGTGCGCACCAAGCATTCCTGCTCAAGCT  3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  CGGCCCTCTGCCCTCCGAGGCCGTGCGCAGTGGCTGTGCGCACCAAGCATTCCTGCTCAAGCT  3300

Qy  3301  GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACGACCCCAGACGCA   3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA    3360

Qy  3361  GCTGAGTCGGGAAGCTCCCGGGACGAGCGTCACTGCCCTGGAGGCCGCAGCCGCCAACCCGGC  3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  GCTGAGTCGGGAAGCTCCCGGGACGAGCGTCACTGCCCTGGAGGCCGCAGCCGCCAACCCGGC  3420

Qy  3421  ACTGCCCTCAGACTTCAAGACCATCCTGACTGATGGCGCCACCCGCCCACCAGCCAGGCCGA   3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  ACTGCCCTCAGACTTCAAGACCATCCTGACTGATGGCGCCACCCGCCCACCAGCCAGGCCCA   3480

Qy  3481  GAGCAGACACCAGCAGCTCCGTGCTCACGCGCTCTACGTCCCAGGCGGCGGAGGGGGCGGC   3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  GAGCAGACACCAGCAGCTCCGTGCTCACGCGCTCTACGTCCCAGGCGGCGGAGGGGGCGGC   3540

Qy  3541  CACACCCAGGCCGCCACCCGCACCCTGGGAGTCTGAGTGAGTGTTTGGCGGCCTGAGGCCTG   3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  CACACCCCAGGCCGCCACCCGCACCCTGGGAGTCTGAGTGAGTGTTTGGCGGCCTGAGGCCTG   3600

Qy  3601  CATGTGTCCGGCTGAAGGCTGAGTGCCGGGTCCGGCTGAGGCTGAGTGTCCAGCCAAGGGCT   3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  CATGTGTCCGGCTGAAGGCTGAGTGCCGGGTCCGGCTGAGGCTGAGTGTCCAGCCAAGGGCT   3660

Qy  3661  GAGTGTCCAGCAGCACCTGCACTTCCCACTGCCTCCCCACCAGGCTGGGCGCTCCACCCCA   3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  GAGTGTCCAGCAGCACCTGCACTTCCCACTGCCTCCCCACCAGGCTGGGCGCTCCACCCCA   3720

Qy  3721  GGGCCAGCGTTTCCTCACCAGGAGCCCCGGCTTCACTCCCCACACTAGGGAATAGTCCATCC  3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  GGGCCAGCGTTTCCTCACCAGGACCCCGGCTTCACTCCCCACATAGGGAATAGTCCATCC    3780

Qy  3781  CCAGATTCGCCATTGTTCACCCCGGACCTTCCACCATCGTCCTTCCTTCCACCCCATCC    3840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  CCAGATTCGCCATTGTTCACCCCGGACCTTCCACCATCGTCCTTCCTTCCACCCCATCC    3840

Qy  3841  AGGTGGAGACCTGAGAAGGACCCCTGGGAGCTCTGGCACGGCTCTGGGATTGGAGTGACCAAAGGTGTG  3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  AGGTGGAGACCTGAGAAGGACCCCTGGGAGCTCTGGCACGGCTCTGGGATTGGAGTGACCAAAGGTGTG  3900

Qy  3901  CCCTTGTACACAGGCGGAGGACCCCTGCACCTGCACCTGCACCCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG  3960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901  CCCTGTACACAGGCGGAGGACCCCTGCACCTGCACCTGGATGTGGGGTCCCTGTGGGTCAAATTGGGGG    3960

Qy  3961  GAGGTGCTGTGGGAGTAAAATACTGAATATGAGTTTTTCAGTTTTGAAAAAAA  4015
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  GAGGTGCTGTGGGAGTAAAATACTGAATATGAGTTTTTCAGTTTTGAAAAAAA  4015
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RESULT 8
AAV72117
ID AAV72117 standard; cDNA; 4042 BP.
XX

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AC   AAV72117;
XX
DT   24-MAY-1999 (first entry)
XX
DE   Human catalytic telomerase sub-unit cDNA.
XX
KW   Human; catalytic telomerase subunit; therapy; diagnosis; hTC; assay;
KW   modulator; treatment; inhibit; cellular disorder; death; defect; cancer;
KW   ageing; antisense; neoplastic cell; telomerase-related condition;
KW   tumour cell; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            63..3461
FT                  /tag= a
FT                  /product= "catalytic telomerase subunit"
XX
PN   WO985904O-A2.
XX
PD   30-DEC-1998.
XX
PF   09-JUN-1998; 98WO-EP03468.
XX
PR   14-APR-1998; 98DE-1016496.
PR   20-JUN-1997; 97DE-1026329.
PR   26-MAR-1998; 98DE-1013274.
XX
PA   (FARB ) BAYER AG.
XX
PI   Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;
XX
DR   WPI; 1999-081276/07.
DR   P-PSDB; AAW90251.
XX
PT   New catalytically active subunit of human telomerase - used in the
PT   modulation of telomerase activity, particularly for treating cancer
PT   and ageing
XX
PS   Claim 4; Fig 1; 76pp; German.
XX
CC   This sequence encodes a novel human catalytic telomerase sub-unit
CC   (hTC). The encoded protein can be used in screening assays to identify
CC   modulators of telomerase and to treat or inhibit cellular disorders,
CC   death, defects and/or other pathological processes involving telomerase,
CC   particularly cancer and ageing (also suitable for this are agents that
CC   stimulate, inhibit or mimic the activity of the subunit). Antisense
CC   nucleic acids inhibit telomerase action (by binding to specific mRNA),
CC   particularly in neoplastic cells and may be expressed in vivo. Antibodies
CC   and fragments of the protein, used as probes or primers, are used to
CC   diagnose telomerase-related conditions (especially neoplasia) by (i)
CC   detecting abnormal levels of the subunit protein in body fluids or
CC   tissues or (ii) by measuring the amount of the encoding nucleic acid.
CC   Expression of the nucleic acid encoding the subunit mRNA is confined to
CC   tumour cells, in contrast to the ubiquitous expression of the telomerase
CC   RNA subunit.
XX
SQ   Sequence 4042 BP; 684 A; 1364 C; 1277 G; 717 T; 0 other;

Query Match             100.0%;  Score 4015;  DB 20;  Length 4042;
Best Local Similarity   100.0%;  Pred. NO. 0;
Matches 4015;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

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Qy      1 GCAGCGCTGCGTCCGTGCTGCTGCGGAGCCCTGGCCACGTGGCCACCCCCGCCACCCCGGATGCC     60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8 GCAGCGCTGCGTCCGTGCTGCTGCGGAGCCCTGGCCACGTGGCCACCCCCGCCACCCCGGATGCC     67

Qy     61 GCGCGCTCCCGTGCCCGGAGCCGTGCGCTCCCGTGCTGCTGCGGCCACCACTACCGGCCGGAGGTGCT    120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     68 GCGCGCTCCCGTGCCCGGAGCCGTGCGCTCCCGTGCTGCTGCGGCCACCACTACCGGCCGGAGGTGCT    127

Qy    121 GCCCCAGCGCTACTGGCAAATGCGCCCTGGCGGCTGGCGGCTGGTGTGCAGCGCGG    180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCCCAGCGCTACTGGCAAATGCGCCCTGGCGGCTGGCGGCTGGTGTGCAGCGCGG    1267
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Qy   1261 GTGCCCTACGGGGTGTCCTCAAGACGCGCACTGCCGCTGCGGAGCTGCGGTCACCCCAGC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1268 GTGCCCTACGGGGTGTCCTCAAGACGCGCACTGCCGCTGCGGAGCTGCGGTCACCCCAGC 1327

Qy   1321 AGCCGGTGTCTGTGCCCGGGAGAAGCCCAGGGCTCTGTGGGGCCCCGAGGAGGAGGA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1328 AGCCGGTGTCTGTGCCCGGGAGAAGCCCAGGGCTCTGTGGGGCCCCGAGGAGGAGGA 1387

Qy   1381 CACAGACCCCCGTCGCTGGTGCAGCTGCTCCGGCAGCACAGCAGCCCTGGCAGTGTA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1388 CACAGACCCCCGTCGCTGGTGCAGCTGCTCCGGCAGCACAGCAGCCCTGGCAGTGTA 1447

Qy   1441 CGGCTTCGTGCTGGGGGCCTGCTGCCGCGGCTGGTGCCCGGCCTGCTCCGGCCTCCAGGCA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1448 CGGCTTCGTGCTGGGGGCCTGCTGCCGCGGCTGGTGCCCGGCCTGCTCCGGCCTCCAGGCA 1507

Qy   1501 CAACGAACGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1508 CAACGAACGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1567

Qy   1561 GCTCCTCGCTGACGCTGAAGATGAGCGTGCGGACACCGTGCGGCTTGGCTGTGAGGATCTGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1568 GCTCCTCGCTGACGCTGAAGATGAGCGTGCGGACACCGTGCGGCTTGGCTGTGAGGATCTGGC 1627

Qy   1621 GAGCCCAGGGGTTGGCTGCTGTGTCGCCGCAGACCGTGGCGGGAGATGAGCGTTCCGGGACTCCGG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1628 GAGCCCAGGGGTTGGCTGCTGTGTCGCCGCAGACCGTGGCGGGAGATGAGCGTTCCGGGACTCCGG 1687

Qy   1681 CAAGTTCCTGCACTGGCTGCGGTCGTGTACGTCGAGCTGTCCAGGTCTTCTTTTA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1688 CAAGTTCCTGCACTGGCTGCGGTCGTGTACGTCGAGCTGTCCAGGTCTTCTTTTA 1747

Qy   1741 TGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1748 TGTCACGGAGACCACGTTCAAAAGAACACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1807

Qy   1801 CAAGTTGCAAAGCATTGGAATCAGACGCACACTTGAGAGAGGTGCAGCTGCGGGAGCTGTC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1808 CAAGTTGCAAAGCATTGGAATCAGACGCACACTTGAGAGAGGTGCAGCTGCGGGAGCTGTC 1867

Qy   1861 GGAAGCAGAGGTCAGGCAGCATGGGAAGCCCAGGGCCGCCCCGTGACGTCCGACTCCG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1868 GGAAGCAGAGGTCAGGCAGCATGGGAAGCCCAGGGCCGCCCCGTGACGTCCGACTCCG 1927

Qy   1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCCGATTGTGAACATGGACTACGTCGTGGGGAGC 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1928 CTTCATCCCCAAGCCTGACGGGCTGCGGCCCGATTGTGAACATGGACTACGTCGTGGGGAGC 1987

Qy   1981 CAGAACGTTCCGCAGAGAAAAGAGGGGCGGGGCCGGGGCGCGGGGCCTACGACACTGTT 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1988 CAGAACGTTCCGCAGAGAAAAGAGGGGCGGGGCCGGGGCGCGGGGCCTACGACACTGTT 2047

Qy   2041 CAGCCGTGCTCAACTACGACGGGGCGGGGCGGGGCGGGGCGGGGCCTCGTGCTGCTGGGG 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2048 CAGCCGTGCTCAACTACGACGGGGCGGGGCGGGGCGGGGCGGGGCCTCGTGCTGCTGGGG 2107

Qy   2101 CCTGGACGATATCCCGGGGCGGCTTCGTTCGTGCTGCTGGGGGGCCCCAGGACCCC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2108 CCTGGACGATATCCCGGGGCGGCTTCGTTCGTGCTGCTGGGGGGCCCCAGGACCCC 2167

Qy   2161 GCCGGCTTGAGCGTGTACTTTGTGCAAGGTGGATGTGACGGGGCGGCCGGGCGCGTACGACAACATCCCCCA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2168 GCCGGCTTGAGCGTGTACTTTGTGCAAGGTGGATGTGACGGGGCGGCCGGGCGCGTACGACAACATCCCCCA 2227

Qy   2221 GGAAGCAGAGGCTCAACTACGAGCCGGGGCTCATCGCCAGCATCATCAAAACCCCAGAAGGCCTTGCTGCG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2228 GGAAGCAGAGGCTCAACTACGAGCCGGGGCTCATCGCCAGCATCATCAAAACCCCAGAAGGCCTTGCTGCG 2287

Qy   2281 TCGGTATGCCGGTGGTCCAGAAGGCCCGGGCCCATGGGCACGTCCCGCACGTCCCAAGAGCCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2288 TCGGTATGCCGGTGGTCCAGAAGGCCCGGGCCCATGGGCACGTCCCGCACGTCCCAAGAGCCA 2347
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Qy   2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2348 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2407

Qy   2401 GACCAGCCCGCTGAGGGATGCCGTCGTCGTCATCGAGCAGCAGCTCCTCCCCTGAATGAGGGCCAG 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2408 GACCAGCCCGCTGAGGGATGCCGTCGTCGTCATCGAGCAGCAGCTCCTCCCCTGAATGAGGGCCAG 2467

Qy   2461 CAGTGGCCTTCTTCATGTCTCATGTGCCGCATGTGCCACCACACCGCGTGCCGCATCAGGGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2468 CAGTGGCCTTCTTCATGTCTCATGTGCCGCATGTGCCACCACACCGCGTGCCGCATCAGGGG 2527

Qy   2521 CAAGTCCTACGTCCAGTGCCAGTGGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2528 CAAGTCCTACGTCCAGTGCCAGTGGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG 2587

Qy   2581 CAGCCTGTGCTACGGCGACATGGAGAACAAGAGCTGTTTCGGTGACACCTCACCTCACCGCGGAAAAC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2588 CAGCCTGTGCTACGGCGACATGGAGAACAAGAGCTGTTTCGGTGACACCTCACCTCACCGCGGAAAAC 2647

Qy   2641 GCTCCTCAGGAACGTGATGATTTCTTGTGGTGACACCTCACCTCACCGCGTGGGTGTGAACTTGCGGAA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2648 GCTCCTCAGGAACGTGATGATTTCTTGTGGTGACACCTCACCTCACCGCGTGGGTGTGAACTTGCGGAA 2707

Qy   2701 CTTCCTCAGGACCCTGGTCCGAGGTGTCCCGAGTATGGCGTCGGTGGTGTGACTTGCGGACGCGGTTTTGTTCAGAT 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2708 CTTCCTCAGGACCCTGGTCCGAGGTGTCCCGAGTATGGCGTCGGTGGTGTGACTTGCGGACGCGGTTTTGTTCAGAT 2767

Qy   2761 GACAGTGGTGAACTTCCCTGTAGAGACGCAGGGCCCTCGTGCGGCACGGGTGGGTGGCACGGGTGGGATACCCGGAGGT 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2768 GACAGTGGTGAACTTCCCTGTAGAGACGCAGGGCCCTCGTGCGGCACGGGTGGGTGGCACGGGTGGGATACCCGGAGGT 2827

Qy   2821 GCCGGCCCACGGCCTATTCCCGTGCGCGCCTGTTCCCGGACCCTGGAGGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2828 GCCGGCCCACGGCCTATTCCCGTGCGCGCCTGTTCCCGGACCCTGGAGGT 2887

Qy   2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCCACCTCAACCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2888 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCCACCTCAACCG 2947

Qy   2941 CGGCTTCAAGGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGGTGAAGTG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2948 CGGCTTCAAGGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGGTGAAGTG 3007

Qy   3001 TCACAGCCTGTTTCGTGTTCTGGATTTGAACATGGACTACGTCGAGGTGAACAGCTGTCGCACCAACATCTA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3008 TCACAGCCTGTTTCGTGTTCTGGATTTGAACATGGACTACGTCGAGGTGAACAGCTGTCGCACCAACATCTA 3067

Qy   3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGGCGTGCTGCAGCTCCCCATTTCA 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3068 CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGGCGTGCTGCAGCTCCCCATTTCA 3127

Qy   3121 TCAGCAAGTTGGAAGAACCCCACATTTTCTGCGTCATCTCTGACACGGGCTCCCT 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3128 TCAGCAAGTTGGAAGAACCCCACATTTTCTGCGTCATCTCTGACACGGGCTCCCT 3187

Qy   3181 CTGCTACTCCATCCTGAAAGCCAAGAACCAGGGGATGTCGCTGCTGCGGCCAAGGGCGCCGCC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3188 CTGCTACTCCATCCTGAAAGCCAAGAACCAGGGGATGTCGCTGCTGCGGCCAAGGGCGCCGCC 3247

Qy   3241 CGGCCCTCTGCCCTCCGAGGGCGTGCAGTGGCGTGTGCCACCAAGCAGCATTCCTGCTCAAGCT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3248 CGGCCCTCTGCCCTCCGAGGGCGTGCAGTGGCGTGTGCCACCAAGCAGCATTCCTGCTCAAGCT 3307

Qy   3301 GACTCGACACCGTGTCACCTACGTGCGGGACACGTACTGCGCGG 3360
          |||||||||||||||||||||||||||||||||||||||||||
Db   3308 GACTCGACACCGTGTCACCTACGTGCGGGACACGTACTGCGCGG 3367

Qy   3361 GCTGAGTCGGAAGCTCCCGGGGACGTCCCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3368 GCTGAGTCGGAAGCTCCCGGGGACGTCCCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCC 3427

Qy   3421 ACTGCCCTCAGACTTCAAGACCATCCTGACTGATGCCGCCCCCACCCCAGCCGGCCGA 3480
```

XX
PS   Example 1; Fig 1; 64pp; English.
XX
CC   The present sequence is that of hTERT cDNA in plasmid pGRN121.
CC   hTERT is the catalytic subunit of human telomerase. Claimed
CC   immortalised cell lines for use in vaccine production are adapted
CC   to express hTERT. Suitable cell lines comprise human diploid
CC   fibroblasts, e.g. MRC-5 or WI38 cells, transfected with hTERT cDNA
CC   or infected by a retrovirus carrying hTERT cDNA, and are capable
CC   of supporting antigen production. A method for preparing such cell
CC   lines using recombinant techniques is provided. The cell lines
CC   are also used as a diagnostic test for the presence of a virus,
CC   such as human cytomegalovirus, and to determine the efficacy of
CC   antiviral agents by testing the capability of a modified virus
CC   containing a reporter gene to infect the cells. The cell lines
CC   have the ability, which can be impaired in cell lines immortalised
CC   by other methods, of being able to support viral replication.
CC   The cells remain morphologically suitable for viral/vaccine
CC   cultivation.
XX
SQ   Sequence 4070 BP; 670 A; 1383 C; 1296 G; 721 T; 0 other;

Query Match   100.0%; Score 4015; DB 24; Length 4070;
Best Local Similarity   100.0%;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GCAGCGCTCGTCCTCGCCACGTGGGAAGCCCTGGCCCGGCCACCCCGCGATGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 GCAGCGCTCGTCCTCGCGCCACGTGGGAAGCCCTGGCCCGGCCACCCCGCGATGCC 80

Qy   61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 140

Qy   121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCCAGGGCCTGGGGCTGGTGCGAGCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCCAGGGCCTGGGGCTGGTGCGAGCGCG 200

Qy   181 GGACCCGGGGCGGCTTTCCCGCGCCGCGCCCCGCCCCTCCGCGCCCGCTGCCGCCCTGGCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 GGACCCGGGGCGGCTTTCCCGCGCCGCGCCCCGCCCCTCCGCGCCCGCTGCCGCCCTGGACGC 260

Qy   241 ACGGCGCGCCCCCCGCCGCCCCCTCCTTCCGCGCGCGGAAGAAGCTGGTGGGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 ACGGCGCGCCCCCCGCCGCCCCCTCCTTCCGCGCGCGGAAGAAGCTGGTGGGC 320

Qy   301 CCGAGTGCTGCAGAGGCTGTGCGAGGGCCCCCCGCGCGCGGAAGAACGTGCTGGCGTTCGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 CCGAGTGCTGCAGAGGCTGTGCGAGGGCCCCCCGCGCGCGGAAGAACGTGCTGGCTTCGC 380

Qy   361 GCTGCTGACGGGGCCCCCGAGGGCCTTCACCACCAGCGTGCCGCAGCTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 GCTGCTGACGGGGCCCCCGAGGGCCTTCACCACCAGCGTGCCGCAGCTA 440

Qy   421 CCTGCCCAACACGGTGACCGACCCGGGGCGTGGGGGCTGCTGCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 CCTGCCCAACACGGTGACCGACCCGGGGCGTGGGGGCTGGCTGCTGCG 500

Qy   481 CCGGCTGGGCGACACGGCTGCTGGTTCACCTGCGGCCGCTCTTTGTGCTGGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 CCGGCTGGGCGACACGGCTGCTGGTTCACCTGCGGCCGCTCTTTGTGCTGGT 560

Qy   541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGGCGTCCCCGTGTACCAGCTGCCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGGCGTCCCCGTGTACCAGCTGCCAC 620

Qy   601 TCAGGCCCGGCCCACACGGTCTAGTGACCTGGGATGGAACGCGGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   621 TCAGGCCCGGCCCACACGGTCTAGTGACCTGGGATGGAACGGGC 680

Qy   661 CTGGAACCATAGCGTCAGGGAGGCCGCGGGGTCCCCTGGCCTGCAGCCCCGGGGTGCGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   681 CTGGAACCATAGCGTCAGGGAGGCCGCGGGGTCCCCTGGCCTGCAGCCCCGGGGTGCGAG 740

Db   3428 ACTTCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACAGCCAGGCCGA 3487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3481 GAGCAGACACCAGCCGTCCCCGGCTCTACGTCCCAGGAGGGGAGGGGCGGCC 3540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3488 GAGCAGACACCAGCCGTCCCCGGCTCTACGTCCCAGGAGGGGAGGGGCGGCC 3547

Qy   3541 CACACCCAGGCCACCCGCCGACCGCCACCCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTGGCCTGAGGCCTG 3600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3548 CACACCCAGGCCACCCGCCGACCGCCACCCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTGGCCTGAGGCCTG 3607

Qy   3601 CATGTGCCGGCTGAAGGCTGAGTGTCCGCTGAGGCCTGAGGCCGAGTGTCCAGCCAAGGGCT 3660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3608 CATGTGCCGGCTGAAGGCTGAGTGTCCGCTGAGGCCTGAGGCCGAGTGTCCAGCCAAGGGCT 3667

Qy   3661 GAGTGTCCAGCACACCTGCCCGTCCACTTCCCCACAGGCTGGCGCTCGGCGTCCACCCCA 3720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3668 GAGTGTCCAGCACACCTGCCCGTCCACTTCCCCACAGGCTGGCGCTCGGCGTCCACCCCA 3727

Qy   3721 GGGCCAGCTGTTTTCCTCACCAGGAGGCCCGGCCTTCCCCACTCCCCACATAGGAATAGTCCATCC 3780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3728 GGGCCAGCTTTTTCCTCACCAGGAGGCCCGGCCTTCCCCACTCCCCACATAGGAATAGTCCATCC 3787

Qy   3781 CCAGATTCGCCATTGTTCACCCCCTCGCCCTCCTTGCCTTCCACCCCACCATCC 3840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3788 CCAGATTCGCCATTGTTCACCCCCTCGCCCTCCTTGCCTTCCACCCCACCATCC 3847

Qy   3841 AGGTGGACCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTTGACCAAAGGTGTG 3900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3848 AGGTGGACCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTTGACCAAAGGTGTG 3907

Qy   3901 CCCTGTACACAGGCGAGGACCCTGCCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3908 CCCTGTACACAGGCGAGGACCCTGCCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3967

Qy   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTGAAAAAAA 4015
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3968 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAAA 4022

RESULT 9
ABL53711
ID   ABL53711 standard; cDNA; 4070 BP.
XX
AC   ABL53711;
XX
DT   17-JUN-2002 (first entry)
XX
DE   Human telomerase catalytic subunit hTERT cDNA.
XX
KW   hTERT; telomerase; reverse transcriptase; immortalisation; human;
KW   vaccine; enzyme; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200216555-A2.
XX
PD   28-FEB-2002.
XX
PF   17-AUG-2001; 2001WO-GB03726.
XX
PR   17-AUG-2000; 2000GB-0020246.
PR   17-AUG-2000; 2000US-225734P.
XX
PA   (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
XX
PI   Jones CJ, Kipling DG, Wilkinson G, McSharry B, Skinner JW;
XX
PR   WPI; 2002-315462/35.
XX
DR   Novel hTERT-immortalized cell line (human telomerase reverse
PT   transcriptase) useful for human vaccine production and preparation of
PT   antigen, such as a virus or virus-derived agent -

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Qy    721  GAGGCGCGGGGCAGTGCCAGCCCGTTGCCCAAGAGGGTGGCGC  780
           |||||||||||||||||||||||||||||||||||||||||||
Db    741  GAGGCGCGGGGCAGTGCCAGCCCGTTGCCCAAGAGGGTGGCGC  800

Qy    781  TGCCCCTGAGCCGGAGCGGACGGCGCCCGTTGGGCAGGGTCCTGGGCCGCCACCCGGGCCAGGAC  840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801  TGCCCCTGAGCCGGAGCGGACGGCGCCCGTTGGGCAGGGTCCTGGGCCGCCACCCGGGCCAGGAC  860

Qy    841  GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCGCGCCGAGAAGC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861  GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCGCGCCGAGAAGC  920

Qy    901  CACCTTCTTTGGAGGGTGCCGCTCTGGCCACGCGCCACTCCCACCCATCCGTGGGCCGCCCA  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921  CACCTTCTTTGGAGGGTGCCGCTCTGGCCACGCGCCACTCCCACCCATCCGTGGGCCGCCCA  980

Qy    961  GCACCACGCGGGCCCCCATCCACATCGCGGCCACCAGTCCCTGGGACACGCCTTGTCC  1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981  GCACCACGCGGGCCCCCATCCACATCGCGGCCACCAGTCCCTGGGACACGCCTTGTCC  1040

Qy   1021  CCCGGTGTACGCCCGAGACCAAGCACTTCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041  CCCGGTGTACGCCCGAGACCAAGCACTTCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1100

Qy   1081  GCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCTCGGAGGCTCGGTCCTGGA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101  GCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCTCGGAGGCTCGGTCGTGGA  1160

Qy   1141  GACCATCTTTCTGGGTTCCAGGGTTCCAGGCCCTGGATGCCAGGTTGCCCCGAGCCCT  1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161  GACCATCTTTCTGGGTTCCAGGGTTCCAGGCCCTGGATGCCAGGTTGCCCCGAGCCCT  1220

Qy   1201  CACAGACCCCCGTCGGCTACTGGCAAATGCGCCCCTGTTCTGGGAACCACGCGCGCA  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221  CACAGACCCCCGTCGGCTACTGGCAAATGCGCCCCTGTTTCTGGGAACCACGCGCGCA  1280

Qy   1261  GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCGCCCGCTGCGAGCTGCGTCACCCAGC  1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281  GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCGCCCGCTGCGAGCTGCGGTCACCCAGC  1340

Qy   1321  AGCCGGTGTCTGTGCCCGGGAGAGCCCCAGGGCTCTGTGTGGCGCCCCCCGAGGAGGAGA  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341  AGCCGGTGTCTGTGCCCGGGAGAGCCCCAGGGCTCTGTGTGGCGCCCCCCGAGGAGGAGA  1400

Qy   1381  CACAGACCCCCGTCGGCTGCTGCCTGCCGTCGTGCAGCAGCAGCCTCTGGCCAGTGTA  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401  CACAGACCCCCGTCGGCTGCTGCCTGCCGTCGTGCAGCAGCAGCCTCTGGCCAGTGTA  1460

Qy   1441  CGGCTTCGTGCGGGGCTGCTGCCTGCCGGCTGGTGCCCGCGGGGCTCTGGGGCTCCAGGCA  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461  CGGCTTCGTGCGGGGCTGCTGCCTGCCGGCTGGTGCCCGCGGGGCTCTGGGGCTCCAGGCA  1520

Qy   1501  CAACGAACGCGCGTTCCTGGCTGCTGCCTCAGGGAAGCTCATCTCCCTGGGGAAGCATGCCAA  1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521  CAACGAACGCGCGTTCCTGGCTGCTGCCTCAGGGAAGCTCATCTCCCTGGGGAAGCATGCCAA  1580

Qy   1561  GCTCTGCTGCCTGCCAGGAGATGAGAGCGTGCGGGACTGCGCTTGGCTGCCAGTGTA  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581  GCTCTGCTGCCTGCCAGGAGATGAGAGCGTGCGGGACTGCGCTTGGCTGCCAGTGTA  1640

Qy   1621  GAGCCCAGGGGTTGCTGCGTTGGCTGCTGCTTCCGGCCCAGAGCACCCGTCTGCGCTGAGGAGATCCTGGC  1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641  GAGCCCAGGGGTTGCTGCGTTGGCTGCTGCTTCCGGCCCAGAGCACCCGTCTGCGCTGAGGAGATCCTGGC  1700

Qy   1681  CAAGTTCCTGCACTGCTGCGATGAGTGTGTACGTCGTACGTCGCTCTTTTTTCAGGTCTCTTTTTA  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701  CAAGTTCCTGCACTGCTGCGATGAGTGTGTACGTCGTACGTCGCTCTTTTTTCAGGTCTCTTTTTA  1760

Qy   1741  TGTCACGGAGACCACGTTTCAAAAGAACACAGGCTCTTTTTTCTACCCGGAAGAGTGTCTGGAG  1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761  TGTCACGGAGACCACGTTTCAAAAGAACACAGGCTCTTTTTTCTACCCGGAAGAGTGTCTGGAG  1820
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Qy   1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACACTGAAGAGGGTGCAGTGCGCGGGAGCTGTC  1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821  CAAGTTGCAAAGCATTGGAATCAGACAGCACACTGAAGAGGGTGCAGTGCGCGGGAGCTGTC  1880

Qy   1861  GGAAGCAGAGGTCAGGCAGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG  1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881  GGAAGCAGAGGTCAGGCAGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG  1940

Qy   1921  CTTCATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTCGTGGGAGC  1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941  CTTCATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTCGTGGGAGC  2000

Qy   1981  CAGAACGTTCCGCAGAGAAAGAGGGCGAGCCTGCTCACCTGCGAGGTGAAGGCACTGTT  2040
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Db   2001  CAGAACGTTCCGCAGAGAAAGAGGGCGAGCCTGCTCACCTGCGAGGGTGAAGGCACTGTT  2060

Qy   2041  CAGCCGTGCTCAACTACGAGCGGCGGCGGCGGCCCGCCCTCCTGGGCGCCTCTGTGCTGGG  2100
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Db   2061  CAGCCGTGCTCAACTACGAGCGGCGGCGGCGGCCCGCCCTCCTGGGCGCCTCTGTGCTGGG  2120

Qy   2101  CCTGGACGATATCCACAGGCCCTGGCGACGTTCGTGCTGCGTGCGGCCCAGGACCC  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121  CCTGGACGATATCCACAGGCCCTGGCGACGTTCGTGCTGCGTGCGGCCCAGGACCC  2180

Qy   2161  GCCGCCTGAGCGTGTACTTTGTCAAGGTGGATGTGACGGGCGGCGTACGACACCATCCCCCA  2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181  GCCGCCTGAGCGTGTACTTTGTCAAGGTGGATGTGACGGGCGGCGTACGACACCATCCCCCA  2240

Qy   2221  GGACAGGCTCACGGAGTCATCGCCAGCAGCATCATCAAACCCAGAACACGTACTGCGTGCG  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241  GGACAGGCTCACGGAGTCATCGCCAGCAGCATCATCAAACCCAGAACACGTACTGCGTGCG  2300

Qy   2281  TCGGTATGCCGTGCGTCCAGAAGGCCGCCCATGGGCACGTCCGAAGGCCTTCAAGAGCA  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301  TCGGTATGCCGTGCGTCCAGAAGGCCGCCCATGGGCACGTCCGAAGGCCTTCAAGAGCCA  2360

Qy   2341  CGTCTCTACCTTGACAGACCTCCAGCGTACATGCGCAGTTCGTGGCTCACCTGCAGGA  2400
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Db   2361  CGTCTCTACCTTGACAGACCTCCAGCGTACATGCGCAGTTCGTGGCTCACCTGCAGGA  2420

Qy   2401  GACCAGCCGCGTGAGGGATGCCGTCGTCATCGAGCAGAGCAGAGCTCCTCGAATGAGGCCAG  2460
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421  GACCAGCCGCGTGAGGGATGCCGTCGTCATCGAGCAGAGCAGAGCTCCTCGAATGAGGCCAG  2480

Qy   2461  CAGTGGCCTCTTCGACGTCTTCATGTGCCACCGCGTGCGCATCAGGGG  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2481  CAGTGGCCTCTTCGACGTCTTCATGTGCCACCGCGTGCGCATCAGGGG  2540

Qy   2521  CAAGTCCTACGTGCCAGTGCCAGGGGATCCGCAGGGCTCCATCCTCCACGCGCTGCTCTG  2580
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Db   2541  CAAGTCCTACGTGCCAGTGCCAGGGGATCCGCAGGGCTCCATCCTCCACGCGCTGCTCTG  2600

Qy   2581  CAGCCTGCGTACGGCCGGGACAACAAGCTGTTTGCGGGGATTCGGCGGGACGCGGCT  2640
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Db   2601  CAGCCTGCGTACGGCCGGGACAACAAGCTGTTTGCGGGGATTCGGCGGGACGCGGCT  2660

Qy   2641  GCTCCTCGGTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCACGCGGAAAAC  2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2661  GCTCCTCGGTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCACGCGGAAAAC  2720

Qy   2701  CTTCCTCAGGACCCTGGTCCGGAGTCTCCCTGAGTATGGCGTGCTGGTGGTGAACTTGCGGAA  2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2721  CTTCCTCAGGACCCTGGTCCGGAGTGTCCCTGAGTATGGCGTGCTGGTGGTGAACTTGCGGAA  2780

Qy   2761  GACACTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGTGGCGGCACGCGGCTTTTGTTCAGAT  2820
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2781  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGTGGCGGCACGCGGCTTTTGTTCAGAT  2840

Qy   2821  GCCGGCCCACGGCCTATTCCCCTGTCGCCTCGTGCTGGATACCCGGACCCTGGAGT  2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2841  GCCGGCCCACGGCCTATTCCCCTGTCGCCTCGTGCTGGATACCCGGACCCTGGAGT  2900

Qy   2881  GCGAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTTCACCTTCACCG  2940
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Db   3981 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA 4035
            ||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10
AAZ08150
ID   AAZ08150 standard; cDNA; 4015 BP.
XX
AC   AAZ08150;
XX
DT   17-JAN-2000 (first entry)
XX
DE   Human telomerase reverse transcriptase cDNA.
XX
KW   Human telomerase reverse transcriptase; hTRT; telomerase; hEST2;
KW   catalytic protein component; cell proliferative capacity;
KW   cell immortality; neoplastic phenotype; diagnostic application;
KW   prognostic application; telomerase related condition; cancer;
KW   therapeutic agent; telomerase expression; telomerase activity; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   CDS   56..3454
FT   /*tag= a
FT   /product= "Human telomerase reverse transcriptase"
FT   /transl_except= (pos:1877..1879, aa:Gln)
XX
PN   WO9950279-A1.
XX
PD   07-OCT-1999.
XX
PF   31-MAR-1999; 99WO-US07160.
XX
PR   31-MAR-1998; 98US-0052919.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1999-610834/52.
DR   P-PSDB; AAZ88881.
XX
PT   Antisense polynucleotides for human telomerase reverse transcriptase
PT   used for diagnosing or treating cancer -
XX
PS   Claim 1; Fig 1; 31pp; English.
XX
CC   The present sequence encodes for human telomerase reverse transcriptase
CC   (hTRT). This is the catalytic protein component of telomerase and is also
CC   referred to as hEST2. This correlates with cell proliferative capacity,
CC   cell immortality, and the development of a neoplastic phenotype. Human
CC   TRT antisense oligonucleotides are useful for diagnostic or prognostic
CC   applications to telomerase related conditions, including cancer. They are
CC   also useful as therapeutic agents, for inhibition of telomerase
CC   expression and activity.
XX
SQ   Sequence 4015 BP; 663 A; 1364 C; 1274 G; 714 T; 0 other;

Query Match   100.0%; Score 4013.4; DB 20; Length 4015;
Best Local Similarity   100.0%; Pred. NO. 0;
Matches 4014; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 GCAGGCGCTGCGTCCGTGCGCACGTGGAAGCCCTGGCCCGCCACCCCGCCGATGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCAGGCGCTGCGTCCGTGCGCACGTGGAAGCCCTGGCCCGCCACCCCGCCGATGCC 60

Qy   61 GGGCGCTCCCGGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGGCGCTCCCGGCCGAGCCGTCCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120

Qy   121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCGTGGTGCAGCGCGGCGG 180

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Db  1201 GCCCCAGCGCTACTGCGGGTGCTCCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1261 GTGCCCCTACGGGGTGCTTCCTCCTCAAGACGCACTGCCCCGCTGCGAGCTGCGCGAGGAGGA      1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GTGCCCCTACGGGGTGCTTCCTCCTCAAGACGCACTGCCCCGCTGCGAGCTGCGCGAGGAGGA      1320
Qy  1321 AGCCGGTGTCTGTGCCCGGGAGAAGCCCAGCAGTCTGCTCCGGAGGCTCGTGTGGCGGCCCCGAGGAGGAGGA 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 AGCCGGTGTCTGTGCCCGGGAGAAGCCCAGCAGTCTGCTCCGGAGGCTCGTGTGGCGGCCCCGAGGAGGAGGA 1380
Qy  1381 CACAGACCCCCGTGCCTGCTCCGTGTCAGCTGCGGCGGCGAGAACGTGCTGCCTTCGGCTTCGC          1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CACAGACCCCCGTGCCTGCTCCGTGTCAGCTGCGGCGGCGAGAACGTGCTGCCTTCGGCTTCGC          1440
Qy  1441 CGGCTTCGTGCTGCCGCGGCCTGTGCCCCGGCTGCCCCAGGGCCTCGGGGCTCTCCCAGGCTA          1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CGGCTTCGTGCTGCCGCGGCCTGTGCCCCGGCTGCCCCAGGGCCTCGGGGCTCTCCCAGGCTA          1500
Qy  1501 CAACGACGCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA               1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 CAACGACGCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA               1560
Qy  1561 GCTCTCGCTCAGGAGCTGACGTGCGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGATCCTGGC         1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 GCTCTCGCTCAGGAGCTGACGTGCGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGATCCTGGC         1620
Qy  1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCCGCCGCTCTGCGTGAGGAGATCCTGCC                  1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCCGCCGCTCTGCGTGAGGAGATCCTGCC                  1680
Qy  1681 CAAGTTCCTGACTGGCTGATGAGTGTGTACGTCGTGAGCTGCGTGAGCTCTTTCTTTA               1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CAAGTTCCTGACTGGCTGATGAGTGTGTACGTCGTGAGCTGCGTGAGCTCTTTCTTTA               1740
Qy  1741 TGTCACGGAGACCACCGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG            1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TGTCACGGAGACCACCGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG            1800
Qy  1801 CAAGTTGCAAAGCATTGAATCAGAGCACACTTGAAGAGGGTCCAGCTGCGGGAGAGC                1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 CAAGTTGCAAAGCATTGAATCAGAGCACACTTGAAGAGGGTCCAGCTGCGGGAGAGC                1860
Qy  1861 GGAAGCAGAGGTCAGGCAGCATCGGAGGCCGCGCCCTGCTGACGTCCTGACGTCGTGGGAGC          1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GGAAGCAGAGGTCAGGCAGCATCGGAGGCCGCGCCCTGCTGACGTCCTGACGTCGTGGGAGC          1920
Qy  1921 CTTCATCCCCCAAGCCTGACGGGGCTCACCTGTCAGCCGAATTGTGAACATGGACTACGTCGTGGGAGC    1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CTTCATCCCCCAAGCCTGACGGGGCTCACCTGTCAGCCGAATTGTGAACATGGACTACGTCGTGGGAGC    1980
Qy  1981 CAGAAACGTTCCCGAGAGAAAAGAGAGGGCCGAGCGTCTCACCTGGTGAAGGCACTCGTT            2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CAGAAACGTTCCCGAGAGAAAAGAGAGGGCCGAGCGTCTCACCTGGTGAAGGCACTCGTT            2040
Qy  2041 CAGCGTGCTCAACTACGAGCGGCGGCGGCCGCGGCCCCTCTGCTGGGGCCGCTCTGTGCTGGGG       2100
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Db  2041 CAGCGTGCTCAACTACGAGCGGCGGCGGCCGCGGCCCCTCTGCTGGGGCCGCTCTGTGCTGGGG       2100
Qy  2101 CCTGGACGGATATCCACAGGGCCTTGCGTCGTGTGTGCGGGGCCCAGGACCCG                    2160
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Db  2101 CCTGGACGGATATCCACAGGGCCTTGCGTCGTGTGTGCGGGGCCCAGGACCCG                    2160
Qy  2161 GCCGCCTGAGTCGTGACTTTGTCAAGGTGGATGTGACGGGCGCGCGGCCGTACGACCATCCCCCA       2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCGCCTGAGTCGTGACTTTGTCAAGGTGGATGTGACGGGCGCGCGGCCGTACGACCATCCCCCA       2220
Qy  2221 GGACAGGCTCACGGAGGTCATCGGCAGCAATCATCAAACCCCAGAAACACGTACTGCGTGCG          2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GGACAGGCTCACGGAGGTCATCGGCAGCAATCATCAAACCCCAGAAACACGTACTGCGTGCG          2280
Qy  2281 TCGGTATGCCGTGGTCCTGTTCCAGAGGCACGTCCGCAAGGCCTTCAAGAGCCA                   2340
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Db  2281 TCGGTATGCCGTGGTCCTGTTCCAGAGGCACGTCCGCAAGGCCTTCAAGAGCCA                   2340
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Db   121 ||||||||||||||||||||||||||||||||||||||||||||||||
         GCCCTGGCCACGGTTCGTCGCCGGGCCTGGGGCTGGTCAGCGGCGCGG  180
Qy   181 GGACCCGGCGGCGGCTTCCGCGCGTGGTCGTGTGCCCTGGTGTGGC  240
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACCCGGCGGCGGCTTCCGCGCGTGGTCGTGTGCCCTGGTGTGGC  240
Qy   241 ACGGCCGCGCCCCCCGCCCCCGCCCCCGCCTTCCGCGTGTCCTGCCTGAAGGAGCTGGTGGC  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACGGCCGCGCCCCCCGCCCCCGCCCCCGCCTTCCGCGTGTCCTGCCTGAAGGAGCTGGTGGC  300
Qy   301 CCGAGTGCTGCAGAGGCGTGCGGACGCGGCGGAGAACGTGCCTGGCCTTCGGCTTCGC  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGAGTGCTGCAGAGGCGTGCGGACGCGGCGGAGAACGTGCCTGGCCTTCGGCTTCGC  360
Qy   361 GCTGCTGGACACGTGACCCGCCGGGGCCCCGCGAGGGGGCCCGCGGGGC  420
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCTGCTGGACACGTGACCCGCCGGGGCCCCGCGAGGGGGCCCGCGGGGC  420
Qy   421 CCTGCCCAACACGTGACCACTGCGGGGAGCCGGTGGGGCGTGGGGCGTGCTGCTGCGG  480
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Qy   481 CCGCGTGGGGGACGACGTGCTGGTTCACCTGCGCACGTGCGCGCTCTTTGTGCTGGT  540
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Qy   541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCCGCTGTGCCACCAGCTCGGCGCTGCCAC  600
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Db   541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCCGCTGTGCCACCAGCTCGGCGCTGCCAC  600
Qy   601 TCAGGCCCGCCCCCGCCCACACGTCAGTGGCGTCGAAGGCGTCTGGGATGCGAACGGGC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCAGGCCCGCCCCCGCCCACACGTCAGTGGCGTCGAAGGCGTCTGGGATGCGAACGGGC  660
Qy   661 CTGGAACCATAGCGTCAGGAGGCCGGGGTCCCCGGGGCCGCAGCCCCGGGGTGCGAG  720
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Qy   721 GAGGCGCGGGGGACAGTCTGCCAGCGAAGTCTGCCGGTTGCCGTGGCGGTCCAGGAC  780
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Db   721 GAGGCGCGGGGGACAGTCTGCCAGCGAAGTCTGCCGGTTGCCGTGGCGGTCCAGGAC  780
Qy   781 TGCCCCTGAGCCGGGACCGGACGGACGCCGTGGGCAGGGTTCTGCACCTGGGGGCCAGGAC  840
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   901 CACCTCTTTGGAGGTGCCCTCTCTGCCACGCGCACGGCCACTCCCACCGTGGGCCGCCA  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CACCTCTTTGGAGGTGCCCTCTCTGCCACGCGCACGGCCACTCCCACCGTGGGCCGCCA  960
Qy   961 GCACCACGCGGGGGCCCCATCCACATCAGCGGCCACCAGTCCCTGGGACACGGCCTTGTCC 1020
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Db   961 GCACCACGCGGGGGCCCCATCCACATCAGCGGCCACCAGTCCCTGGGACACGGCCTTGTCC 1020
Qy  1021-CCCGGTACGCCGTAGCCCTCCTACTCCTGAGGCCCAGCTGACTGGCTCAGGGCTCGCG    1080
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Qy  1081 GCCCTCCTACTCCAGCTCTCAGGGTTCACCTGAGGCCCAGCTGACTGGCGCTCGGAGGGCTCGGA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 GCCCTCCTACTCCAGCTCTCAGGGTTCACCTGAGGCCCAGCTGACTGGCGCTCGGAGGGCTCGGA 1140
Qy  1141 GACCATCTTTCTGGGTTCCAGGCCCTCGGAGCTGCTTGGGAGCTGCTTGGGAACCACGCGCA 1200
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2341 CGTCTCTACCTTGACAGACCTCCAGCCTGGCTGTGGCTCACCTGCAGGA 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CGTCTCTACCTTGACAGACCTCCAGCCTGGCTGTGGCTCACCTGCAGGA 2400

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Qy  2461 CAGTGGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGG 2520
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Db  2461 CAGTGGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGG 2520

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Db  2521 CAAGTCCTACGTCCAGTGCCAGGGATCCCGCAGGGCTTCCATCCTCTCCACGCTGCTCTG 2580

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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CAGCCCTGCTACGGCGACATGGAGAACAAGTGTTTGCGGGGATTCGGCGGGACGGGGCT 2640

Qy  2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTACCCACCGCGAAAAC 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTACCCACCGCGAAAAC 2700

Qy  2701 CTTCCTCAGGACCCTGGTCCGAGGTGTGCGGTGGTGAACTTGCGGAA 2760
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CTTCCTCAGGACCCTGGTCCGAGGTGTGCGGTGGTGAACTTGCGGAA 2760

Qy  2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGCTGGCACGGCTTTTGTTCAGAT 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGCTGGCACGGCTTTTGTTCAGAT 2820

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Qy  2881 GCAGAGCCACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTTCACCTTCAACCG 2940
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Db  2941 CGGCTTCAAGGCTGGAGGAACATGCGCTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000

Qy  3001 TCACAGCCGTGTTCTGGATTTGCGAGGTGAACAGCGTGTGCACCAACATCTA 3060
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Db  3001 TCACAGCCGTGTTCTGGATTTGCGAGGTGAACAGCGTGTGCACCAACATCTA 3060

Qy  3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCACGTGTCTGCTGCAGCTCCCATTTCA 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCACGTGTCTGCTGCAGCTCCCATTTCA 3120

Qy  3121 TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCTCATCTCTTGACACGGCCTCCT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCTCATCTCTTGACACGGCCTCCT 3180

Qy  3181 CTGCTACTCCATCCTGAAAGCCAAGAGACGCAGGGATGCGTCGCTGGGGGCCAAGGGCGCGC 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CTGCTACTCCATCCTGAAAGCCAAGAGACGCAGGGATGCGTCGCTGGGGGCCAAGGGCGCGC 3240

Qy  3241 CGGCCCTTCTGCCCTCCACCCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CGGCCCTTCTGCCCTCCACCCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy  3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGTCACTCAGGACAGCCCAGACGCA 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGTCACTCAGGACAGCCCAGACGCA 3360

Qy  3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTCCCGGGGACGACGCTGACTCAGGACAGCC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTCCCGGGGACGACGCTGACTCAGGACAGCC 3420
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Qy  3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGCAGTTCAAGAACCTCCAGCCTGCCGA 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGCAGTTCAAGAACCTCCAGCCTGCCGA 3480

Qy  3481 GAGCAGACACCAGCAGCCCCGACCCCGTGTCACGCGCGGCTCTACGTCCCGGGAGGGGCGGCC 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GAGCAGACACCAGCAGCCCCGACCCCGTGTCACGCGCGGCTCTACGTCCCGGGAGGGGCGGCC 3540

Qy  3541 CACACCCAGGCCGCCACCGCACCGTGAGGCCTGAGGGTCTGAGGCCTGAGTGGTTGGCCGAGCCTG 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CACACCCAGGCCGCCACCGCACCGTGAGGCCTGAGGGTCTGAGGCCTGAGTGGTTGGCCGAGCCTG 3600

Qy  3601 CATGTCCGGCTGAAGGCTGAGGCTGAGTCCGGCGTGAGCCTGGCCGCTCGGCTCGGCTCCACGGCTC 3660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CATGTCCGGCTGAAGGCTGAGGCTGAGTCCGGCGTGAGCCTGGCCGCTCGGCTCGGCTCCACGGCTT 3660

Qy  3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCACAGGCTGGCGCTCGGCTCGGCTCCACCCCA 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCACAGGCTGGCGCTCGGCTCGGCTCCACCCCA 3720

Qy  3721 GGGCCAGCTTTTCCTCACCTCACCTCCCCAGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GGGCCAGCTTTTCCTCACCTCACCTCCCCAGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780

Qy  3781 CCAGATTCGCCATTGTTCACCCTCCTTGCCTTCCTTGCCTTCCACCCCCACCATCC 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 CCAGATTCGCCATTGTTCACCCTCCTTGCCTTCCTTGCCTTCCACCCCCACCATCC 3840

Qy  3841 AGGTTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGACTGACCAAAGGTGTG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 AGGTTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGACTGACCAAAGGTGTG 3900

Qy  3901 CCCTGTACACAGGCCGAGGACCCTGCACCTGGGGGTCCTGTGGGTCAAATTGGGGG 3960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 CCCTGTACACAGGCCGAGGACCCTGCACCTGGGGGTCCTGTGGGTCAAATTGGGGG 3960

Qy  3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA 4015
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA 4015
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PT New immunogenic polynucleotides or polypeptides useful for diagnosing,
PT preventing and treating cancer expressing CT or CP mRNA antigens, and
PT in virology, immunology, microbiology, molecular biology and
PT recombinant DNA techniques -
XX
PS Claim 1; SEQ ID 817; 207pp; English.
XX
CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present
CC invention. (I) and (II) have cytostatic activity and can be used in gene
CC therapy and vaccines. (I), (II), antibodies and compositions from the
CC present invention are useful for diagnosing, preventing and treating
CC cancer, which expresses CT or CP mRNA antigens. They are useful for
CC stimulating immune response. They can also be useful in virology,
CC immunology, microbiology, molecular biology and recombinant DNA
CC techniques.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4015 BP; 664 A; 1363 C; 1275 G; 713 T; 0 other;

Query Match   100.0%; Score 4013.4; DB 25; Length 4015;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 4014; Conservative   0; Mismatches   0; Indels   1; Gaps   0;

Qy   1 GCAGCGCTGCGTCCGTGCTGCCACGTGGGAAGCCCTGGCCCCGGCCCACCCCGGCCGATGCC   60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCAGCGCTGCGTCCGTGCTGCCACGTGGGAAGCCCTGGCCCCGGCCCACCCCGGCCGATGCC   60

Qy   61 GCGGGCTCCCGGCCGTGCCGCTCCCTGCTGCGCAGGCCCTGGGCCGCTGGCGCGGCCAGGCGCGG 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCGGGCTCCCGGCCGTGCCGCTCCCTGCTGCGCAGGCCCTGGGCCGCTGGCGCGGCCAGGCGCGG 120

Qy   121 GCCGCTGGCCACGTTCGTGCGGCCGCCTGGGCGGCCTGGGCGGCTGGTGCAGCGCGG 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCCGCTGGCCACGTTCGTGCGGCCGCCTGGGCGGCCTGGGCGGCTGGTGCAGCGCGG 180

Qy   181 GGACCCGGCGGCTTTCCGGCGCGCCTGGTGCCCAGTGCCTGTGCGTCGCCTGGGACGC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACCCGGCGGCTTTCCGGCGCGCCTGGTGCCCAGTGCCTGTGCGTCGCCTGGGACGC 240

Qy   241 ACGGCGCGCGCCCCCCGCGCGCCCCCTTCCGCGCCAGTGTCCTGCCTGAAGGAGCTGGTGGC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACGGCGCGCGCCCCCCGCGCGCCCCCTTCCGCGCCAGTGTCCTGCCTGAAGGAGCTGGTGGC 300

Qy   301 CCGAGTGCTGCAGAGGCGTGGGGAGCGCGGGGCGTGGGGCGTGGGGAGCGCGG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGAGTGCTGCAGAGGCGTGGGGAGCGCGGGGCGTGGGGCGTGGGGAGCGCGG 360

Qy   361 GCTGCTGGACGGGGCCCGGGGGCCCCCGGGGCCTTCACCACCAGCGTGCGCAGCTA 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCTGCTGGACGGGGCCCGGGGGCCCCCGGGGCCTTCACCACCAGCGTGCGCAGCTA 420

Qy   421 CCTGCCAACACGGTGACCGACGCTGCCGGGGAGCGGGGCGTGGGGCTGCTGCGCG 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTGCCAACACGGTGACCGACGCTGCCGGGGAGCGGGGCGTGGGGCTGCTGCGCG 480

Qy   481 CCGGCTGGGCGACGACGCTGGTTCACCTGCTGCACCTGCTGCTCTTTGTGCTGGT 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCGGCTGGGCGACGACGCTGGTTCACCTGCTGCACCTGCTGCTCTTTGTGCTGGT 540

Qy   541 GGCTCCCAGCTGCGCCTACCAGGTGCGCGGGGCCCGCGTCTGCCGCGCTGCCGCCAC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCTCCCAGCTGCGCCTACCAGGTGCGCGGGGCCCGCGTCTACCAGCGCCGCCCAC 600

Qy   601 TCAGGCCCGCCCCCGCCACCACGCTAGTGACCCGCGTCTGGGATGCGGAACGGGC 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCAGGCCCGCCCCCGCCACCACGCTAGTGACCCGCGTCTGGGATGCGGAACGGGC 660

Qy   661 CTGGAACCATAGCGTCAGGGAGGGCTCAGGAGGGCCGGCGGGGTCCCCCTGGGCCTGCCAGCCCGGCCGGTGCGAG 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGGAACCATAGCGTCAGGGAGGGCTCAGGAGGGCCGGCGGGGTCCCCCTGGGCCTGCCAGCCCGGCCGGTGCGAG 720

Qy   721 GAGGCCGGGGGGGGGGGCAGTGCCAGCGCCGAAGTCTGCCGTTGCCGAGAGGAGGCCCAGGCGGCTGGCGC 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GAGGCCGGGGGGGGGGGCAGTGCCAGCGCCGAAGTCTGCCGTTGCCGAGAGGAGGCCCAGGCGGCTGGCGC 780

Qy   781 TGCCCCTGAGCCGGAGCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGCCCGGGCCAGGAC 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGCCCCTGAGCCGGAGCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGCCCGGGCCAGGAC 840

Qy   841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGCACGCGCCACTCCCACCATCCGTGGGCCGCCA 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGCACGCGCCACTCCCACCATCCGTGGGCCGCCA 900

Qy   901 CACCTCTTTGGAGGGTGCGCTCTGGCACGCGCCACTCCCTGGCACGCGCCGTTGTCC 960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CACCTCTTTGGAGGGTGCGCTCTGGCACGCGCCACTCCCTGGCACGCGCCGTTGTCC 960

Qy   961 GCACCACGCGGGGCCCCCATCCACATCGCGGCCACCAGTCCCTGGCACGCGCCTTGTCC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GCACCACGCGGGGCCCCCATCCACATCGCGGCCACCAGTCCCTGGGACACGCGCCTTGTCC 1020

Qy   1021 CCCGGGTACGGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCAGCTCGCG 1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCCGGTGTACGGCCGAGACCAAGCACTTCCTCTACTCCTCAGGGACAAGGAGCAGCAGCTCG 1080

Qy   1081 GCCCTCCTTCCTACTCAGCTCTCGAGGCCCAGCTGGCGCTGGACTGGCGCTCGGAGGCTCGTGA 1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCCCTCCTTCCTACTCAGCTCTCGAGGCCCAGCTGGCGCTGGACTGGCGCTCGGAGGCTCGTGGA 1140

Qy   1141 GACCATCTTCTGGGTTCCAGGCCTGGATGCGCCGGCCACTACCGGCGCAGGTGCT 1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GACCATCTTCTGGGTTCCAGGCCTGGATGCGCCGGCCACTACCGGCGCAGGTGCT 1200

Qy   1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCGGTTTCTGGAGCTGCTTGGGAACCAGCGGCA 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCGGTTTCTGGAGCTGCTTGGGAACCAGCGGCA 1260

Qy   1261 GTGCCCCTACGGGGTGCTCCTCAAGAGCCACTGCCCGTCGCCCGCTGGGGACGGC 1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGCCCCTACGGGGTGCTCCTCAAGAGCCACTGCCCGTCGCCCGCTGGGGACGGC 1320

Qy   1321 AGCCGGTGCTGTGTGCCCGGGAGGAGGCTCGTGCCTGCCAGTGTCCTGCCCTGAAGGAGGAGGA 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGCCGGTGTCTGTGTGCCCGGGAGGAGGCTCGTGCCTGCCAGTGTCCTGCCCTGAAGGAGGAGGA 1380

Qy   1381 CACAGACCCCCGTCGCCTGGTGCAGCGTGCCGGGGAAGAACGTGCCCTGGCCTTCGCC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CACAGACCCCCGTCGCCTGGTGCAGCGTGCCGGGGAAGAACGTGCCCTGGCCTTCGC 1440

Qy   1441 CGGCTTGCGGACGGGGGCCCCCGGGGGGGGCCCCCCCCAGGCCTCTGGGCGCTCTGGGGCTCCAGGCA 1500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CGGCTTGCGGACGGGGGCCCCCGGGGGGGGCCCCCCCCAGGCCTCTGGGCGCTCTGGGGCTCCAGGCA 1500

Qy   1501 CAACGAACGCCGCTTCCTCAGGGACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CAACGAACGCCGCTTCCTCAGGGACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

Qy   1561 GCTCTCGCTGACGAGCTGGAGATGAGCGTCCGGGACTGCGTTGGCTGCGTTGCCCAG 1620
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GCTCTCGCTGACGAGCTGGAGATGAGCGTCCGGGACTGCGTTGGCTGCGTTGCCCAG 1620

Qy   1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGATCCTGGC 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGCCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680

Qy   1681 CAAGTTCCTGCCTGACTGGTGTAGTGACCGTCTGGGATGTGACGGGC 1740
             |||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CAAGTTCCTGCCTGACTGGTGTAGTGACCGTCTGGGATGTGACGGGC 1740

Qy   1741 TGTCACCGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGCTGGAG 1800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 TGTCACCGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGCTGGAG 1800

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Qy  1801 CAAGTTGCAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTGTC 1860
         ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860

Qy  1861 GGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCCGGCGCCCGCCCTGCTGACGACTCCG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCCGGCGCCCGCCCTGCTGACGACTCCG 1920

Qy  1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTCGGGAGC 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTCGGGAGC 1980

Qy  1981 CAGAACGTTCCCAGAGAAAAGAGGGCCAGCCGTCTCACCTGAGGGTGAAGGCACTGTT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CAGAACGTTCCCAGAGAAAAGAGGGCCAGCCGTCTCACCTGAGGGTGAAGGCACTGTT 2040

Qy  2041 CAGCGTGCTCAACTACGAGCGCGGCCTGGCCCTTCGTGCGCCCAGGCCCTCCTGCTGTGGG 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 CAGCGTGCTCAACTACGAGCGCGGCCTGGCCCTTCGTGCGCCCAGGCCCTCCTGCTGTGGG 2100

Qy  2101 CCTGGACGATATCCCACAGGGCCTGGCCGTGCGGCCCCAGACCC 2160
         ||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCTGGACGATATCCCACAGGGCCTGGCCGTGCGGCCCCAGACCC 2160

Qy  2161 GCCGGCCTGAGCTGTACTTTGTCAAGGTGGATGCAGGGCCGCGTACGACACCATCCCCA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCGGCCTGAGCTGTACTTTGTCAAGGTGGATGCAGGGCCGCGTACGACACCATCCCCA 2220

Qy  2221 GGACAGGCTCACGGAGTCATCGCCAGCATCAAAACCCAGAAACACGTACTACTGCGTGCG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GGACAGGCTCACGGAGTCATCGCCAGCATCAAAACCCAGAAACACGTACTACTGCGTGCG 2280

Qy  2281 TCGGTATGCCGTGGTCCAGAAGGCACGTCCCGCAAGGCCTTCAAGAGCA 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TCGGTATGCCGTGGTCCAGAAGGCACGTCCCGCAAGGCCTTCAAGAGCA 2340

Qy  2341 CGTCTCTACCTTGACAGACCTTCGTGCTCACTGCAGGA 2400
         ||||||||||||||||||||||||||||||||||||||
Db  2341 CGTCTCTACCTTGACAGACCTTCGTGCTCACTGCAGGA 2400

Qy  2401 GACCAGCCCGTCGAGGGATGCGTCGTCATCGAGCAGAGCTCCTGGAATGAGGCCCAG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GACCAGCCCGTCGAGGGATGCGTCGTCATCGAGCAGAGCTCCTGGAATGAGGCCCAG 2460

Qy  2461 CAGTGGCCTCTTCGACGTCTTCATGTGCCACCACCACCTGGGGG 2520
         ||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGTGGCCTCTTCGACGTCTTCATGTGCCACCACCACCTGGGGG 2520

Qy  2521 CAAGTCCTACGTCCAGTGCCCAGGGATCCCATCCTGCTCCACGCTGCTCTG 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CAAGTCCTACGTCCAGTGCCCAGGGATCCCATCCTGCTCCACGCTGCTCTG 2580

Qy  2581 CAGCCTGTCTACGGCGACATGTGTTGCGGGGATTCGGCGGGACGGGGCT 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CAGCCTGTCTACGGCGACATGTGTTGCGGGGATTCGGCGGGACGGGGCT 2640

Qy  2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCACCGGAAAAC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCACCGGAAAAC 2700

Qy  2701 CTTCCTCAGGACCCTGTCCCGAGTGTCCCGAGTATTGGCTGCGTGTGTGACTTGCGGAA 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CTTCCTCAGGACCCTGTCCCGAGTGTCCCGAGTATTGGCTGCGTGTGTGACTTGCGGAA 2760

Qy  2761 GACAGTGGTGACTTCCCTGTAGAAGACGAGGCCCTGGTGGCACGGCTTTTGTTGTTCAGAT 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 GACAGTGGTGACTTCCCTGTAGAAGACGAGGCCCTGGTGGCACGGCTTTTGTTGTTCAGAT 2820

Qy  2821 GCCGGCCCACCGGCCTATTCCCCTGGTGCGCTGCTGTCCTGCGGGACCCCTGGAGGT 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 GCCGGCCCACCGGCCTATTCCCCTGGTGCGCTGCTGTCCTGCGGGACCCCTGGAGGT 2880

Qy  2881 GCAGAGCGACTACTCCCGGACCTATGCCCGGACCTCCATCAGAGACGCCAGTTCAACCG 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 GCAGAGCGACTACTCCCGGACCTATGCCCGGACCTCCATCAGAGACGCCAGTTCAACCG 2940
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Qy  2881 GCAGAGCGACTACTCCCGGACCTATGCCCGGACCTCCATCAGAGACGCCAGTTCAACCG 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 GCAGAGCGACTACTCCCGGACCTATGCCCGGACCTCCATCAGAGACGCCAGTTCAACCG 2940

Qy  2941 CGGCTTCAAGGCTGGGAGGAACTCGTCGAGGAGAACTCTTGGGGTCTTGCGGCTGAAGTG 3000
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Db  2941 CGGCTTCAAGGCTGGGAGGAACTCGTCGAGGAGAACTCTTGGGGTCTTGCGGCTGAAGTG 3000

Qy  3001 TCACAGCCTGTTCTGGATTGCAGGTGAACAGCCTCCAACAGCGTGTCACCAACATCTA 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 TCACAGCCTGTTCTGGATTGCAGGTGAACAGCCTCCAACAGCGTGTCACCAACATCTA 3060

Qy  3061 CAAGATCCCTCCTGCTGCAGCCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 CAAGATCCCTCCTGCTGCAGCCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120

Qy  3121 TCAGCAAGTTTGAAGAGAACCCCCACATTTTCCTGCCGCGTCATCTCGACACTCTGACACGCCCT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 TCAGCAAGTTTGGAAGAACCCCACATTTTCCTGCCGCGTCATCTCGACGGTCACGGCGGCCCCT 3180

Qy  3181 CTGCTACTCCATCCTGAAAGCCAAGAACCAGGAGATGTCGCTGGGGGCCAGCCAACCCGGC 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CTGCTACTCCATCCTGAAAGCCAAGAACCAGGAGATGTCGCTGGGGGCCAGCCAACCCGGC 3240

Qy  3241 CGGGCCCTGCCCTGCCCTCCGAGCCCGTGCAGTTGCCGTGGTCGTGCCACCAAGCATTCTGCTCAAGCT 3300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CGGGCCCTGCCCTGCCCTCCGAGCCCGTGCAGTTGCCGTGGTCGTGCCACCAAGCATTCTGCTCAAGCT 3300

Qy  3301 GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA 3360

Qy  3361 GCTGAGTCGGAAGCTCCCGGAACGCTGACGCTGCCCTGACGCTGACTGCTGGAGGCCGCAGCCAACCCGGC 3420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 GCTGAGTCGGAAGCTCCCGGAACGCTGACGCTGCCCTGACGCTGACTGCTGGAGGCCGCAGCCAACCCGGC 3420

Qy  3421 ACTCCCTCAGACTTCAAGACCATCCTGGCTCACACTCGAGGA 3480
         ||||||||||||||||||||||||||||||||||||||||||
Db  3421 ACTCCCTCAGACTTCAAGACCATCCTGGCTCACACTCGAGGA 3480

Qy  3481 GAGCAGACACCAGCAGCCCTGTCACGCCGGGCCTCACGTCCCGGGCCAGGGAGGGGCGGCC 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GAGCAGACACCAGCAGCCCTGTCACGCCGGGCCTCACGTCCCGGGCCAGGGAGGGGCGGCC 3540

Qy  3541 CACACCCAGGCCGCCACCGCCACCGGCCTGGAGTCTGAGGCCTGAGTGAGTGTTGGCCGGAGGCCTG 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CACACCCAGGCCGCCACCGCCACCGGCCTGGAGTCTGAGGCCTGAGTGAGTGTTGGCCGGAGGCCTG 3600

Qy  3601 CATGTCCGGCTGAAGGCTGAGGCTGAGTGTCGGCTGAGGCGAGTGTCGAGCGAGCCAAGGGCT 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 CATGTCCGGCTGAAGGCTGAGGCTGAGTGTCGGCTGAGGCGAGTGTCGAGCGAGCCAAGGGCT 3660

Qy  3661 GAGTGTCAGCACACCTGTCTTCACTTCCCGCTGGCTGCGCTGCGCTCGGCTGCTGCGGCTCCCCA 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GAGTGTCAGCACACCTGTCTTCACTTCCCACTTCACTTCCCGCTGGCTGCGCTCGGCTGCTGCGGCTCACCCCA 3720

Qy  3721 GGGCCAGCTTTTCCTCACCCCGGCTTCGCCCTTCGCCCCTCCTTTGCCTTCCCCACCATCC 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 GGGCCAGCTTTTCCTCACCCCGGCTTCGCCCTTCGCCCCTCCTTTGCCTTCCCCACCATCC 3780

Qy  3781 CCAGATTCGCATTGTTCACCCTGAGTTGGCTGCTGTGAACTTGCGGAA 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 CCAGATTCGCATTGTTCACCCTGAGTTGGCTGCTGTGAACTTGCGGAA 3840

Qy  3841 AGGTGGAGACCCTGAGAAGGCCGAGAGGACCCTCGGGAATTTGGAGTTTGGACCAAAGGTGTG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 AGGTGGAGACCCTGAGAAGGCCGAGAGGACCCTCGGGAATTTGGAGTTTGGACCAAAGGTGTG 3900

Qy  3901 CCCTGTACAACAGGCGAGAGACCCTGCCTTCGCCTTCCTTGCCTTCCACCCCCCACCATCC 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 CCCTGTACAACAGGCGAGAGACCCTGCCTTCGCCTTCCTTGCCTTCCACCCCCCACCATCC 3960

Qy  3961 GAGGTGCTGTGGGAGTAAATATGCAGTAAATATGAGTTTTTCAGTTTGAAAAAA 4015
         ||||||||||||||||||||||||||||||||||||
```

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Db  3961 GAGGTGCTGCTGTGGGAGTAAAAAAACTGAATATATGAGTTTTTCAGTTTTGAAAAAA 4015
```

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RESULT 12
AAV60320
ID   AAV60320 standard; cDNA; 4023 BP.
XX
AC   AAV60320;
XX
DT   04-DEC-1998 (first entry)
XX
DE   Human telomerase gene referred to as hEST2.
XX
KW   Catalytic subunit; human; telomerase; telomere maintenance;
KW   diagnosis; treatment; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             59..3458
FT                   /*tag= a
XX
PN   WO9837181-A2.
XX
PD   27-AUG-1998.
XX
PF   20-FEB-1998;  98WO-US03404.
XX
PR   30-OCT-1997;  97US-0064322.
PR   20-FEB-1997;  97US-0038750.
PR   20-MAY-1997;  97US-0047151.
PR   01-AUG-1997;  97US-0054549.
PR   14-AUG-1997;  97US-0055762.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Counter CM, Meyerson M, Weinberg RA;
XX
DR   WPI; 1998-495367/42.
DR   P-PSDB; AAW71376.
XX
PT   New isolated human telomerase catalytic sub-unit gene - used to
PT   develop products for increasing or reducing the life span of cells
PT   such as cancer cells or transformed cells
XX
PS   Claim 5; Fig 5A-B; 96pp; English.
XX
CC   The present sequence encodes the catalytic subunit of a human
CC   telomerase holoenzyme. Disruption of the telomerase gene alters
CC   telomere maintenance. The DNA is essential for telomerase activity,
CC   and the protein is physically associated with telomerase and a
CC   constituent of active telomerase complex. The products can be used
CC   for increasing or reducing the lifespan of cells such as cancer cells
CC   or transformed cells. They can also be used in the diagnosis and
CC   treatment of malignancies. In addition, cells with a longer lifespan
CC   can be transplanted into or grafted onto an individual (e.g. as skin
CC   grafts, as systems for delivery of therapeutic proteins, such as hormones
CC   and enzymes), to whom they provide therapeutic benefit.
XX
SQ   Sequence 4023 BP; 668 A; 1363 C; 1277 G; 715 T; 0 other;
```

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Query Match          99.9%; Score 4011.8; DB 19; Length 4023;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4013;  Conservative  0;  Mismatches 2;  Indels 0;  Gaps 0;

Qy    1 GCAGGCCTGCCTGCTCCCCGCTGCCGAGCCGTGGCCCCGGCGATGCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    4 GCAGGCCTGCCTGCTCCCCGCTGCCGAGCCGTGGCCCCGGCGATGCC 63

Qy   61 GCGGCCTGCCTCCCCGCTGCCGAGCCGTGGCCTCCTGCTGCGGCCACTACCGGAGGTGCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 GCGGCCTGCCTCCCCGCTGCCGAGCCGTGGCCTCCTGCTGCGGCCACTACCGGAGGTGCT 123

Qy  121 GCGGCTGCCACGTTCGTGCTGCGCGGCCTGGCGGCCTGGGCGTGCTCGGTGCAGCGCGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  124 GCGGCTGCCACGTTCGTGCTGCGCGGCCTGGCGGCCTGGGCGTGCTCGGTGCAGCGCGG 183

Qy  181 GGACCGGCGGCTTCCCGCGGCTGGTGGCCGCCAGTGCCTGGTGTGCGTGCCCTGGGACGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  184 GGACCGGCGGCTTCCCGCGGCTGGTGGCCGCCAGTGCCTGGTGTGCGTGCCCTGGGACGC 243

Qy  241 ACGGCGCGCCCCCGCCCCGCGCCCCTTCCGCCCAGTGTCCTGCTGCTGAAGGAGCTGGTGGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  244 ACGGCGCGCCCCCGCCCCGCGCCCCTTCCGCCCAGTGTCCTGCTGCTGAAGGAGCTGGTGGC 303

Qy  301 CCGAGTGCTGCAGAGGTGTGCGAGCCGGCGGCGCCGAAGAACGTCTGGCCTTCGGCTTCCC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  304 CCGAGTGCTGCAGAGGTGTGCGAGCCGGCGGCGCCGAAGAACGTCTGGCCTTCGGCTTCGC 363

Qy  361 GCTGCTGACGGGGCCCCGCCGGGGCCCCGAGGGCCTTCACCACCAGCGTGCGCAGCTA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  364 GCTGCTGACGGGGCCCCGCCGGGGCCCCGAGGGCCTTCACCACCAGCGTGCGCAGCTA 423

Qy  421 CCTGCCCAACACGTGACCGACACGTGCGGGGGCGGGGGGAGCGGGGCGTGCTGCTGCGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  424 CCTGCCCAACACGTGACCGACACGTGCGGGGGCGGGGGGAGCGGGGCGTGCTGCTGCGG 483

Qy  481 CCGCGTGGGCGACGACGTGCTGTTCACCTGCGTGCGCGGCCTGCTCTTTGTGCTGTGT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  484 CCGCGTGGGCGACGACGTGCTGTTCACCTGCGTGCGCGGCCTGCTCTTTGTGCTGTGT 543

Qy  541 GGCTCCAGCTGCGGCCTACCAGTGTGCGGGCCGCTGTACCAGCTCGGCGGCCTGCCAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  544 GGCTCCAGCTGCGGCCTACCAGTGTGCGGGCCGCTGTACCAGCTCGGCGGCCTGCCAC 603

Qy  601 TCAGGGCCCGGCCCCCGCCACACGGTAGTGGACCCCGAAGGCGGTCTGGGATGCGAACGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  604 TCAGGGCCCGGCCCCCGCCACACGGTAGTGGACCCCGAAGGCGGTCTGGGATGCGAACGGGC 663

Qy  661 CTGGAACCATAGCGTCAGGGAGGCCGGGGGTCCCCTGGGGCTCCCCGGGGTGCGGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  664 CTGGAACCATAGCGTCAGGGAGGCCGGGGGTCCCCTGGGGCTCCCCGGGGTGCGGAG 723

Qy  721 GAGGCGCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGGCTGGCGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  724 GAGGCGCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGGCTGGCGC 783

Qy  781 TGCCCCTGAGCCCGAGCGACGCCCGTTGGCCAGGGGTCCTGGGCCCACCCGGGCGAGAC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  784 TGCCCCTGAGCCCGAGCGACGCCCGTTGGCCAGGGGTCCTGGGCCCACCCGGGCAGGAC 843

Qy  841 GGGTGGACCGAGTGACCGTGGTTCTGTGTGGTCACCTGCCAGACCCGCCGAAGAAGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  844 GCGTGGACCGAGTGACCGTGGTTCTGTGTGGTCACCTGCCAGACCCGCCGAAGAAGC 903

Qy  901 CACCTCTTTGGAGGGTGGCTCTCTGGCACGCGCCACTCCACCATCGTGGGCCGCCA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  904 CACCTCTTTGGAGGGTGGCTCTCTGAGCACGCGCCACTCCACCATCGTGGGCCGCCA 963

Qy  961 GCACCACGCGGGCCCCATCCAGCTCCCTGGGACGCCCCAGTGTCCCTTGTCC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  964 GCACCACGCGGGCCCCATCCAGCTCCCTGGGACACGCCCAGTGTCCTTGTCC 1023

Qy 1021 CCCGGTGACGCCGAGACCAAGCACTTCCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1024 CCCGGTGACGCCGAGACCAAGCACTTCCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1083

Qy 1081 GCCCTCCTTCTCTACTCAGCTCTGAGGCCGTGACTGGCGCTCGGAGGCTCGTGA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1084 GCCCTCCTTCTCTACTCAGCTCTCGAGGCCGTGACTGGCGCTCGGAGGCTCGTGA 1143

Qy 1141 GACCATCTTTCTGGGTTCCAGGGATGCCAGGGACTCCCCGCAGTTGCCCCGGCCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1144 GACCATCTTTCTGGGTTCCAGGGATGCCAGGGACTCCCCGCAGTTGCCCCGGCCT 1203

Qy 1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAACCACGCGCA 1260
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Right column:

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Db  2284  TCGGTATGCGTGGTCCAGAAGGCCGCCCATGGCACGTCCGAAGGCCTCAAGAGCCA  2343
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2341  CGTCTCTACCTTGACAGACCTCCAGCGTTCGTGGCTCACCTGCAGGA  2400
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  2344  CGTCTCTACCTTGACAGACCTCCAGCGTTCGTGGCTCACCTGCAGGA  2403

Qy  2401  GACCAGCGCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG  2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2404  GACCAGCGCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG  2463

Qy  2461  CAGTGGCCTCTTCCTTGACGTTCTCCTACGCGTTCATCGTGCCACCAGCCGTGCGATCAGGGG  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2464  CAGTGGCCTCTTCCTTGACGTTCTCCTACGCGTTCATCGTGCCACCAGCCGTGCGATCAGGGG  2523

Qy  2521  CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCCACGCTGCCTCTG  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2524  CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCCACGCTGCCTCTG  2583

Qy  2581  CAGCCTGTTGCTACGGCCGCACATGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGGCT  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2584  CAGCCTGTTGCTACGGCCGCACATGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGGCT  2643

Qy  2641  GCTCCTGCGGTTTGGTTGGTGGATGATTCTTGTGGTGACACCTCACCTCACCCACGCGAAAAC  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2644  GCTCCTGCGGTTTGGTTGGTGGATGATTCTTGTGGTGACACCTCACCTCACCCACGCGAAAAC  2703

Qy  2701  CTTCCTCAGGACCCTGGTCCGAGTGTCCCGAGTGTCCCGAGTGTGGTGGTGAACTTGCGGAA  2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2704  CTTCCTCAGGACCCTGGTCCGAGTGTCCCGAGTGTCCCGAGTGTGGTGGTGAACTTGCGGAA  2763

Qy  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT  2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2764  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT  2823

Qy  2821  GCCGGCCCACGGCCTATTCCCCTGCCTGCTGCCTGCTGCTGGATACCCGGAGGT  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2824  GCCGGCCCACGGCCTATTCCCCTGCCTGCTGCCTGCTGCTGGATACCCGGAGGT  2883

Qy  2881  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTTTGGGGTCTTGCGGCTGAAGTG  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2884  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTTTGGGGTCTTGCGGCTGAAGTG  2943

Qy  2941  CGGCTTCAAGGCTGGGAGGAACATGCGTCGCCAAACTCTTTCGCGCTGAGACTCCG  3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2944  CGGCTTCAAGGCTGGGAGGAACATGCGTCGCCAAACTCTTTCGCGCTGAGACTCCG  3003

Qy  3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGTGTGACCAACATCTA  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3004  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGTGTGACCAACATCTA  3063

Qy  3061  CAAGATCTCCTCGCTGCTCAGGTTCACGGCATGTGCTGCGAGCTCCATTCA  3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3064  CAAGATCTCCTCGCTGCTCAGGTTCACGGCATGTGCTGCGAGCTCCATTTCA  3123

Qy  3121  TCAGCAAGTTGGAAGAACCCCACCATTTTCCTGCGCGTCATCTCTGACGCGTCCCT  3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3124  TCAGCAAGTTGGAAGAACCCCACCATTTTCCTGCGCGTCATCTCTGACGCGTCCCT  3183

Qy  3181  CTGCTACTCCATCCTGAAAGCCAAGAACCGCAGGATGTGCTGGGGGCCCAAGGGCCGC  3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3184  CTGCTACTCCATCCTGAAAGCCAAGAACCGCAGGATGTGCTGGGGGCCCAAGGGCCGC  3243

Qy  3241  CGGCCCCTGCTCCTGCGCCTCCGGAGCCGTGCAGTGGCTGTGCTGCCACCAAGCATTCCTGCTCAAGCT  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3244  CGGCCCCTGCTCCTGCGCCTCCGGAGCCGTGCAGTGGCTGTGCTGCCACCAAGCATTCCTGCTCAAGCT  3303

Qy  3301  GACTCGACACCGTGTCACTCGACGTGCCCACTCCTCGGGGTCACTCAGGACAGCCCAGACGCA  3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3304  GACTCGACACCGTGTCACTCGACGTGCCCACTCCTCGGGGTCACTCAGGACAGCCCAGACGCA  3363

Qy  3361  GCTGAGTCGGAAGCTCCCGGGACGACCCGGGACCGCAGCCGCCAACCCGGC  3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3364  GCTGAGTCGGAAGCTCCCGGGACGACCCGGGACCGCAGCCGCCAACCCGGC  3423
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Left column:

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Db        ||||||||||||||||||||||||||||||||||||||||||||||||||
          GCCCCAGCGCTACTGGCAAATGCGGCCCGTGTTCTGGAGCTGCTTGGGACCACGCGGCA  1263
Qy  1261  GTGCCCCTACGGGGTGCTGTGTCGCCCGGGAGAAGCCCAGAGGCTCTGTGTGGGCCCCGAGGAGGAGGA  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1264  GTGCCCCTACGGGGTGCTGTGTCGCCCGGGAGAAGCCCAGAGGCTCTGTGTGGGCCCCGAGGAGGAGGA  1323

Qy  1321  AGCCGGTGTCTGTGCCGGGAGAAGCCCAGAGGCTCTGTGTGGGCCCCGAGGAGGAGGA  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1324  AGCCGGTGTCTGTGCCGGGAGAAGCCCAGAGGCTCTGTGTGGGCCCCGAGGAGGAGGA  1383

Qy  1381  CACAGACCCCCGTCGCCTGGTCAGCGTCGTCCGCCAGCAGCAGCCCCTGGCCAGGTGTA  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1384  CACAGACCCCCGTCGCCTGGTCAGCGTCGTCCGCCAGCAGCAGCCCCTGGCCAGGTGTA  1443

Qy  1441  CGGCTTCGTGCGGCCCGCCTGCCTGCGCCCGGCTGGTGCCCCCAGGGCTCCTGGGGCTCCTCCAGGCA  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1444  CGGCTTCGTGCGGCCCGCCTGCCTGCGCCCGGCTGGTGCCCCCAGGGCTCCTGGGGCTCCTCCAGGCA  1503

Qy  1501  CAACGAACGCGCCTTCTCCAGGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1504  CAACGAACGCGCCTTCTCCAGGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1563

Qy  1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGACTGCCGTTGGCTGCGCAG  1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1564  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGACTGCCGTTGGCTGCGCAG  1623

Qy  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCGCACCGTCTGCGTGAGGGAGATCCTGGC  1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1624  GAGCCCAGGGGTTGGCTGTGTTCCGGCGCACCGTCTGCGTGAGGGAGATCCTGGC  1683

Qy  1681  CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCTGCGTGCTTCGTCTTTCTTTTA  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1684  CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCTGCGTGCTTCGTCTTTCTTTTA  1743

Qy  1741  TGTCACGGAGACCACGTTTCAAAAGAACAGGCCTCTTTTCTACCGGAAGAGTGTCTGGAG  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1744  TGTCACGGAGACCACGTTTCAAAAGAACAGGCCTCTTTTCTACCGGAAGAGTGTCTGGAG  1803

Qy  1801  CAAGTTGCAAAGCATTGAAATCAGACAGCACTTGAAGAGGGTGCAGTGCAGTGTC  1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1804  CAAGTTGCAAAGCATTGAAATCAGACAGCACTTGAAGAGGGTGCAGTGCAGTGTC  1863

Qy  1861  GGAAGCAGAGGTCAGGCAGCATCGGGAGCGGCGGCCCGCCCACCTTCGTGACTCCGGAGTCCGACTCCG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1864  GGAAGCAGAGGTCAGGCAGCATCGGGAGCGGCGGCCCGCCCACCTTCGTGACTCCGGAGTCCGACTCCG  1923

Qy  1921  CTTCATCCCCAAGCCTGACGGGCCTGCGGCCGATTGTGAACATGGACTACGTCCTGGGAGC  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1924  CTTCATCCCCAAGCCTGACGGGCCTGCGGCCGATTGTGAACATGGACTACGTCCTGGGAGC  1983

Qy  1981  CAGAACGTTCCCAGAGAGAAAGAGAGGGGCCGGAAGGTGAAGGCACTGTT  2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1984  CAGAACGTTCCCAGAGAGAAAGAGAGGGGCCGGAAGGTGAAGGCACTGTT  2043

Qy  2041  CAGCAGGCGTCAACTAGGCGAGGTCATCGCGAGGTCATCGCCTCGGGCTCTGTGCTGGGG  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2044  CAGCAGGCGTCAACTAGGCGAGGTCATCGCGAGGTCATCGCCTCGGGCTCTGTGCTGGGG  2103

Qy  2101  CCTGGACGATATCCACAGGCCCTGACGGGCTGCGGCCGACCTCGTTCGTGCCTGCTGCCTGCGGCCCGTGTGCCTGCTGCCTGCGGCCCAGGACCC  2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2104  CCTGGACGATATCCACAGGCCCTGACGGGCTGCGGCCGACCTCGTTCGTGCCTGCTGCCTGCGGCCCGTGTGCCTGCTGCCTGCGGCCCAGGACCC  2163

Qy  2161  GCCGGCCTGAGCTGTACTTTGTCAAGGTGATGTGAAGGTGATGTGACGGGTGATGAGGTGAAGGCACCATCCCCCA  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2164  GCCGGCCTGAGCTGTACTTTGTCAAGGTGATGTGAAGGTGATGTGACGGGTGATGAGGTGAAGGCACCATCCCCCA  2223

Qy  2221  GGACAGGTTCCGGACAGAGAAGAGAGGCGGCGGCCGCGGCCGCGGCCCCCAGAGCCCAGAGCCGCG  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2224  GGACAGGTTCCGGACAGAGAAGAGAGGCGGCGGCCGCGGCCGCGGCCCCCAGAGCCCAGAGCCGCG  2283

Qy  2281  TCGGTATGCGTGGTCCAGAAGGCCGCCCATGGCACGTCCGAAGGCCTCAAGAGCCA  2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3421  ACTGCCTCAGACTTCAAGACCATCCTGGACTGAGGCCACCCGCCCACAGCCAGGCCGA  3480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3424  ACTGCCTCAGACTTCAAGACCATCCTGGACTGAGGCCACCCGCCCACAGCCAGGCCGA  3483

Qy   3481  GAGCAGACACCAGCAGCCCTGTCACGCCCGGCTCTACGTCCCAGGGAGGGAGGGCGGCC  3540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3484  GAGCAGACACCAGCAGCCCTGTCACGCCCGGCTCTACGTCCCAGGGAGGGAGGGCGGCC  3543

Qy   3541  CACACCCAGGCCCGCCACCGCCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCAGGCCCTG  3600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3544  CACACCCAGGCCCGCCACCGCCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTG  3603

Qy   3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT  3660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3604  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTCCAGCCAAGGGCT  3663

Qy   3661  GAGTGTCCAGCACACCTGCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCGTCCACCCCA  3720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3664  GAGTGTCCAGCACACCTGCGTCTCACTTCCCCACAGGCTGGCGCTCGGCGTCCACCCCA  3723

Qy   3721  GGGCCAGCAGCTTTTCCTCACCAGGAGCCCGGCTTCACTCCCCACATAGGAATAGTCCATCC  3780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3724  GGGCCAGCGTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC  3783

Qy   3781  CCAGATTCGCCATTGTTCACCCCTCGCCCCTCCTTTGCCTTCCACCCCCACCATCC  3840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3784  CCAGATTCGCCATTGTTCACCCCTCGCCCTCCTTTGCCTTCCACCCCCACCATCC  3843

Qy   3841  AGGTGGAGACCCTGAGAAGGACCCTCTGGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTG  3900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3844  AGGTGGACCCTGAGAAGGACCCTCTGGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTG  3903

Qy   3901  CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGTCCTGTGGGTCAAATTGGGGG  3960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3904  CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGTCCTGTGGGTCAAATTGGGGG  3963

Qy   3961  GAGGTGCTGTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA  4015
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   3964  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAAA  4018
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RESULT 13
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AAV22428
ID   AAV22428   standard; cDNA; 4037 BP.
XX
AC   AAV22428;
XX
DT   13-AUG-1998   (first entry)
XX
DE   Human telomerase reverse transcriptase encoding cDNA refined sequence.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
KW   prognosis; cell proliferation; cancer; ageing; ribonucleoprotein; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            56..3454
FT                  /tag= a
FT                  /product= "telomerase reverse transcriptase"
FT                  /note= "refined sequence"
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-0020890.
XX
PR   14-AUG-1997;   97US-0915503.
PR   01-OCT-1996;   96US-0724643.
PR   18-APR-1997;   97US-0844419.
PR   25-APR-1997;   97US-0846017.
```

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Query Match             99.8%;  Score 4007;  DB 19;  Length 4037;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 4007;  Conservative  4;  Mismatches  4;  Indels  0;  Gaps  0;

Qy    1  GCAGCGCTGCGTCCTGCTGCCACGTGGGAAGCCTGGCCCGGCCCACCCCCGCGAGATGCC  60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  GCAGCGCTGCGTCCTGCTGCCACGTGGGAAGCCTGGCCCGGCCCACCCCCGCGAGATGCC  60

Qy   61  GGGCGGCTCCCCGTGCGCCTGCCAGCCGCTGCGCTCCCTGCGCCAGCCACTACCGCGAGGCTGCT  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GGGCGGCTCCCCGTGCGCCTGCCAGCCGCTGCGCTCCCTGCGCCAGCCACTACCGCGAGGTGCT  120

Qy  121  GCCGCTGCCACGTGCGCAGGCTCGGCGGCGGCCCTGGGCGGGCCCTGGCGGCTGGGTGCAGCGCGGG  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GCCGCTGCCACGTTCGTGCGCAGGCTCGGCGGCGGCCCTGGGCGGGCCCTGGCGGCTGGGTGCAGCGCGGG  180

Qy  181  GGACCCGGCGGCTTTCCGCCGCTTCCGGCAGCTGCTCCGGTGCCCTGGTGTGCCCTGGGACGC  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  GGACCCGGCGGCTTTCCGCCGCTTCCGGCAGCTGCTCCGGTGCCCTGGTGTGCCCTGGGACGC  240

Qy  241  ACGGGCCCGCCCCCGCCCCCGCCCCTCCTTCCGCCGCCGCGCCCTGGTGTCCTGCCTGAGGCCTGGTGGCC  300
         ||||||||||||||||||||| ||||||||| |||||||||||||||||||||||||||
Db  241  AGCCCGCCCCCGCCCCCGCCCCCTCCTTCCGCCAGCGTGTCCTGCCTGAGGCCTGGTGTGCC  300

Qy  301  CCGAGTGCTGCAGAGGCTGTGGCGGGGCCCCGGCCGGCGGAAGAACGTGCTGGCCTCGGCTTCGC  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  CCGAGTGCTGCAGAGGCTGTGGCGAGCGCGGGGCCGGCGGAAGAACGTGCTGGCCTTCGGCTTCGC  360

Qy  361  GCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1501 CAACGAACGCCGCTTCCTCAGGAGACCACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 CAACGAACGCCGCTTCCTCAGGAGACCACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

Qy  1561 GCTCTCGCTGCAGGAGCTGACGTGCTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAG 1620
         |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  1561 GCTCTCGCTGCAGGAGCTGACGTGCTGTGTTCGGCGGCTCTTTGCTGGT 1620

Qy  1621 GAGCCCAGGGGTTGGCTGTGTGTTCCGGCCGCCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 GAGCCCAGGGGTTGGCTGTGTGTTCCGGCCGCCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680

Qy  1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGCGAGCTGCTCAGGTCTTCAGGTCTTCTTTTA 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGCTGCGAGCTGCTCAGGTCTTCAGGTCTTCTTTTA 1740

Qy  1741 TGTCACGGAGGACCACGTTTCAAAAGAACAGGCTCTTTTTCTTACCGGCCGAAGAGTGTCTGGAG 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TGTCACGGAGGACCACGTTTCAAAAGAACAGGCTCTTTTTCTTACCGGCCGAAGAGTGTCTGGAG 1800

Qy  1801 CAAGTTGCAAAGATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTC 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 CAAGTTGCAAAGATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTC 1860

Qy  1861 GGAAGCAGAGTCAGGCAGCAGCATCGGGAAGCCAGGCCCGTGCGACGTCCAGACTCCG 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GGAAGCAGAGTCAGGCAGCAGCATCGGGAAGCCAGGCCCGTGCGACGTCCAGACTCCG 1920

Qy  1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGTGGAGC 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGTGGAGC 1980

Qy  1981 CAGAACGTTCCGCAGAGAAAGAGGGCCGAGCCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CAGAACGTTCCGCAGAGAAAGAGGGCCGAGCCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040

Qy  2041 CAGCGTGCTCAACTACGACAGGGCCCGGGCGCCCCTCTGTGCTGGG 2100
         |||||||||||||||||||||||||||||||||||||||||||||
Db  2041 CAGCGTGCTCAACTACGACAGGGCCCGGGCGCCCCTCTGTGCTGGG 2100

Qy  2101 CCTGGACGATATCCACAGGGCCTGCGCCACCTTCGTGCGTGCGGGCCCAGGACCC 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCTGGACGATATCCACAGGGCCTGCGCCACCTTCGTGCGTGCGGGCCCAGGACCC 2160

Qy  2161 GCCGCCTGAGCGTGTACTTTGTCAAGGTGACGTGGATGTGACGGGCGCGTACGACACCATCCCCA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCCCCTGAGCGTGTACTTTGTCAAGGTGACGTGGATGTGACGGGCGCGTACGACACCATCCCCA 2220

Qy  2221 GGACAGGCTCACGGAGGTCATCATCAAACCCCAGAACATCATCAAAACCCAGAACACGTACTGCGTGCG 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GGACAGGCTCACGGAGGTCATCATCAAACCCCAGAACATCATCAAAACCCAGAACACGTACTGCGTGCG 2280

Qy  2281 TCGGTATGCCGTGGTCCAGAAGGCCGCGGACATGGCCAGTCCGGACAGTTCGTGGCTCACCTGCAGGA 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TCGGTATGCCGTGGTCCAGAAGGCCGCGGACATGGCCAGTCCGGACAGTTCGTGGCTCACCTGCAGGA 2340

Qy  2341 CGTCTCTTGACAGACCTCCAGCCGTACATGCGACAGTCCTCGGCTCGTCACCTGCAGTTCGTGGCTCAGGA 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CGTCTCTTGACAGACCTCCAGCCGTACATGCGACAGTCCTCGGCTCGTCACCTGCAGTTCGTGGCTCAGGA 2400

Qy  2401 GACCAGCCCGCCGGATGGCCGTCGTCATCGAGAGCTCCTCCTGAATGAGGCCAGAGAGGA 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GACCAGCCCGCCGGATGGCCGTCGTCATCGAGAGCTCCTCCTGAATGAGGCCAGAGAGGA 2460

Qy  2461 CAGTGGCTCTTCTTCGACGCTTCCATCGTGCGGTGCAGGGTACTCCACCACCGTGCGGGG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGTGGCTCTTCTTCGACGCTTCCATCGTGCGGTGCAGGGTACTCCACCACCGTGCGGGG 2520

Qy  2521 CAAGTCCTACGTCCAGTGCCCAGGGATCCCGGCCTCCTCTCCACGCGTGCTCTG 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CAAGTCCTACGTCCAGTGCCCAGGGATCCCGGCCTCCTCTCCACGCGTGCTCTG 2580
```

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Db   361 GCTGCTGCTGGACGGGGCCCGCGGGGGCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCGTGGGGGCGTGCTGCTGCG 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCGTGGGGGCGTGCTGCTGCG 480

Qy   481 CCGCGTGGGCGACGACGTGCTGTTCACCTGCGTCGCGCGCTTCTTTGTGCGGCTGGT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCGCGTGGGCGACGACGTGCTGTTCACCTGCGTCGCGCGCTTCTTTGTGCGGCTGGT 540

Qy   541 GGCTCCCAGCTGCGCTACCAGGTGTCGCCGCCCGTACCAGCTGCGGCCGGCGCGCCGCCAC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCTCCCAGCTGCGCTACCAGGTGTCGCCGCCCGTACCAGCTGCGGCCGGCGCGCCGCCAC 600

Qy   601 TCAGGCCCGGCCACACGTCGGGGATGGCAGTGGGACCCCGAAGGGCGTCTGGGATGCGGAACGGGC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCAGGCCCCGGCCACACGTCCGGGGATGGCAGTGGGACCCCGAAGGGCGTCTGGGATGCGGAACGGGC 660

Qy   661 CTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCGTGCCCAGCCCCGGGTGCCAG 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCGTGCCCAGCCCCGGGTGCCAG 720

Qy   721 GAGGCGGGGGCAGTGCCAGCGGAGTCTGCCCGTTGCCCAAGAGGCCGGCCAGGCGTGCGC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GAGGCCGCGGGCAGTGCCAGCGGAGTCTGCCCGTTGCCCAAGAGGCCGGCCAGGCGTGCGC 780

Qy   781 TGCCCCTGAGCCGGGAGCCGGACGCCCGGTTGGGCAGGGGTCCTGGGCCCCACCCGGGCAGGAC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGCCCCTGAGCCGGGAGCCGGACGCCCGGTTGGGCAGGGGTCCTGGGCCCCACCCGGGCAGGAC 840

Qy   841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTCACCTGCGTCAGGGCCGAGACCGCCGAAGAAGC 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCGTGGGACCGAGTGACCGTGGTTTCTGTGTGTCACCTGCGTCAGGGCCGAGACCGCCGAAGAAGC 900

Qy   901 CACCTGCTTGGAGGGTGCGCTCTGCGACGCACTCACCATCGCCACTCCACCCATCCGTGGGGCCGGCCA 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CACCTGCTTTGGAGGGGTCGCGCTCTGCGACGCACTCACCATCGCCACTCCACCCATCCGTTGGGCCCGCCA 960

Qy   961 GCACCACGCGGGCCCCCCATCCACATGCGGGCCACAGTCCCTGGGACACGGCCTTGTCC 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GCACCACGCGGGCCCCCCATCCACATCGCGGGCCACAGTCCCTGGGACACGGCCTTGTCC 1020

Qy  1021 CCCGGTGTACGCCGAGACCAAGAGCACTGCGGGCACAGGGAGCAGTGCAGCTGCG 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 CCCGGTGTACGCCGAGACCAAGAGCACTGCGGGCACAGGGAGCAGTGCAGCTGCG 1080

Qy  1081 GCCCTCCTTCAGCTCTCTACTGCGCAGCCCAGCTGGCCTGCAGGGGTCTGGAGGCCTCGGTCGTGGA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 GCCCTCCTTCAGCTCTCTACTGCGCAGCCCAGCTGGCCTGCAGGGGTCTGGAGGCCTCGGTCGTGGA 1140

Qy  1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCCAGGACTCCCCGAGGTTGCCCCCGCCT 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCCAGGACTCCCCGAGGTTGCCCCCGCCT 1200

Qy  1201 GCCCCAGCGCTACTGGCAAATGCGGGCCCTGTTTTCTGGAGCTGCTTGGGAACCACCGCGGCA 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GCCCCAGCGCTACTGGCAAATGCGGGCCCTGTTTTCTGGAGCTGCTTGGGAACCACCGCGGCA 1260

Qy  1261 GTGCCCCTACGGGTGCTCCTCAAGACGCACTGCGGTCGCGTGCTCACCCCAGC 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GTGCCCCTACGGGTGCTCCTCAAGACGCACTGCGGTCGCGTGCTCACCCCAGC 1320

Qy  1321 AGCCCGGTGTCTTGTGCCCCGAGGAGGAGGA 1380
         |||||||||||||||||||||||||||||||
Db  1321 AGCCCGGTGTCTTGTGCCCCGAGGAGGAGGA 1380

Qy  1381 CACAGACCCCGCTGCTCCGCCACAGCCTGCTCCGCCACCACAGCCCTGCGAGGTGTA 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CACAGACCCCGCTGCTCCGCCACAGCCTGCTCCGCCACCACAGCCCTGCGAGGTGTA 1440

Qy  1441 CGGCTTCGTCGTGCGCGGCGCTGCCTGCCCCGGCTGCTCGGGGCCTCGGGGCTCCAGGCA 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CGGCTTCGTCGTGCGCGGCGCTGCCTGCCCCGGCTGCTCGGGGCCTCGGGGCTCCAGGCA 1500
```

Qy   2581 CAGCCTGTCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCCGGGACGGGCT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 CAGCCTGTCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCCGGGACGGGCT 2640

Qy   2641 GCTCCTGCGTTGGTGGTGGGATGATTCTTGTTGGTGACACCTCACCTCACCCACGCGGAAAAAC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCTCCTGCGTGGTGGTGGGATGATTCTTCTTCTGTGGTGACACCTCACCTCACCCACGCGGAAAAAC 2700

Qy   2701 CTTCCTCAGGACCCTGTCCGAGGTGTCCCTGAGATGGCGTGGTGTGAACTTGCGGAA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTTCCTCAGGACCCTGTCCGAGGTGTCCCTGAGATGGCGTGGTGTGAACTTGCGGAA 2760

Qy   2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGGCTTTGTTGTTCAGAT 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGGCTTTGTTGTTCAGAT 2820

Qy   2821 GCCGGGCCCACGGCCTATTCCCGTGGTGCGCTGGGCTGCTGATACCCGGACCCTGGAGGT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GCCGGGCCCACGGCCTATTCCCGTGGTGCGCTGGGCTGCTGATACCCGGACCCTGGAGGT 2880

Qy   2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCAGAGCCCAGTCTCACCTTCAACCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCAGAGCCCAGTGTCACCTTCAACCG 2940

Qy   2941 CGGCTTCAAGGCTGGGAGGAACAATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCTGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000

Qy   3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCCTCCGAGACGGTGCACCAACATCTA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCCTCCGAGACGGTGCACCAACATCTA 3060

Qy   3061 CAAGATCCTCCTGCTCGCAGGGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CAAGATCCTCCTGCTCGCAGGGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120

Qy   3121 TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCCTGACACGGCCTCCCT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCCTGACACGGCCTCCCT 3180

Qy   3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGCGCTGCTGGGGCCAAGGGCCGGC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCAAGGGCCGGC 3240

Qy   3241 CGGCCCTCTGCCTCCGAGGCCGTGCAGTGGCCGTGCCACCAAGCATTCCTGCTCAAGCT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CGGCCCTCTGCCTCCGAGGCCGTGCAGTGGCCGTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy   3301 GACTCGACACCGTGTCACCTACGTGCACTCCTGGGTCACTCAGGACAGCCCCAGACGCA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GACTCGACACCGTGTCACCTACGTGCACTCCTGGGTCACTCAGGACAGCCCCAGACGCA 3360

Qy   3361 GCTGAGTCGGAAGTCCCCGGGGACGTCCTCCCTGAGGCCTGAGGTCAGCCAACCGGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GCTGAGTCGGAAGTCCCCGGGGACGTCCTGACTCGGGGACGTCCTCCCTGAGGCCTGAGGTCAGCCAACCGGC 3420

Qy   3421 ACTGCCCTCAGACTTCAAGACCATCTGGACTGAGCTCCTGGACTGATGGCCACCGCGGCCGA 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 ACTGCCCTCAGACTTCAAGACCATCTGGACTGAGCTCCTGGACTGATGGCCACCGCGGCCGA 3480

Qy   3481 GAGCAGACACCAGCAGCCCTGTCACGTCCACGGGCTCTACGTCCCAGGAGGAGGGCCGGCC 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GAGCAGACACCAGCAGCCCTGTCACGTCCACGGGCTCTACGTCCCAGGAGGAGGGCCGGCC 3540

Qy   3541 CACACCCAGGCCCGCCACCGCGTCGGAGTCTGGAGTCTGAGTGAGTGTTTGGCCAGGCCTG 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CACACCCAGGCCCGCCACCGCGTCGGAGTCTGGAGTCTGAGTGAGTGTTTGGCCAGGCCTG 3600

Qy   3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGTGAGCTGGAGTGTCCAGCCAAGGGCT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGTGAGCTGGAGTGTCCAGCCAAGGGCT 3660

Qy   3661 GAGTGTCCAGCACACCTGCCGCTCTTCACTTCCCACAGGCGTGGCCGCTCGGCCTCCACCCCA and 3720

Qy   3661 GAGTGTCCAGCACACCTGCCGCTCTTCACTTCCCACAGGCGTGGCCGCTCGGCCTCCACCCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGTGTCCAGCACACCTGCCGCTCTTCACTTCCCACAGGCGTGGCCGCTCGGCCTCCACCCCA 3720

Qy   3721 GGGCCAGCTTTTCCTACCAGGAGCCCGGCTTCCACTCCCACAGGAATAGGAATAGTCCATCC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCACAGGAATAGGAATAGTCCATCC 3780

Qy   3781 CCAGATTCGCCATTGTTCACCCCGCCCCTGCCCCTCGTTCTTTTGCCTTCCACCCCACCATCC 3840
          ||||||||||||||||||||||::||||||||||||||||||||||||||||||||||
Db   3781 CCAGATTCGCCATTGTTCACCCCYTCGCCCYTCGCCCTGCCYTCCTTGCCTTCCACCCCACCATCC 3840

Qy   3841 AGTGGAGACCCTGAGAAGGACCCTGGGAGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 AGTGGAGACCCTGAGAAGGACCCTGGGAGAGCTCTGGGAGTTTGGAGTGACCAAAGGTGTG 3900

Qy   3901 CCCTGTACACAGGCGACGAGCCCTGCACCTGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CCCTGTACACAGCGCGAGACCCTGCACCTGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960

Qy   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA 4015
          ||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA 4015

RESULT 14
AAX89424
ID   AAX89424 standard; cDNA; 4027 BP.
XX
AC   AAX89424;
XX
DT   22-SEP-1999 (first entry)
XX
DE   Human EST2 coding sequence.
XX
KW   EST2; proliferative capacity; cellular proliferation; decubitus ulcer;
KW   telomerase-activating therapeutic agent; cell life-span extension;
KW   venous disease; venous stasis ulcer; excessive pressure; arterial ulcer;
KW   tissue regeneration enhancer; atherosclerosis; therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9935243-A2.
XX
PD   15-JUL-1999.
XX
PF   12-JAN-1999;   99WO-US00682.
XX
PR   21-APR-1998;   98US-0063657.
PR   12-JAN-1998;   98US-0071220.
PR   13-JAN-1998;   98US-0071455.
XX
PA   (COLD-) COLD SPRING HARBOR LAB.
XX
PI   Beach DH, Hannon GJ, Wang J;
XX
DR   WPI; 1999-444196/37.
DR   P-PSDB; AAY28401.
XX
PT   Increasing proliferative capacity of cells useful for promoting
PT   wound healing
XX
PS   Claim 4; Page 65-70; 73pp; English.
XX
CC   This sequence encodes the human EST2 protein, and can be used in the
CC   method of the invention. The method is for increasing the proliferative
CC   capacity of cells , and comprises contacting the cell with a
CC   telomerase-activating therapeutic agent (TATA). The method can be used
CC   for extending the life-span of cells, e.g. by increasing the number of
CC   mitotic divisions. They can be used for e.g. the extension of skin or
CC   other epithelial cell cultures or grafts, the expansion of mesenchymal
CC   cell cultures or grafts, and the expansion of chondrocyte or osteocyte
CC   cultures or grafts. They can be applied to e.g. neuronal, haematopoietic,
CC   epithelial, pancreatic, hepatic, chondrocytic and osteocytic stem and

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CC    progenitor cells in in vivo, in vitro or ex vivo protocols. The methods
CC    can be used for promoting the healing of wounds resulting from
CC    e.g. surgery, burns, inflammation or irritation or ulcers resulting from
CC    e.g. venous disease (venous stasis ulcers), excessive pressure (decubitus
CC    ulcers) or arterial ulcers. They can also be used to enhance tissue
CC    regeneration processes, e.g. of the skin, hair and/or fingernails. They
CC    can also be used for treating age-related conditions, e.g. atrophy of the
CC    skin through loss of extracellular matrix homeostasis in dermal
CC    fibroblasts, age-related macular degeneration caused by accumulation of
CC    liofuscin and downregulation of a neuronal survival factor in retinal
CC    pigmented epithelial (RPE) cells, and atherosclerosis caused by loss of
CC    proliferative capacity and overexpression of hypertensive and thrombotic
CC    factors in endothelial cells. Expanded populations of normal or
CC    genetically engineered rejuvenated cells could be used for autologous or
CC    allogeneic cell and gene therapy. They can also be used for prolonging
CC    the lifespan of a culture of normal cells or tissue being used to secrete
CC    therapeutic or other commercially significant proteins and products.
XX
SQ    Sequence 4027 BP; 674 A; 1361 C; 1277 G; 715 T; 0 other;

Query Match             99.7%;  Score 4002;  DB 20;  Length 4027;
Best Local Similarity   99.9%;  Pred. NO. 0;
Matches  4005;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;
```

(The remainder of the page consists of a paired Query/Database DNA sequence alignment, with sequence position numbers ranging approximately from 6/65 through 1806/1865, displayed as paired Qy and Db rows of nucleotide sequence connected by vertical match bars.)

```
Db   1807  TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAG  1866

Qy   1866  CAGAGGTCAGGCAGCATCGGGAAGGCCCAGGCCCGCCGCCCTGACGTCCGACTCCGCTTCA  1925
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1867  CAGAGGTCAGGCAGCATCGGGAAGGCCCAGGCCCGCCGCCCTGACGTCCGACTCCGCTTCA  1926

Qy   1926  TCCCCAAGCCTGACGGCGTGCCGGCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAA  1985
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1927  TCCCCAAGCCTGACGGCGTGCCGGCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAA  1986

Qy   1986  CGTTCCCGCAGAGAAAAGAGGGGCGAGCGTCTCACCTGCGAAGGCACTGTTCAGCG  2045
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1987  CGTTCCCGCAGAGAAAAGAGGGGCGAGCGTCTCACCTGCGAAGGCACTGTTCAGCG  2046

Qy   2046  TGCTCAACTACGAGCGGGCGGGGCGGGCGGCGCGGGCGGCGGGCGGCGGCGGGCCTG  2105
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2047  TGCTCAACTACGAGCGGGCGGGGCGGGCGGCGCGGGCGGCGGGCGGCGGCGGGCCTG  2106

Qy   2106  ACGATATCCACAGGCCCTGGCGACACTTCGTGCGCGTGCGTGCGGGACCCCGCCC  2165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2107  ACGATATCCACAGGCCCTGGCGACACTTCGTGCGCGTGCGTGCGGGACCCCGCCC  2166

Qy   2166  CTGAGCTGTACTTTGTGTCAAGGTGGATGGATGTGACGGCGGCGGTACGACCAGGACA  2225
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2167  CTGAGCTGTACTTTGTGTCAAGGTGGATGGATGTGACGGCGGCGGTACGACCAGGACA  2226

Qy   2226  GGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGT  2285
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2227  GGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGT  2286

Qy   2286  ATGCCGTGGTGCCAGAAGGCCGCCGCCATGGGCACGTCCGACGTTCGCAGGAGCCACGTCT  2345
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2287  ATGCCGTGGTGCCAGAAGGCCGCCGCCATGGGCACGTCCGACGTTCGCAGGAGCCACGTCT  2346

Qy   2346  CTACCTTGACAGACCTCCAGCGTCGTCGTCTACGCGTACATGCGACAGTTCGTGGCCTGCTCACCTGCAGGAGGACCA  2405
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2347  CTACCTTGACAGACCTCCAGCGTCGTCGTCTACGCGTACATGCGACAGTTCGTGGCCTGCTCACCTGCAGGAGGACCA  2406

Qy   2406  GCCCCGCTGAGGGATGCCGTCGTCTGCATCGAGACAGAGCTCCACCACCGCGGCTCCCTGAATGAGGCCAGCAGTG  2465
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2407  GCCCCGCTGAGGGGATGCCGTCGTCTGCATCGAGACAGAGCTCGAGCAGCTCCACCACCGCGGCTCCCTGAATGAGGCCAGCAGTG  2466

Qy   2466  GCCTCTTCGACGTCTTCCTACGCGTTTCATCGTGGCCCACCACCGCCTCCATCTCTCGCTGCGAGGGGCAAGT  2525
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2467  GCCTCTTCGACGTCTTCCTACGCGTTTCATCGTGGCCCACCACCGCCTCCATCTCTCGCTGCGAGGGGCAAGT  2526

Qy   2526  CCTACGTCCAGTCCAGTGGTCCGGAGGGGGATCCCGCCAGGGCGTCCATCCTGCGCTGCTCTGCGAC  2585
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2527  CCTACGTCCAGTCCAGTGGTCCGGAGGGGGATCCCGCCAGGGCGTCCATCCTGCGCTGCTCTGCGAC  2586

Qy   2586  TGGTGTACGGCGACAATGGGAACATGGGAAACAAGCTGTGTTGCGGGGATTCGGCGCGGACGGCTGCTCC  2645
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2587  TGGTGTACGGCGACAATGGGAACATGGGAAACAAGCTGTGTTGCGGGGATTCGGCGCGGACGGCTGCTCC  2646

Qy   2646  TGCGTTTGGTGGTGGATGATTTCTTGGTGGTGACACCTCACCTCACCTCACCCGCGAAAACCTTCC  2705
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Db   2647  TGCGTTTGGTGGTGGATGATTTCTTGGTGGTGACACCTCACCTCACCTCACCCGCGAAAACCTTCC  2706

Qy   2706  TCAGGACCCTGGTCCGGAGTGTCCTGAGTATGGCTGCGGTGGTGGGAACTTGCGGGAAGACAG  2765
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Db   2707  TCAGGACCCTGGTCCGGAGTGTCCTGAGTATGGCTGCGGTGGTGGGAACTTGCGGGAAGACAG  2766

Qy   2766  TGGTGAACTTCCCGTGTAGAGAATGTGAGAGAGGAGAGGCTTTTGTTCAGATGCCGG  2825
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Db   2767  TGGTGAACTTCCCGTGTAGAGAATGTGAGAGAGGAGAGGCTTTTGTTCAGATGCCGG  2826

Qy   2826  CCCACGGGCCTATTCCCGTGTCGCGGCCCGCTGCTCGATACCCGGACCCCTGAGGTGCAGA  2885
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2827  CCCACGGGCCTATTCCCGTGTCGCGGCCCGCTGCTCGATACCCGGACCCCTGAGGTGCAGA  2886

Qy   2886  GCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCAACCGCGGCT  2945
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Db   2887  GCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCAACCGCGGGCT  2946


Qy   2946  TCAAGGCTGGAGGAACATGCTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACA  3005
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2947  TCAAGGCTGGAGGAACATGCTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACA  3006

Qy   3006  GGCTGTTCTGGATTTGCAGGTGAACAGCTCCAGACGGTGCACCAACATCTACAAGA  3065
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Db   3007  GGCTGTTCTGGATTTGCAGGTGAACAGCTCCAGACGGTGCACCAACATCTACAAGA  3066

Qy   3066  TCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGCTGCAGCTCCATTCATCAGC  3125
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3067  TCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGCTGCAGCTCCATTCATCAGC  3126

Qy   3126  AAGTTTGGAAGAACCCCACATTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCT  3185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3127  AAGTTTGGAAGAACCCCACATTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCT  3186

Qy   3186  ACTCCATCCTGAAAGCCAAGAACGCAGGATCGTCGTGGGGGCCAAGGGCGCCGCCGCC  3245
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3187  ACTCCATCCTGAAAGCCAAGAACGCAGGATCGTCGTGGGGGCCAAGGGCGCCGCCGCC  3246

Qy   3246  CTCTGCCCTCCGAGGGCGTGCTGCTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC  3305
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3247  CTCTGCCCTCCGAGGGCGTGCTGCTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC  3306

Qy   3306  GACACCCGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCAGCCAGCTGA  3365
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Db   3307  GACACCCGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCAGCCAGCTGA  3366

Qy   3366  GTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGGAGGCCCGCCCAACCCGGCCACTGC  3425
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Db   3367  GTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGGAGGCCCGCCCAACCCGGCCACTGC  3426

Qy   3426  CCTCAGACTTCAAGACCATCCTGGACTGATGAGCCACCCGGCAGCCGGAGCA  3485
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Db   3427  CCTCAGACTTCAAGACCATCCTGGACTGATGAGCCACCCGGCAGCCGGAGCA  3486

Qy   3486  GACACCAGCAGCCCTGTTCACGCGGGCTCTACGTCCCGGCGGGAGGGAGGGGCGCCCACAC  3545
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Db   3487  GACACCAGCAGCCCTGTTCACGCGGGCTCTACGTCCCGGCGGGAGGGAGGGGCGCCCACAC  3546

Qy   3546  CCAGGCTGAAGGCTGAGTGTCCGGCTGAGGCGTCGAGCCTGAGCGAGTGTGCATGT  3605
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3547  CCAGGCTGAAGGCTGAGTGTCCGGCTGAGGCGTCGAGCCTGAGCGAGTGTGCATGT  3606

Qy   3606  CCGGCTGAAGGTGAGTGTCCGGCTCACTTGCCTGCGCTCGCCTCACCCAGGGCCAAGT  3665
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3607  CCGGCTGAAGGTGAGTGTCCGGCTCACTTGCCTGCGCTCGCCTCACCCAGGGCCAAGT  3666

Qy   3666  TCCAGCACACCTGCCTGCTTCACTTGGGGAATTTGGAGTGACCAAAGGTGTGCCCAC  3725
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Db   3667  TCCAGCACACCTGCCTGCTTCACTTGGGGAATTTGGAGTGACCAAAGGTGTGCCCAC  3726

Qy   3726  AGTTTTCCTCACCAGGAGCCCGCTTCCACTCCCAGAGTAGTCCATCCCCAGA  3785
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3727  AGTTTTCCTCACCAGGAGCCCGCTTCCACTCCCAGAGTAGTCCATCCCCAGA  3786

Qy   3786  TTTCGGCCATTGTTCACCCCTCGCCCTTTGCCTTCACCCACCATCCAGGTG  3845
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3787  TTTCGGCCATTGTTCACCCCTCGCCCTTTGCCTTCACCCACCATCCAGGTG  3846

Qy   3846  GAGAAGGAGGAGAAGGACCCTGCGGAGTGACCAAAGGTGTGCCCTG  3905
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Db   3847  GAGAAGGAGGAGAAGGACCCTGCGGAGTGACCAAAGGTGTGCCCTG  3906

Qy   3906  TACACAGGCGAGGAGTAAAATTGGGGGGAGGT  3965
           ||||||||||||||||||||||||||||||||
Db   3907  TACACAGGCGAGGAGTAAAATTGGGGGGAGGT  3966

Qy   3966  GCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTTGAAAAAAA  4015
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Db   3967  GCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTTGAAAAAAA  4016
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us-10-054-295-224.rng

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RESULT 15
AAA29388
ID   AAA29388 standard; cDNA; 4027 BP.
XX
AC   AAA29388;
XX
DT   12-SEP-2000  (first entry)
XX
DE   hEST2, a human telomerase catalytic subunit homologue cDNA.
XX
KW   hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
KW   retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW   proliferation; immortal; tumour therapy; macular degeneration; activator;
KW   INK4; ss.
XX
OS   Homo sapiens.
XX
FH                  Location/Qualifiers
FT   Key
FT   CDS             57..3455
FT                   /*tag=  a
FT                   /product= human_telomerase_catalytic_subunit
XX
PN   WO20031238-A2.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;  99WO-US27907.
XX
PR   25-NOV-1998;  98US-0109891.
PR   17-FEB-1999;  99US-0120549.
XX
PA   (GENE-) GENETICA INC.
XX
PI   Hannon GJ, Beach DH;
XX
DR   WPI; 2000-400055/34.
DR   P-PSDB; AAY96566.
XX
PT   New method for increasing the proliferative capacity of cell lines
PT   comprises administering agents reversibly activating telomerase
PT   activity and reversibly inactivating Rb/Ink4 and/or p53 pathways useful
PT   in treating age related diseases
XX
PS   Claim 14; Page 112-116; 123pp; English.
XX
CC   This cDNA, designated hEST2, is a human telomerase catalytic subunit
CC   homologue of yeast EST2p and Euplotes p123. hEST2 is a member of the
CC   reverse transcriptase family of enzymes.
CC   The invention concerns methods and reagents for extending the life-span,
CC   e.g. the number of mitotic divisions, of a cell. The method relies on
CC   activation of a telomerase activity and inhibition of one or both of a
CC   retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb
CC   by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
CC   division cycle. Binding of INK4 family members, e.g. the tumour
CC   suppressor p16INK4a, inhibits kinase activity and results in growth
CC   arrest. Rb inactivators can selectively and reversibly inactivate an
CC   Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
CC   is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
CC   and can also be used in the methods. Other molecules which can be used
CC   include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
CC   differs from at one or more residues K22, R24, H95 and/or D97.
CC   Additional constructs include a papilloma virus E7 protein, or other
CC   viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
CC   the Rb and p16INK4a genes may also be used. The methods are useful for
CC   increasing the proliferative capacity of cells. The cells are
CC   subsequently of use in pharmaceutical and cosmetic preparations used to
CC   treat conditions related to (premature) ageing, e.g. macular degeneration
CC   and arteriosclerosis. The cells can also be used to replace tumour cell
CC   lines in vitro and for studies on biochemical and physiological aspects
CC   of growth and differentiation. Long lived (immortal) cells could also be
CC   of use in the production of normal or genetically engineered
CC   biotechnology products.
XX
SQ   Sequence 4027 BP; 674 A; 1361 C; 1277 G; 715 T; 0 other;

Query Match             99.7%;  Score 4002;  DB 21;  Length 4027;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 4005; Conservative  0; Mismatches  0; Indels  5; Gaps  0;

Qy          6 GCTGCGTCCTGCTGCCGCAGTGGGAAGCCCTGGCCCGGCCACCCCGGCACCCCGGCACCGCGGCCG 65
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 GCGTGGTCCTGCTGCCGCAGTGGGAAGCCCTGGCCCGGCCACCCCGGCACCCCGGCATGCCGGCCG 66

Qy         66 CTCCCCGCTGCCGAGCCGTGCGCTGCCCTGCTCCCTGCGCCAGGGTGCCCAGGGGCCGCGGCCG 125
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CTCCCCGCTGCCGAGCCGTGCGCTGCCCTGCTCCCTGCGCCAGGGTGCCCAGGGGCCGCGGCCG 126

Qy        126 TGGCCACGTTCGTGCGGGCCGCCTGGGGCCCCAGGGCTGGGCGGCTGGTGTGCAGCGCGGGGACC 185
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGGCCACGTTCGTGCGGGCCGCCTGGGGCCCCAGGGCTGGGCGGCTGGTGTGCAGCGCGGGGACC 186

Qy        186 CGGCGGGCCTTTCCGCGCGCTGGTGGCCCAGTGCCCTGGTGCGTGCCCTGGGGACGGCACGGC 245
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CGGCGGGCCTTTCCGCGCGCTGGTGGCCCAGTGCCCTGGTGCGTGCCCTGGGGACGGCACGGC 246

Qy        245 CGCCCCCGCGCGCCCCTCCTTCCCGCAGTGTCCTGCCCAGGAGCTGTGGCCGGAG 305
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGCCCCCGCGCGCCCCTCCTTCCCGCAGTGTCCTGCCCAGGAGCTGTGGCCCGGAG 306

Qy        306 TGCTGCAGAGGCTGTGCGAGCGCGGCGCCGAAGAACGTGCTGGCCTTCGGCCTTCGCGCTGC 365
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Db        307 TGCTGCAGAGGCTGTGCGACGGCGGCGCCGAAGAACGTGCTGGCCTTCGGCCTTCGCGGTGC 366

Qy        366 TGGACGGGGCCCGCGGGGCCCCGGGGGCCTTCACCACCAGCGTGCCAGCTACCTGC 425
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TGGACGGGGCCCGCGGGGCCCCGGGGGCCTTCACCACCAGCGTGCCAGCTACCTGC 426

Qy        426 CCAACACGGTGACCGACGCACTGCGGGGCGGGGCGTGGGGGTGCTCTGCGCGCGCG 485
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CCAACACGGTGACCGACGCACTGCGGGGCGGGGCGTGGGGGCTGGGCTGTTGCGCCG 486

Qy        486 TGGGCGACGACGTGCTGGTTCACCTGCTGCCACCGTGCGCGCGCTGCTTGTTGGTGGTGGCTC 545
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGCGACGACGTGCTGGTTCACCTGCTGCCACCGTGCGCGCGCTCTTTGTTGTGTGGTGGCTC 546

Qy        546 CCAGCTGCGCCTACCAGGTGTGCGGGGCCGCCGCTCGTGTACCAGTCTCGGCCGTGCCACTCAGG 605
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCAGCTGCGCCTACCAGGTGTGCGGGGCCGCCGCTCGTGTACCAGTCTCGGCCGTGCCACTCAGG 606

Qy        606 CCCGGCCCCCGCCAGTGCTAGTGACCCGAAGGCGTCTGGGATGCGAACGGGCCTGGA 665
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CCCGGCCCCCGCCAGTGCTAGTGACCCGAAGGCGTCTGGGATGCGAACGGGCCTGGA 666

Qy        666 ACCATAGCGTCAGGGAGGCCGGGTCCCCTGGGGGCTGCCAGCCCCGGTGCGAGGAGGC 725
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 ACCATAGCGTCAGGGAGGCCGGGTCCCCTGGGGGCCTGCCAGCCCCGGTGCGAGGAGGC 726

Qy        726 GGGGGGCAGTGCCAGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGGGCTGCCC 785
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 GCGGGGGCAGTGCCAGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGGGCTGCCC 786

Qy        786 CTGAGCCGGAGCGGACGCCCGTTGGCAGGGTCTCAGGGTCAGGGGTCCACCCGGGCCAGGACGCGTG 845
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CTGAGCCGGAGCGGACGCCCGTTGGCAGGGTCTCAGGGTCAGGGGTCCACCCGGGCCAGGACGCGTG 846

Qy        846 GACCGAGTGACCGTGGTTTCGTGGTGTCACCTGCCAGAGACCCGAAGAAGCCACCT 905
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 GACCGAGTGACCGTGGTTTCGTGGTGTCACCTGCCAGAGACCCGAAGAAGCCACCT 906

Qy        906 CTTTGGAGGTGCGCTCTCTGGCACGCGCACTCCACATCCGTGGGCCGGCCAGCACC 965
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CTTTGGAGGTGCGCTCTCTGGCACGCGCACTCCACATCCGTGGGGCCGGCCAGCACCT 966

Qy        966 ACGGGGCCCCCATCCACATCGCGCCGCCACCACGTCCCTGGGCACACGTCCCTGTCCCCGG 1025
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Left column (positions 967–2106):

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Db   967  ACGCGGGCCCCCATCCACATCGCGGCACCACGTCCTGGGACACGCCTCCTGTCCCCCGG 1026
Qy  1026  TGTACCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCT 1085
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Db  1027  TGTACCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCGGCCCT 1086

Qy  1086  CCTTCTACTCAGCTCTCTGAGGCCCTGACTGGCCTCGGCGGGCTCGGCGACCA 1145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1087  CCTTCTACTCAGCTCTCTGAGGCCCTGACTGGCCTCGGCGGGCTCGGCGGACCA 1146

Qy  1146  TCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCTGCCCC 1205
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Db  1147  TCTTTCGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCTGCCCC 1206

Qy  1206  AGCGGCTACTGGCAAATGCGGCCCCTGTTTCTGGGAGCTGCTGGGAACCACGCGCAGTGCC 1265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1207  AGCGGCTACTGGCAAATGCGGCCCCTGTTTCTGGGAGCTGCTGGGAACCACGCGCAGTGCC 1266

Qy  1266  CCTACGGGGTGTCTCCTCAAGACGCACTGCCCGCTGCGGTGCGGAGCTGCGAGCTGCGAGCCG 1325
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Db  1267  CCTACGGGGTGTCTCCTCAAGACGCACTGCCCGCTGCGGTGCGGAGCTGCGAGCTGCGAGCCG 1326

Qy  1326  GTGTCGTGTGCCCGGAGAAGCCCAGGGCTCGTGTGCGGAGCAGCAGGAGGAGGACAGCAG 1385
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Db  1327  GTGTCGTGTGCCCGGAGAAGCCCAGGGCTCGTGTGCGGAGCAGCAGGAGGAGGACAGCAG 1386

Qy  1386  ACCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCAGCACAGGCCCTGGCAGGTGTACGGCT 1445
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1387  ACCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCAGCACAGGCCCTGGCAGGTGTACGGCT 1446

Qy  1446  TCGTGCGGGGCCTGCCCTGGTGCCCCAGGCCTCGGGGCTCCAGGCGCACAACG 1505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1506  AACGCGCGCTTCCTCAGGAACACCAAGAAGTCATCTCCCTGGGGAAGCATGCCCAAGCTCT 1565
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 569978 seqs, 220691566 residues

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	4015	100.0	4015	3	US-08-851-843A-224	Sequence 224, App
2	4015	100.0	4015	3	US-08-974-549A-1	Sequence 1, Appli
3	4015	100.0	4015	4	US-08-854-050-224	Sequence 224, App
4	4015	100.0	4015	4	US-09-430-323-224	Sequence 224, App
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23	1877.2	46.8	2171	3	US-08-851-843A-100	Sequence 100, App
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33	1514.2	37.7	51552	4	US-09-733-294A-30	Sequence 30, Appl
34	385.8	9.6	389	3	US-08-851-843A-62	Sequence 62, Appl
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c 45	67.6	1.7	90	3	US-08-974-549A-697	Sequence 697, App

ALIGNMENTS

RESULT 1
US-08-851-843A-224
; Sequence 224, Application US/08851843A
; Patent No. 6093809

GENERAL INFORMATION:
.;;   APPLICANT: Cech, Thomas R.
.;;   APPLICANT: Lingner, Joachim
.;;   APPLICANT: Nakamura, Toru
.;;   APPLICANT: Chapman, Karen B.
.;;   APPLICANT: Morin, Gregg B.
.;;   APPLICANT: Harley, Calvin
.;;   APPLICANT: Andrews, William H.
.;;   TITLE OF INVENTION: 603809el Telomerase
.;;   NUMBER OF SEQUENCES: 225
.;;   CORRESPONDENCE ADDRESS:
.;;   ADDRESSEE: Townsend and Townsend and Crew LLP
.;;   STREET: Two Embarcadero Center, 8th Floor
.;;   CITY: San Francisco
.;;   STATE: California
.;;   COUNTRY: United States of America
.;;   ZIP: 94111
.;;   COMPUTER READABLE FORM:
.;;   MEDIUM TYPE: Floppy disk
.;;   COMPUTER: IBM PC compatible
.;;   OPERATING SYSTEM: PC-DOS/MS-DOS
.;;   SOFTWARE: PatentIn Release #1.0, Version #1.30
.;;   CURRENT APPLICATION DATA:
.;;   APPLICATION NUMBER: US/08/851,843A
.;;   FILING DATE: 06-MAY-1997
.;;   CLASSIFICATION:
.;;   PRIOR APPLICATION DATA:
.;;   APPLICATION NUMBER: US 08/846,017
.;;   FILING DATE: 25-APR-1997
.;;   CLASSIFICATION:
.;;   PRIOR APPLICATION DATA:
.;;   APPLICATION NUMBER: US 08/844,419
.;;   FILING DATE: 18-APR-1997
.;;   CLASSIFICATION:
.;;   PRIOR APPLICATION DATA:
.;;   APPLICATION NUMBER: US 08/724,643
.;;   FILING DATE: 01-OCT-1996
.;;   CLASSIFICATION:
.;;   ATTORNEY/AGENT INFORMATION:
.;;   NAME: Apple, Randolph T.
.;;   REGISTRATION NUMBER: 36,429
.;;   REFERENCE/DOCKET NUMBER: 015389-002930US
.;;   TELECOMMUNICATION INFORMATION:
.;;   TELEPHONE: (415) 576-0200
.;;   TELEFAX: (415) 576-0300
.;; INFORMATION FOR SEQ ID NO: 224:

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;   STRANDEDNESS: single
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Qy   541  GGCTCCCAGTCGCGCGCTACCAGTGTGCGGCCGCGGGGCCCCAGCCCGTGGGGTGCCAC  600
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Db   541  GGCTCCCAGTCGCGCGCTACCAGTGTGCGGCCGCGGGGCCCCAGCCCGTGGGGTGCCAC  600

Qy   601  TCAGGGCCCGGCCCACGCTAGTGGACCCCGAAGGCGTCTGGGGATGCGGAACGGGC  660
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Db   601  TCAGGGCCCGGCCCACGCTAGTGGACCCCGAAGGCGTCTGGGGATGCGGAACGGGC  660

Qy   661  CTGGGAACCATAGCGCTGGGGCAGTCGCCAGTCGCCGAAGTCTGCGGCGGCCGGG  720
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Db   661  CTGGGAACCATAGCGCTGGGGCAGTCGCCAGTCGCCGAAGTCTGCGGCGGCCGGG  720

Qy   721  GAGGGCGCGGGGGGCAGTCGCCAGCCGAAGTCGCTGCCGTTGCGGCGTGCGCC  780
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Db   721  GAGGGCGCGGGGGGCAGTCGCCAGCCGAAGTCGCTGCCGTTGCGGCGTGCGCC  780

Qy   781  TGCCCCTGAGCCGACCGGACGCCCGTTCTGGGCCCAGGGGTCTTCGGGCCAGGAGGAC  840
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Db   781  TGCCCCTGAGCCGACCGGACGCCCGTTCTGGGCCCAGGGGTCTTCGGGCCAGGAGGAC  840

Qy   841  GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTTCTCACCTGCGTGTGTGTCACTGC  900
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Db   841  GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTTCTCACCTGCGTGTGTGTCACTGC  900

Qy   901  CACTCTTTTGGAGGGTGCGCTCTGCGCTCTGCGCACGCGCCACTCCACCACCATCCGTGGGCCGCCA  960
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Db   901  CACTCTTTTGGAGGGTGCGCTCTGCGCTCTGCGCACGCGCCACTCCACCACCATCCGTGGGCCGCCA  960

Qy   961  GCACCACGCGGGGCCCCCATCCACATCCGCGCCACCACGTCCGGCCACCACGTCCCTGTGTCC  1020
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Db   961  GCACCACGCGGGGCCCCCATCCACATCCGCGCCACCACGTCCGGCCACCACGTCCCTGTGTCC  1020

Qy  1021  CCGGGTGTACGCGCGAGACCAAGACACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1080
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Qy  1081  GCCCTCCTTCCTACTCAGCTTCTCTGAGGCCCTGAGCTGACTGGCGCTCGGAGGCTCCTGA  1140
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Qy  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCGCAGGGACTCCCCGCGCTTGCCCCGCCT  1200
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Db  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCGCAGGGACTCCCCGCGCTTGCCCCGCCT  1200

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Qy  1261  GTGCCCTACGGGGTGCTCTCCAAGACGACTGCCCGCGTGCGCGGTGCGGTGCGGGACGC  1320
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Db  1261  GTGCCCTACGGGGTGCTCTCCAAGACGACTGCCCGCGTGCGCGGTGCGGTGCGGGACGC  1320

Qy  1321  AGCCGGTGTCGTGCGCCCGGGAGAAGCCCCAGGGGCTCGTGGCGGCCCCGGAGGAGGA  1380
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Qy  1381  CACAGACCCCGTGCGCTGCCTCGTGCTGCTCCCTGGCACGCACAGCCCCTGGCCAGGTGTA  1440
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Qy  1501  CAACGAACGCCGCTTCCTCAGGAACACCACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAA  1560
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Qy  1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGCGGGACTGCGCGGCTTGGCTGCGCAG  1620
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Db  1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGCGGGACTGCGCGGCTTGGCTGCGCAG  1620

Qy  1621  GAGCCCAGGGTTGGCTGTGTTCCGCGGCCACGCGTCTGCGCGGAGATCCTGGC  1680
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Qy  1681  CAAGTTCCTCACTGCCTGACTGAGTGTGTAGTGTGTGCACTTTCTTTTA  1740
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Db  1681  CAAGTTCCTCACTGCCTGACTGAGTGTGTAGTGTGTGCACTTTCTTTTA  1740

Qy  1741  TGTCACGGAGACCACGTTCAAAAGAACAGGCGTCTCTTTTTCTACCGGAAGAGTGTCTGAG  1800
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Db  1741  TGTCACGGAGACCACGTTCAAAAGAACAGGCGTCTCTTTTTCTACCGGAAGAGTGTCTGAG  1800

Qy  1801  CAAGTTGCAAAGCATTGAATACAGCAGCACTTGAAGAGGGTGCGGGAGCGTGTC  1860
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Db  1801  CAAGTTGCAAAGCATTGAATACAGCAGCACTTGAAGAGGGTGCGGGAGCGTGTC  1860

Qy  1861  GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCCAGGAGCCAGGCCCGCCCCACCCGGCCAGGAC  1920
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Db  1861  GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCCAGGAGCCAGGCCCGCCCCACCCGGCCAGGAC  1920
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Left column (positions 1921–3000):

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Qy  1921  CTTCATCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980
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Db  1921  CTTCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980

Qy  1981  CAGAACGTTCCCGAGAGAAAAGAGGGCCGAGCGCTCACCTGAAGGCACTGTT  2040
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Db  1981  CAGAACGTTCCGAGAGAGAAAAGAGGGCCGAGCGCTCACCTGAAGGCACTGTT  2040

Qy  2041  CAGCCGTGCTCAACTACGAGCGGGCCGCGGGCCGCCCCGGCCTTCTGTGCTGTGGG  2100
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Qy  2101  CCTGGACGATATCCACAGGGGCTGGCGCACCTTCGTGCTGTGCGGGGGCCAGGACCCC  2160
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Db  2101  CCTGGACGATATCCACAGGGGCTGGCGCACCTTCGTGCTGTGCGGGGGCCAGGACCCC  2160

Qy  2161  GCGCCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGTACGACACCATCCCCCA  2220
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Db  2161  GCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGTACGACACCATCCCCCA  2220

Qy  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAAACACGTACTGCGTGCG  2280
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Db  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAAACACGTACTGCGTGCG  2280

Qy  2281  TCGGTATGCCGGTGGTCCAGAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA  2340
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Db  2281  TCGGTATGCCGGTGGTCCAGAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA  2340

Qy  2341  CGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA  2400
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Db  2341  CGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA  2400

Qy  2401  GACCAGCCCGTGTGAGGGATGCGGCCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG  2460
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Db  2401  GACCAGCCCGTGTGAGGGATGCGGCCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG  2460

Qy  2461  CAGTGGCTCCTCGCGCTCTTCCTACGCTTCATGTGCCACCACGCCGTGCCGCATCAGGGGG  2520
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Db  2461  CAGTGGCTCCTCTTCGCGCTCTTCCTACGCTTCATGTGCCACCACGCCGTGCCGCATCAGGGGG  2520

Qy  2521  CAAGTCCTACGTCCAGTCCGCAGGGATCCCGCAGGGCTCCATCCTCTCCCACGCTGCTCTG  2580
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Db  2521  CAAGTCCTACGTCCAGTCCGCAGGGATCCCGCAGGGCTCCATCCTCTCCCACGCTGCTCTG  2580

Qy  2581  CAGCCTGTGTACGGGCAACATGGAGAACAAGCTGTTTGCGGGATTCGGCGGGACGGGCT  2640
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Db  2581  CAGCCTGTGTACGGGCAACATGGAGAACAAGCTGTTTGCGGGATTCGGCGGGACGGGCT  2640

Qy  2641  GCTCCCTGCGTTGGTCGATGATTTCTTGTTGGTGACACCTCACCTGAACTTGCCGAAAAC  2700
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Db  2641  GCTCCCTGCGTTGGTCGATGATTTCTTGTTGGTGACACCTCACCTGAACTTGCCGAAAAC  2700

Qy  2701  CTTCCCTCAGGAGCCCTGGTCTCCGAGGTGTCCCTGAGTATGGCTGCGCTGGTGAACTTGCCGAA  2760
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Db  2701  CTTCCCTCAGGAGCCCTGGTCTCCGAGGTGTCCCTGAGTATGGCTGCGCTGGTGAACTTGCCGAA  2760

Qy  2761  GACAGTTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGTGGCACGGCTTTTGTTCAGAT  2820
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Db  2761  CAGCCTGTTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGTGGCACGGCTTTTGTTCAGAT  2820

Qy  2821  GCCGGCCCTATTCCCCGGTCTGGTGCGGCCTGCTGCTGCTGTCGGATACCCGGACCCTGGAGGT  2880
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Right column (positions 3001–4015):

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Qy  3001  TCACAGCCTGTTCTGGATTTGGAGGTGAACAGCTCCAGACGCGTGTGCGACCAACATCTA  3060
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Db  3001  TCACAGCCTGTTCTGGATTTGGAGGTGAACAGCTCCAGACGCGTGTGCGACCAACATCTA  3060

Qy  3061  CAAGATCTCCTCCTGCTCGCTACAGGTTCACGCATGTGCTGCTGCAGCTCCATTTCA  3120
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Db  3061  CAAGATCTCCTCCTGCTCGCTACAGGTTCACGCATGTGCTGCTGCAGCTCCATTTCA  3120

Qy  3121  TCAGCAAGTTGGAAGAACCCCACATTTTCCTGCGCGTCATCTGACACGGCCTCCCT  3180
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Qy  3181  CTGCTACTCCATCCTGAAAGCCAGAACGCAGGGGATGTCGCTGGTGCTGCCAAGGGCGCGCGC  3240
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Db  3181  CTGCTACTCCATCCTGAAAGCCAGAACGCAGGGGATGTCGCTGGTGCTGCCAAGGGCGCGCGC  3240

Qy  3241  CGGCCCTCCTGCCCTCCGAGGCCGTGCAGTGGCTGGTGCTGCCACCAAGCATTCCTGCTCAAGCT  3300
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Db  3241  CGGCCCTCCTGCCCTCCGAGGCCGTGCAGTGGCTGGTGCTGCCACCAAGCATTCCTGCTCAAGCT  3300

Qy  3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA  3360
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Db  3361  GCTGAGTGGAAGCTCCCGGGGACGAGCGTGACTGCCCTGGAGGCCGCAGCCAACCCGGC  3420

Qy  3421  ACTGCCCTCAGACTTCAAGACCATCCTGGCTCACCTGCAGGACTGATGGCCACCGGCCGA  3480
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Db  3421  ACTGCCCTCAGACTTCAAGACCATCCTGGCTCACCTGCAGGACTGATGGCCACCGGCCGA  3480

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Qy  3721  GGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCCACTCCCCACAATAGTCCATCC  3780
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Qy  3781  CCAGAATTCGCCATTGTTCACCCCCATGTTGCTCCTTTGCCTTCCGCTCCACCATCC  3840
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GENERAL INFORMATION:
  APPLICANT: Cech, Thomas R.
  APPLICANT: Lingner, Joachim
  APPLICANT: Nakamura, Toru
  APPLICANT: Chapman, Karen B.
  APPLICANT: Morin, Gregg B.
  APPLICANT: Harley, Calvin B.
  APPLICANT: Andrews, William H.
  TITLE OF INVENTION: Human Telomerase Catalytic Subunit
  NUMBER OF SEQUENCES: 727
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94111-3834
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/974,549A
    FILING DATE: 19-NOV-1997
    CLASSIFICATION: 536
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/724,643
    FILING DATE: 01-OCT-1996
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/844,419
    FILING DATE: 18-APR-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/846,017
    FILING DATE: 25-APR-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/851,843
    FILING DATE: 06-MAY-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/854,050
    FILING DATE: 09-MAY-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/911,312
    FILING DATE: 14-AUG-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/912,951
    FILING DATE: 14-AUG-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/915,503
    FILING DATE: 14-AUG-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: WO PCT/US97/17618
    FILING DATE: 01-OCT-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: WO PCT/US97/17885
    FILING DATE: 01-OCT-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Apple, Randolph Ted
    REGISTRATION NUMBER: 36,429
    REFERENCE/DOCKET NUMBER: 015389-002610US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX: (415) 576-0300
  INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 4015 base pairs
    TYPE: nucleic acid
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    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
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    NAME/KEY: CDS
    LOCATION: 56..3454

; OTHER INFORMATION: /product= "hTRT"
; OTHER INFORMATION: /note= "human telomerase reverse
; OTHER INFORMATION: transcriptase (hTRT) catalytic protein
; OTHER INFORMATION: component"

US-08-974-549A-1

Query Match   100.0%; Score 4015; DB 3; Length 4015;
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Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   61 GCGGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCCACTACCGCGAGGTGCT   120

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Db   181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC   240

Qy   241 ACGGCGCGCCCCCGCGCCCCTCCTTCGCCAGTGTCCTGCCTGAAGGAGCTGGTGGC   300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/854,050
  FILING DATE: 09-MAY-1997
  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/851,843
  FILING DATE: 06-MAY-1997
  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
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PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
  CLASSIFICATION: 536
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TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
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INFORMATION FOR SEQ ID NO: 224:
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US-08-854-050-224

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Db  2461  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACCGTGCGCATCAGGGG  2520

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Db  2521  CAAGTCCTACGTCCAGTGCCAGTGGGATCCCGCAGGGCTCCATCCTCTCCACCGCTGCTCTG  2580

Qy  2581  CAGCCTGTGCTACGGCGACATGGAGAACAGCTGTGTTGCGGGATTCGGCGGGACGGGGCT  2640
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Db  2581  CAGCCTGTGCTACGGCGACATGGAGAACAGCTGTGTTGCGGGATTCGGCGGGACGGGGCT  2640

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Qy  3781  CCAGATTCGGCCATTGTTCACCCCTGCCTCCTTTGCCTTCCACCCCCACCATCC  3840
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RESULT 4
US-09-430-323-224
; Sequence 224, Application US/09430323
; Patent No. 6309867

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
          Lingner, Joachim
          Nakamura, Toru
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          Harley, Calvin
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TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
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CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017

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; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
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INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4015 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
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FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 56..3454
;   OTHER INFORMATION: /product= "hTRT"
;   /note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
;
US-09-430-323-224
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Query Match      100.0%;  Score 4015;  DB 4;  Length 4015;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 4015;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    361 GCTGCTTGGACGGGGCCCGGCCCCGAGGGCGGGGGAGGGCCCCGGGGCTTCACCACCAGCGTA   420
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Qy    901 CACCTCTTTGGAGGTGCGCTCTCGCACGCGCCACTCCACCATCCGTGGGCCGCCA   960
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Qy    961 GCACCACGGCGGGGCCCCCATCACATCGGCGGCCACAGTCCCTGGGACACGCCTTGTCC   1020
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Db   2521 CAAGTCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG 2580

Qy   2581 CAGCCTGTGCTACGGCGGACATGGAGAACAAGCTGTTGCGGCGGGATTCGGCGGACGGGCT 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 CAGCCTGTGCTACGGCGGACATGGAGAACAAGCTGTTGCGGCGGGATTCGGCGGACGGGCT 2640

Qy   2641 GCTCCTGCGTTTGGTGATGATTCTTGTTGGTGACACCTCACTGTGCGTGTGACACCCACGCGAAAC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCTCCTGCGTTTGGTGATGATTCTTGTTGGTGACACCTCACTGTGCGTGTGACACCCACGCGAAAC 2700

Qy   2701 CTTCCTCAGGACCTGGTCCGAGGTGTCCCTGCGTTATGGCGTGTGTAGTTGGCGTGCTGGTGAACTTGCCGGAA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTTCCTCAGGACCTGGTCCGAGGTGTCCCTGCGTTATGGCGTGTGTAGTTGGCGTGCTGGTGAACTTGCCGGAA 2760

Qy   2761 GACAGTGGTGAACTTCCCTGTAGAAGAGGAGGCCCTGGGTGGCACGGCTTTGTTCAGAT 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2761 GACAGTGGTGAACTTCCCTGTAGAAGAGGAGGCCCTGGGTGGCACGGCTTTGTTCAGAT 2820

Qy   2821 GCCGGCCCACGGCCTATTCCCTGCTGCGCCCTCGCTGCTGGATACCCGGAGGT 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GCCGAGCCCACGGCCTATTCCCTGCTGCGCCCTCGCTGCTGGATACCCGGAGGT 2880

Qy   2881 GCAGAGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTCTCAACCTTCAACCG 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCAGAGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTCTCAACCTTCAACCG 2940

Qy   2941 CGGCTTCAAGGTCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CGGCTTCAAGGTCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000

Qy   3001 TCACAGCCTGTTCTGCAGTTGCAGGTGAACAGCAGCCTCCAGACGGTGTGCACCAACATCTA 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TCACAGCCTGTTCTGCAGTTGCAGGTGAACAGCAGCCTCCAGACGGTGTGCACCAACATCTA 3060

Qy   3061 CAAGATCCTCCTGCTGCGCAGGCGTACAGGTTCACGCCGCTCGTGCTGCGCAGCTCCCATTTCA 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CAAGATCCCTCCTGCTGCGCAGGCGTACAGGTTCACGCCGCTCGTGCTGCGCAGCTCCCATTTCA 3120

Qy   3121 TCAGCAAGTTGGAAGAACCCCACATTTCCTGCGCGTCATCTCTGACACGGCCTCCT 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 TCAGCAAGTTGGAAGAACCCCACATTTCCTGCGCGTCATCTCTGACACGGCCTCCT 3180

Qy   3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGCGGGGGCCAGGGGCCCGC 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGCGGGGGCCAGGGGCCCGC 3240

Qy   3241 CGGCCCCTCTGCCCTCCGAGGCCGTGCAGTGGCCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CGGCCCCTCTGCCCTCCGAGGCCGTGCAGTGGCCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy   3301 GACTCCGACACCGTGTCACCTACGGGTCACTGGGTCACTCCTCGGAGGCCGCAGCGCCAGCAGCCA 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GACTCCGACACCGTGTCACCTACGGGTCACTGGGTCACTCCTCGGAGGCCGCAGCGCCAGCAGCCA 3360

Qy   3361 GCTGAGTCGGAAGCTCGGAAGCTCCCGGGACGACGTGACTCGGAGGCCGCCGCAGCCAACCCGGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GCTGAGTCGGAAGCTCGGAAGCTCCCGGGACGACGTGACTCGGAGGCCGCCGCAGCCAACCCGGC 3420

Qy   3421 ACTGCCCTCAGACTTCAAGACCATCCTGACTGATGGCCCGGCCACCCGGCCCAGGCCGGA 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 ACTCCCTCAGACTTCAAGACCATCCTGACTGATGGCCCGGCCACCCGGCCCAGGCCGGA 3480

Qy   3481 GAGCAGACCAGCAGCCCCCACCCGGCTCTGTCACGTCGCCCGGGCTGCGGGGAGGGAGGCGGCC 3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GAGCAGACACCAGCAGCCCCCACCCGGCTCTGTCACGTCGCCCGGGCTGCGGGGAGGGAGGCGGCC 3540

Qy   3541 CACACCCAGCCCGGCCCACCCGGGGTCTGAGGCCTGAGTGAGTTTGGCCGGGCTG 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CACACCCAGCCCGGCCCGCCCACCCGGGGTCTGAGGCCTGAGTGAGTTTGGCCGGGCTG 3600

Qy   3601 CATGTCCCGCTGAAGGCTGAGTGTCCGGCCTGAGGCGCTGAGGCCAAGGGCT 3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CATGTCCCGCTGAAGGCTGAGTGTCCGGCCTGAGGCGCTGAGGCCAAGGGCT 3660

Qy   3661 GAGTGTCCGCACACCGGGGATTCGGCGGGACGGGCTCGGCTCCACCCCA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGTGTCCAGCACACCGGGGATTCGGCGGGACGGGCTCGGCTCCACCCCA 3720

Qy   3721 GGGCCAGCTTTTCCTCACCGAGCCCGCTTCCCACATAGGAATAGTCCATCC 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GGGCCAGCTTTTCCTCACCGAGCCCGCTTCCCACATAGGAATAGTCCATCC 3780

Qy   3781 CCAGATTGCCATTGTTCACCCTGTTGCGTTGTGGTGTGAACTTGCGGAA 3840
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CCAGATTGCCCATTGTTCACCCTGTTGCGTTGTGGTGTGAACTTGCGGAA 3840

Qy   3841 AGGTGGAGACCCCTGAGAGGACCCTGGGAGCTGGGAATTTGGAGTGACCAAAGGTGTG 3900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 AGGTGGAGACCCCTGAGAGGACCCTGGGAGCTGGGAATTTGGAGTGACCAAAGGTGTG 3900
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Qy   3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGTCAAATTGGGGG  3960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGTCAAATTGGGGG  3960

Qy   3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAATATATGAGTTTTTGAAAAAA     4015
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAATATATGAGTTTTTGAAAAAA     4015
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RESULT 5
US-09-572-423B-3
; Sequence 3, Application US/09572423B
; Patent No. 6331399
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William A. Gaarde
; APPLICANT: Edward Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0462
; CURRENT APPLICATION NUMBER: US/09/572,423B
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-572-423B-3

Query Match   100.0%; Score 4015; DB 4; Length 4015;
Best Local Similarity 100.0%;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  GCAGGCTGCGTCCTCTGTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGGCGATGCC   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GCAGGCTGCGTCCTCTGTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGGCGATGCC   60

Qy     61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCGCGAGCCACTACCGCGAGGTGCT    120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCGCGAGCCACTACCGCGAGGTGCT    120

Qy    121  GCGCTGGCCACGTTCGTGCGCGGCCTGGGCGGTGGCGGCGGCGGG               180
           ||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCGCTGGCCACGTTCGTGCGCGGCCTGGGCGGTGGCGGCGGCGGG               180

Qy    181  GGACCCGGCGGCTTCGTGCCCGCGCCCCGCGCCCCTGGGGGCGTGCCCGTCTGGGACGC   240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GGACCCGGCGGCTTCGTGCCCGCGCCCCGCGCCCCTGGGGGCGTGCCCGTCTGGGACGC   240

Qy    241  ACGGGCGGCCGCCCGCGCCCCGCGCCCCGCGCCCCGCCCCCCGAGTCCTGGGGCGGC    300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ACGGGCGGCCGCCCGCGCCCCGCGCCCCGCGCCCCGCCCCCCGAGTCCTGGGGCGGC    300

Qy    301  CCTGCCCAACGCCGTGGAGCGCGGCGACCGCCACGACGCGGTGTCGGGGGCGTGGGGG   360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CCTGCCCAACGCCGTGGAGCGCGGCGACCGCCACGACGCGGTGTCGGGGGCGTGGGGG   360

Qy    361  GCTGCTGGACGGGGCCCGCCGGGGCCCCCCGAGCGCTGCGCCCAGCAGCGTGCGCAGCTA   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GCTGCTGGACGGGGCCCGCCGGGGCCCCCCGAGCGCTGCGCCCAGCAGCGTGCGCAGCTA   420

Qy    421  CCTGCCCAACACGGTGACCGACGCGCTGCGGGGGTCGGGGGCGGTGGGGGCGTGCTCGCG   480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CCTGCCCAACACGGTGACCGACGCGCTGCGGGGGTCGGGGGCGGTGGGGGCGTGCTCGCG   480

Qy    481  CGGCTGGACGGGGCCCGCCGGGGCCCCCCGCGCCCCTGGTTCACCTGTTCACCTGTGGT   540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CGGCTGGACGGGGCCCGCCGGGGCCCCCCGCGCCCCTGGTTCACCTGTTCACCTGTGGT   540

Qy    541  GGCTCCCAGCTGCGCCTACCAGGTGTGCGGCGGCGCCGCTGTACCAGCTCGGCGGCTGCCAC   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GGCTCCCAGCTGCGCCTACCAGGTGTGCGGCGGCGCCGCTGTACCAGCTCGGCGGCTGCCAC   600

Qy    601  TCAGGCCCGGCCGGCCGGCCCCCGCCCCGCCGTGATGGCGCTAGTGGACGCTGGGATGGCGAACGGGC   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TCAGGCCCGGCCGGCCGGCCCCCGCCCCGCCGTGATGGCGCTAGTGGACGCTGGGATGGCGAACGGGC   660

Qy    661  CTGGAACCATAGCGTCAGGGAGGCCGGAGGCCGGGGCCGTGCCGGGGTGCCCCCTGGGCTGCTGCGAG   720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTGGAACCATAGCGTCAGGGAGGCCGGAGGCCGGGGCCGTGCCGGGGTGCCCCCTGGGCTGCTGCGAG   720

Qy    721  GAGGCGGGGGCAGTGCCGCCGGCGAAGTCTGCCGTTGCCGTGGCGC                          780
           ||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GAGGCGGGGGCAGTGCCGCCGGCGAAGTCTGCCGTTGCCGTGGCGC                          780

Qy    781  TGCCCCTGAGCCGGAGCCGGACGCCCGTTGGGCAGGGGTCCTGGCAGGGGTCCTGGCAGGGGCCAGGAC   840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TGCCCCTGAGCCGGAGCCGGACGCCCGTTGGGCAGGGGTCCTGGCAGGGGTCCTGGCAGGGGCCAGGAC   840

Qy    841  GGGTGGACCGAGTGACGTGGTTTCTGTGTGTGTCACCTGGCGACGCGCCACTGCCGAAGAGCGCCGAAGAAGC   900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GGGTGGACCGAGTGACGTGGTTTCTGTGTGTGTCACCTGGCGACGCGCCACTGCCGAAGAGCGCCGAAGAAGC   900

Qy    901  CACCTCTTTGGAGGGTGCGCTCTCGGACGCGGCCACTCCCACCCATCCGTGGGCCGCCA               960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CACCTCTTTGGAGGGTGCGCTCTCGGACGCGGCCACTCCCACCCATCCGTGGGCCGCCA               960

Qy    961  GCACCACGCGGCGGCCCCCCATCCACATCGCGGCCACAGTCCTGGGACACGCCCTTGTCC            1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  GCACCACGCGGCGGCCCCCCATCCACATCGCGGCCACAGTCCTGGGACACGCCCTTGTCC            1020

Qy   1021  CCGGTGTACGCGCCGAGACCAAGACCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGAGCTCG   1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  CCGGTGTACGCGCCGAGACCAAGACCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGAGCTCG   1080

Qy   1081  GCCCTCCTTCCTACTCAGCTCTCTCCTGAGGCCCAGCCAGTCCGGCGCTCGACTGGGCTCGTCGTGA   1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  GCCCTCCTTCCTACTCAGCTCTCTCCTGAGGCCCAGCCAGTCCGGCGCTCGACTGGGCTCGTCGTGA   1140

Qy   1141  GACCATCTTTTCTGGGTTCCAGGCCCTGATGCCGCTGCGCCTCACCGCGAGGTGCT                1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GACCATCTTTTCTGGGTTCCAGGCCCTGATGCCGCTGCGCCTCACCGCGAGGTGCT                1200

Qy   1201  GCCCCAGGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGGTTGGGAACCACGCGGCCA         1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  GCCCCAGGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGGTTGGGAACCACGCGGCCA         1260

Qy   1261  GTGCCCTACGGGGTGCTGCCTCAAGACGCACTGCCCGCTGGCGAGCTGGGACGGCGTGGTGGC        1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  GTGCCCTACGGGGTGCTGCCTCAAGACGCACTGCCCGCTGGCGAGCTGGGACGGCGTGGTGGC        1320

Qy   1321  AGCCGGTGTCTGTGCGCGGGGCCCCCGCCTCGTGTGGGCCTGGGACGAGTCTGGTGGC            1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  AGCCGGTGTCTGTGCGCGGGGCCCCCGCCTCGTGTGGGCCTGGGACGAGTCTGGTGGC            1380

Qy   1381  CACAGAGCCCCCGTGCGGGCGGCGGCACGCACCAGAGTTCATCTCCTGGGCAGGTGTA            1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CACAGAGCCCCCGTGCGGGCGGCGGCACGCACCAGAGTTCATCTCCTGGGCAGGTGTA            1440

Qy   1441  CGGCTTCGTGCGGGCCTGCCTGCGGCGACTCGTGCCTTCACCACCAGCGTGCCGCAGCTA         1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  CGGCTTCGTGCGGGCCTGCCTGCGGCGACTCGTGCCTTCACCACCAGCGTGCCGCAGCTA         1500

Qy   1501  CAACGAACGCGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAA       1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  CAACGAACGCGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAA       1560

Qy   1561  GCTCTCGCTCGCAGGAGCTGACGTGGAAGATGAGCGTGCGCGGGACTGCCTTGGCTGCGGT      1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  GCTCTCGCTCGCAGGAGCTGACGTGGAAGATGAGCGTGCGCGGGACTGCCTTGGCTGCGGT      1620

Qy   1621  GAGCCCCAGGGGTTGGCTGTGTTCCGGCCGCCGCCACCGTCTGCGTGAGATCCTGGC          1680
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Db  1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTCGCGTGAGGAGATCCTGGC 1680

Qy  1681 CAAGTTCCTGCACTGGCTGGCTGATGAGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTA 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CAAGTTCCTGCACTGGCTGGCTGATGAGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTA 1740

Qy  1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800

Qy  1801 CAAGTTGCAAAGCATTGGAATCAGACACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 CAAGTTGCAAAGCATTGGAATCAGACACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860

Qy  1861 GGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCCCTGCTGACGTCCAGACTCCG 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCCCTGCTGACGTCCAGACTCCG 1920

Qy  1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTCGGGGAGC 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTCGGGGAC 1980

Qy  1981 CAGAACGTTCCGCAGAGAAAAGAGGGCTCTCTTTTCTCACCTCAGGGGTGAAGGCACTGTT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CAGAACGTTCCGCAGAGAAAAGAGGGCTCTCTTTTCTCACCTCAGGGGTGAAGGCACTGTT 2040

Qy  2041 CAGCCGTGCTCAACTACGAGCGGGGCGGGCGCCCGGCCTCCTGGGCGCCTCGTGTGCTGGG 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 CAGCCGTGCTCAACTACGAGCGGGGCGGGCGCCCGGCCTCCTGGGCGCCTCGTGTGCTGGG 2100

Qy  2101 CCTGGACGATATCCACACAGGGCCTTGGCTGTCGTGTGCGTTGCGGCCCCAGGACCC 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCTGGACGATATCCACACAGGGCCTTGGCTGTCGTGTGCGTTGCGGCCCCAGGACCC 2160

Qy  2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACCACCATCCCCA 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACCACCATCCCCA 2220

Qy  2221 GGACAGGCTCACGGAGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGG 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 GGACAGGCTCACGGAGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGG 2280

Qy  2281 TCGGTATGCCGGTGTGGTCCAGAGAAGGCCGCCATGGGCACGTTCGGCAAGGCCTTCAAGAGCCA 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TCGGTATGCCGGTGTGGTCCAGAGAAGGCCGCCATGGGCACGTTCGGCAAGGCCTTCAAGAGCCA 2340

Qy  2341 CGTCTCTTACCTTGACAGACCTCCAGCCGTACACGCGGCGACAGTTCGGCTCACCTGCAGGA 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CGTCTCTTGACAGACCTCCAGCCGTACACGCGGCGACAGTTCGGCTCACCTGCAGGA 2400

Qy  2401 GACCAGCCCGCTGAGGGATGGCCGTCGTCATCGAGCAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GACCAGCCCGCTGAGGGATGGCCGTCGTCATCGAGCAGCAGAGCTCCTCCCTGAATGAGGCCAG 2460

Qy  2461 CAGTGGGCTCTTCGACGTTCATGTCCGCCATGCGTCCGCATGCAGGGG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGTGGGCTCTTCGACGTTCATGTCCGCCACCACGCCGCATGCAGGGG 2520

Qy  2521 CAAGTCTGCACGTGCCAGTGCCGGATCCCGCAGGGGATCTCCATCCTGCTCCACCGCTGCTCTG 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CAAGTCTCCGGCTACGTGCCAGTGCCGGATCCCGCAGGGGATCTCCATCCTGCTCCACCGCTGCTCTG 2580

Qy  2581 CAGGTCCTGTGCTACGGCGACAATGGAGAACAAGCTGTTTCGGCGGGATTCGGCGGGACGGGCT 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CAGCCCTGTGCTACGGCGACAATGGAGAACAAGCTGTTTCGGCGGGATTCGGCGGGACGGGCT 2640

Qy  2641 GCTCCTGCGTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCTCACCACCACCACGGAAAAC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 GCTCCTCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCTCACCACCACCACGGAAAAC 2700

Qy  2701 CTTCCTCAGGACCCTGTCCCTGGAGGTGTCCCTGGAGTATGGCTGCGTTGCGTTGTGTGAACTTGCGGAA 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CTTCCTCAGGACCCTGTCCCTGGAGGTGTCCCTGGAGTATGGCTGCGTTGCGTTGTGTGAACTTGCGGAA 2760
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Db  2761 GACAGTGGTGAACTTCCCTGTGTTAGAGACGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820

Qy  2761 GACAGTGGTGAACTTCCCTGTGTTAGAGACGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 GACAGTGGTGAACTTCCCTGTGTTAGAGACGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820

Qy  2821 GCCGGCCCACGGCCTATTCCCTGCGGCCTGCTCGTGCTGCTGGATACCCGGACCCTGGAGGT 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 GCCGGCCCACGGCCTATTCCCTGCGGCCTGCTCGTGCTGCTGGATACCCGGACCCTGGAGGT 2880

Qy  2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940

Qy  2941 CGGCTTCAAGGCTGGGAGGAACATGCTCGCCAAACTCTTTGGGGTCTTGCCGGCTGAAGTG 3000
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Db  2941 CGGCTTCAAGGCTGGGAGGAACATGCTCGCCAAACTCTTTGGGGTCTTGCCGGCTGAAGTG 3000

Qy  3001 TCACAGCCTGTTTCTGGATTTGCAGGCGTGAACAGCGTGTGCACCAACATCTA 3060
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Db  3001 TCACAGCCTGTTTCTGGATTTGCAGGCGTGAACAGCGTGTGCACCAACATCTA 3060

Qy  3061 CAAGATCCTCTGCTGCAGGCGTACAGGTTTCACGCAGTGTGCTGCGCAGTCTCCCATTTCA 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 CAAGATCCTCTGCTGCAGGCGTACAGGTTTCACGCAGTGTGCTGCGCAGTCTCCCATTTCA 3120

Qy  3121 TCAGCAAGTTTGGAAGAACCCCACATTTTCCTGCGCGTCATCTCTGACACGCGGCTCCCT 3180
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Db  3121 TCAGCAAGTTTGGAAGAACCCCACATTTTCCTGCGCGTCATCTCTGACACGCGGCTCCCT 3180

Qy  3181 CTGCTACTCCATCCTGCCCATCCTGCGAGGCCGTGCCACTCCTGGGTCTGCCACTCGTGTCCCGTGCGCGC 3240
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Db  3181 CTGCTACTCCATCCTGCCCATCCTGCGAGGCCGTGCCACTCCTGGGTCTGCCACTCGTGTCCCGTGCGC 3240

Qy  3241 CGGCCCCTCTTGCCCTTCCGAGGCCGTGCAGTGGCTGCTGCCACCAAGCATTCCTGCTCAAGCT 3300
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Db  3241 CGGCCCCTCTTGCCCTTCCGAGGCCGTGCAGTGGCTGCTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy  3301 GACTCGACACCGTGTCACTCACGTCGCCACTCCTGGGTCACTCAGGACAGCCCAGACGCA 3360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GACTCGACACCGTGTCACTCACGTCGCCACTCCTGGGTCACTCAGGACAGCCCAGACGCA 3360

Qy  3361 GCTGAGTCGGAAGCTCCCGGACCGCAGGTTCCCTGAGGCCGCAACCCGGC 3420
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Db  3361 GCTGAGTCGGAAGCTCCCGGACCGCAGGTTCCCTGAGGCCGCAACCCGGC 3420

Qy  3421 ACTGCCCTCAGACTTCAAGACCATCCTGATGGCCACCCGGCCCGGCGCCAGCCCAGGGCCGA 3480
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Db  3421 ACTGCCCTCAGACTTCAAGACCATCCTGATGGCCACCCGGCCCGGCGCCAGCCCAGGGCCGA 3480

Qy  3481 GAGCAGACACCAGCAGCCGCCGCACCCGCACCGGCCGCGGCCGGGGAGGGGGCGGGCC 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GAGCAGACACCAGCAGCCGCCGCACCCGCACCGGCCGCGGCCGGGGAGGGGGCGGGCC 3540

Qy  3541 CACACCCAGGCCGCTGAGGCTGAGTGTCCGGCTGAGTGCGCGAGGCCTGAGGGCCTG 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CACACCCAGGCCGCTGAGGCTGAGTGTCCGGCTGAGTGCGCGAGGCCTGAGGGCCTG 3600

Qy  3601 CATGTCCGGCTGAAGGCTGTTCCGGCTGAGTGTCCAGCGCTGAGCGCTGTCCAAGGGCT 3660
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Db  3601 CATGTCCGGCTGAAGGCTGTTCCGGCTGAGTGTCCAGCGCTGAGCGCTGTCCAAGGGCT 3660

Qy  3661 GAGTGTCCAGCACACCTGTCTTCACTTCCCACAGGCTCGGCTCGGCTCCCACCCCA 3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3721 GGGCCAGCTTTTCTCACTCCCGCTTCCCACTCCCACATAGGAATAGTTCCATCC 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3781 CCAGATTCGCCATTGTTCACCCCTGAGTATGGCGTGGTGGTGAACTTGCGGAA 3840
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Db  3781 CCAGATTCGCCATTGTTCACCCCTGAGTATGGCGTGGTGGTGAACTTGCGGAA 3840
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Qy   3841  AGGTGGAGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG  3900
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Db   3841  AGGTGGAGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG  3900

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Db   3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGTCCCTGTGGGTCAAATTGGGGG  3960

Qy   3961  GAGTGCTGTGGGAGTAAAATACTGAATATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA  4015
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RESULT 6
US-09-128-354-1

; Sequence 1, Application US/09128354
; Patent No. 6337200
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 015389-003310US
; CURRENT APPLICATION NUMBER: US/09/128,354
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 08/851,843
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: US 08/854,050
; EARLIER FILING DATE: 1997-05-09
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 09/052,864
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT) cDNA
US-09-128-354-1

Query Match   100.0%;   Score 4015;   DB 4;   Length 4015;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 4015;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy      1  GCAGCGCTGCGGCTCCGTCTGCGCCGCAGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC    60
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Db     61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCAGCCACTACCGCGAGGTGCT   120

Qy    121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGCG   180
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Db    121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGCG   180

Qy    181  GGACCCGGCGGCGCTTCCGCGGCGCCCCCTCCTTCCGCGGCGCCCCCTCCTTCCGCGGCCGGCGG  240
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Db    181  GGACCCGGCGGCGCTTCCGCGGCGCCCCCTCCTTCCGCGGCGCCCCCTCCTTCCGCGGCCGGCGG  240

Qy    241  ACGGCGCCCAACACGGTGACCGACACTGCGCTCGGGCGGCTGCGGCTCCTGGGCTGCCTGCG   300
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Db    241  ACGGCGCCCAACACGGTGACCGACACTGCGCTCGGGCGGCTGCGGCTCCTGGGCTGCCTGCG   300

Qy    301  CCGAGTCGTGCAGAGGCTGTGCGAGCGCGGCGGCGAAGAACGTGCTGGCCTTCGGCCTTCGC   360
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Db    301  CCGAGTCGTGCAGAGGCTGTGCGAGCGCGGCGGCGAAGAACGTGCTGGCCTTCGGCCTTCGC   360

Qy    361  GCTGCTGACGCGGCCCCGCGGGGGCCCCCCGAGGGCCTTCACCACCAGCGTGCGCAGCTA   420
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Db    361  GCTGCTGACGCGGCCCCGCGGGGGCCCCCCGAGGGCCTTCACCACCAGCGTGCGCAGCTA   420

Qy    421  CCTGCCCAACACGGTGACCGACACTGCGCTCGGGCGGCTGCGGCTCCTGCTCTTTGTGCTGGT  480
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Db    421  CCTGCCCAACACGGTGACCGACACTGCGCTCGGGCGGCTGCGGCTCCTGCTCTTTGTGCTGGT  480

Qy    481  CCGCGTGGGCGACGACGTGCTGGTTCACCTGCCCGTGTCGGGGCCGCGTACCAGCTCGGCCTGCAC  540
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Db    481  CCGCGTGGGCGACGACGTGCTGGTTCACCTGCCCGTGTCGGGGCCGCGTACCAGCTCGGCCTGCAC  540

Qy    541  GGCTCCCAGTGCTGGCCTACCAGTGTGCGGGGCCGCGCACAGCTAGTGGACCCCGAAAGGGC   600
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Db    541  GGCTCCCAGTGCTGGCCTACCAGTGTGCGGGGCCGCGCACAGCTAGTGGACCCCGAAAGGGC   600

Qy    601  TCAGGGCCCGCGCCCCGCCAGGACCCCGAAGGCGTCTGGGATGCGAACGGGC   660
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Db    601  TCAGGGCCCGCGCCCCGCCAGGACCCCGAAGGCGTCTGGGATGCGAACGGGC   660

Qy    661  CTGGAACCATAGCGTCAGGGAGGCCCGGGTCCCCGGGCCTGCCAGCCCCGGGTGGGAG   720
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Db    661  CTGGAACCATAGCGTCAGGGAGGCCCGGGTCCCCGGGCCTGCCAGCCCCGGGTGGGAG   720

Qy    721  GAGGCGCGGGGCAGTGCCGCCGAAGTCTGCGCGTTGGGCAGGGCCAGGGCTGGCGC   780
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Db    721  GAGGCGCGGGGCAGTGCCGCCGAAGTCTGCGCGTTGGGCAGGGCCAGGGCTGGCGC   780

Qy    781  TGCCCCTGAGCGGAGCGGACGCCCGTTGGGCAGGGCCTGGCCCACCCGGCAGGAC   840
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Db    781  TGCCCCTGAGCGGAGCGGACGCCCGTTGGGCAGGGCCTGGCCCACCCGGCAGGAC   840

Qy    841  GCGTGACCGAGTGACCGTGGTTTCTGTGTGGTGTGTGTCACCTGCCGCCCACTCGTGGCCGGCCA   900
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Db    841  GCGTGACCGAGTGACCGTGGTTTCTGTGTGGTGTGTGTCACCTGCCGCCCACTCGTGGCCGGCCA   900

Qy    901  CACCTCTTTGGAGAGGTGCGCTCTCGGGCCTGGGCCGCCA   960
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Db    901  CACCTCTTTGGAGAGGTGCGCTCTCGGGCCTGGGCCGCCA   960

Qy    961  GCACCACGCGGGCCCCCATCACAATCGCGGCACGCTCCTGGACACGCCCTTGTCC  1020
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Db    961  GCACCACGCGGGCCCCCATCACAATCGCGGCACGCTCCTGGACACGCCCTTGTCC  1020

Qy   1021  CCCGGTGTACGGCGACCGAGACCACCAAGACCACTTCCTCTACTCCTCAGGCGCAGCAGCTGCG  1080
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Db   1021  CCCGGTGTACGGCGACCGAGACCACCAAGACCACTTCCTCTACTCCTCAGGCGCAGCAGCTGCG  1080

Qy   1081  GCCCTCCTCCTACTCAGCTCTCTGAGGCCGTCGGACTGGCGCTCGGAGGCTCGTTGA  1140
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Db   1081  GCCCTCCTCCTACTCAGCTCTCTGAGGCCGTCGGACTGGCGCTCGGAGGCTCGTTGA  1140

Qy   1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCGAGGTGCT  1200
           |||||||||||||||||||||||||||||||||||||||||
Db   1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCGAGGTGCT  1200

Qy   1201  GCCCAGCGCTACTGGCAAATGCGCGCCCCGTTTCTGGAGCTGCTTGGGAACCACGCGG  1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  GCCCAGCGCTACTGGCAAATGCGCGCCCCGTTTCTGGAGCTGCTTGGGAACCACGCGG  1260

Qy   1261  GTGCCCCTACGGGTGCTTCCTCCTCAAGACGCGCACTCCCGGGTGTTGCCTGCCCTGGGACGGC  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 1261 GTGCCCCTACGGGGTGCTTCCTCAAGACGCACTGCCCGCTGCCGAGCTGCGGTCACCCCAGC 1320

Qy 1321 AGCCGGTGTCTGTGCCCGGAGAAGCCCCAGGGGCTCTGTGGCCGGCCCCGAGGAGGAGGA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 AGCCGGTGTCTGTGCCCGGAGAAGCCCCAGGGGCTCTGTGGCCGGCCCCGAGGAGGAGGA 1380

Qy 1381 CACAGACCCCGTCGCCTGGTCAGCTGCTCCGCCAGCACAGCCCTGCCAGGTGTA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 CACAGACCCCGTCGCCTGGTCAGCTGCTCCGCCAGCACAGCCCTGCCAGGTGTA 1440

Qy 1441 CGGCTTCGTGCCGGGCCTGCCTGCCGGCCGGCTGCGGCCGCTGCCCCAGGCCTCTTGGGGGCTCCAGGCA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 CGGCTTCGTGCCGGGCCTGCCTGCCGGCCGGCTGCGGCCGCTGCCCCAGGCCTCTTGGGGGCTCCAGGCA 1500

Qy 1501 CAACGAACGCCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGAAGCATGCCAA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501 CAACGAACGCCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGAAGCATGCCAA 1560

Qy 1561 GCTCTCGCTGCCGGAGCTGACGTGGAAGATAGCGTGCGGGACTGCGCTTGGCTGCCGCAG
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Db 1561 GCTCTCGCTGCCGGAGCTGACGTGGAAGATAGCGTGCGGGACTGCGCTTGGCTGCCGCAG 1620

Qy 1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCACCGCCTGCTGCGTGGCGAGGAGATCCTGGC
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Db 1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCACCGCCTGCTGCGTGGCGAGGAGATCCTGGC 1680

Qy 1681 CAAGTTCCTGACTGGCTGACTGAGTGTGTACGTCGTCGAGCTCTCAGGTCTTTCTTTTA
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Db 1681 CAAGTTCCTGACTGGCTGACTGAGTGTGTACGTCGTCGAGCTCTCAGGTCTTTCTTTTA 1740

Qy 1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTTGTCTGGAG
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Qy 1801 CAAGTTGCAAAGCATTGGAATCAGAACAGCACTTGAACAGGGTGCAGCTGCGCGGGAGCTGTC
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Db 1801 CAAGTTGCAAAGCATTGGAATCAGAACAGCACTTGAACAGGGTGCAGCTGCGCGGGAGCTGTC 1860

Qy 1861 GGAAGCAGAGTCAGGCAGCATCGGAGCGGCGCGGCCAGCCCGCGCCCCGGAAGCCAGCTCCG
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Db 1861 GGAAGCAGAGTCAGGCAGCATCGGAGCGGCGCGGCCAGCCCGCGCCCCGGAAGCCAGCTCCG 1920

Qy 1921 CTTCATCCCCAAGCCTGACGGCGTGCCGATTGTGAACATGGACTACGTCGTGGGGAGC
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Db 1921 CTTCATCCCCAAGCCTGACGGCGTGCCGATTGTGAACATGGACTACGTCGTGGGGAGC 1980

Qy 1981 CAGAACCTTCCCGCAGAGAAAAAGAGAGGGCGTCACCTGTGAGGGTGAAGGCCACTGTT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1981 CAGAACCTTCCCGCAGAGAAAAAGAGAGGGCGTCACCTGTGAGGGTGAAGGCCACTGTT 2040

Qy 2041 CAGCAGGCTGTCAACTACGAGCGGCGCGCGGCCTCCGGCTCCTGTGCTGGGG
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Db 2041 CAGCAGGCTGTCAACTACGAGCGGCGCGCGGCCTCCGGCTCCTGTGCTGGGG 2100

Qy 2101 CCTGGACGATATCCACAGAGCCTGGCCACCTTCGTGCTGCGTGTGCCCAGGACCC
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Db 2101 CCTGGACGATATCCACAGAGCCTGGCCACCTTCGTGCTGCGTGTGCCCAGGACCC 2160

Qy 2161 GCCGCCTGAGCGTGTACTTGTCAAGGTGGATGTGACGGCGCCGCTACGACACCATCCCCCA
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Db 2161 GCCGCCTGAGCGTGTACTTGTCAAGGTGGATGTGACGGCGCCGCTACGACACCATCCCCCA 2220

Qy 2221 CAGCAGGCTGTCAACTACGAGGTCATCGCCAGCATCATCAAAAACCCCAGAACGTACTGCGTTGCG
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Db 2221 CAGCAGGCTGTCAACTACGAGGTCATCGCCAGCATCATCAAAAACCCCAGAACGTACTGCGTTGCG 2280

Qy 2281 TCGGTATGCCGTGGTCAGAAGGCCACGTCCCCATGGGCACGGCCTTCAAGGACCA
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Db 2281 TCGGTATGCCGTGGTCAGAAGGCCACGTCCCCATGGGCACGGCCTTCAAGGACCA 2340

Qy 2341 CGTCTCTACCTTGACAGACCTTCCAGCCTGCTACATGCGACCAGTTCGTGCTGCTCACCTGCAGGA
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Db 2341 CGTCTCTACCTTGACAGACCTTCCAGCCTGCTACATGCGACCAGTTCGTGCTGCTCACCTGCAGGA 2400

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Qy 2461 CAGTGGCCTCTTCGACGTCTTCGACGTCTTCATGTGCCACACGCGTGCGCATCAGGGG
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Db 2641 GCTCTCGCTGCGTTGGTGGATGATTTCTTGTGGTGACACCTCACCCACGCGCGAAAAC 2700

Qy 2701 CTTCCTCAGGACCCCGGTCCGGAGTGTCCCGAGTGTCCCGAGTATGGCTGCGTGGTGAACTTGCGGAA
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Qy 2761 GACAGTGGTGAACTTCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAGAT
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Db 2761 GACAGTGGTGAACTTCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAGAT 2820

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Db 3001 CAAGATCCTGCTGCTACAGGTTCACGCGTACAGGGTTCACGCGTACAGGTGGCTGTGCCACTCCCATTTCA 3060

Qy 3061 TCAGCAAGTTGGAAGAACCCCACCATTTTCCTGCGCATCTCGACACGGCCTCCCT
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Qy 3121 CTGCTACTCCATCCTGAAAGCCAGGCCGCCGTCCCGGGGGCCCGCCGCAGGCGGCGC
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Db 3121 CTGCTACTCCATCCTGAAAGCCAGGCCGCCGTCCCGGGGGCCCGCCGCAGGCGGCGC 3180

Qy 3181 CGGCCCCTGCTCGCCCTCGCCCGGAGGCGGCGCATTCCTGCCACCAAGCCATTCCTGCTCCAAGCT
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Db 3181 CGGCCCCTGCTCGCCCTCGCCCGGAGGCGGCGCATTCCTGCCACCAAGCCATTCCTGCTCCAAGCT 3240

Qy 3241 GACTCGACAACGGTGCTCACTCAGGGTGCCACCTACGGGGTCACTCAGGACGACGCA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3241 GACTCGACAACGGTGCTCACTCAGGGTGCCACCTACGGGGTCACTCAGGACGACGCA 3300

Qy 3301 GCTGAGTCCGAAGCTGACTCCCGGGAACGCCAGCGTCGACTGCCTTCAAGAGCCGGC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3301 GCTGAGTCCGAAGCTGACTCCCGGGAACGCCAGCGTCGACTGCCTTCAAGAGCCGGC 3360

Qy 3361 ACTGCCCTCAGACTTCAAGAACTCCTGACTGAATGGCGCCATCCTGGACTGATGGGCCGCCGGA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3361 ACTGCCCTCAGACTTCAAGAACTCCTGACTGAATGGCGCCATCCTGGACTGATGGGCCGCCGGA 3420

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Qy    61  GCGCGCTCCCGGTGCCGAGCCGTGCCGCTCCTGCGCAGCCACTACCGGAGGTGCT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GCGCGCTCCCGGTGCCGAGCCGTGCCGCTCCTGCGCAGCCACTACCGGAGGTGCT  120

Qy   121  GCCCTGCTGGCCACGTTCGTGCGGCGCGCTGGGAGTCTGAGGCTGAGTGAGTGTTTGGGCCGGAGGCCTG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GCCCTGCTGGCCACGTTCGTGCGGCGCGCTGGGAGTCTGAGGCTGAGTGAGTGTTTGGGCCGGAGGCCTG  180

Qy   181  GGACCCGGCGGCTTCCGGGCTGCTGAGGGCTGAGCCGGCAGTCCAGCCAAGGGCT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  GGACCCGGCGGCTTCCGGGCTGCTGAGGGCTGAGCCGGCAGTCCAGCCAAGGGCT  240

Qy   241  ACGGCCGCACCACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ACGGCCGCACCACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA  300

Qy   301  CCGAGTGCTGCGCAGAGGCTGTGCGAGCGGCCGGCGGGCGCGAAGAACGTGGCCTTCGGCTTCGC  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CCGAGTGCTGCGCAGAGGCTGTGCGAGCGGCCGGCGGGCGCGAAGAACGTGGCCTTCGGCTTCGC  360

Qy   361  GCTGCTGGACGGGGCCGCCGGGGGCCCCCCGAGGGCCTTCACCACCAGCCTGCCGCAGCTA  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GCTGCTGGACGGGGCCGCCGGGGGCCCCCCGAGGGCCTTCACCACCAGCCTGCCGCAGCTA  420

Qy   421  CCTGCCCACACGTGACCGACGCGACTGCGGGGAGCGGGCGTGGGGCGTCGGCGCTCTGCTGCGG  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  CCTGCCCACACGTGACCGACGCGACTGCGGGGAGCGGGCGTGGGGCGTCGGCGCTCTGCTGCGG  480

Qy   481  CCCGGTGGGCGACGACGTGCTGCCACCTGCGCCACGTGCTTGTTCACCTGGGTCTCTTTGTGCTGGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  CCCGGTGGGCGACGACGTGCTGCCACCTGCGCCACGTGCTTGTTCACCTGGGTCTCTTTGTGCTGGT  540

Qy   541  GGCTCCCAGTGCCGCCTACCAGGTGCCGGGGCCCGCGTGTACCAGCTCGGCGCGCTGCCAC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GGCTCCCAGTGCCGCCTACCAGGTGCCGGGGCCCGCGTGTACCAGCTCGGCGCGCTGCCAC  600

Qy   601  TCAGGCCCGGCCCCCCGCCACACGTGAGTGGACCCGCGAAGGCGTCTGGGATGCGAACGGGC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TCAGGCCCGGCCCCCCGCCACACGTGAGTGGACCCGCGAAGGCGTCTGGGATGCGAACGGGC  660

Qy   661  CTGGAACCATAGCGTCAGGAGGCCCGGTCCCCGTGGGTGCGGGAG  720
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  CTGGAACCATAGCGTCAGGAGGCCCGGTCCCCGTGGGTGCGGGAG  720

Qy   721  GAGGCGGGGGCAGTCCAGCGAAGTCTGCCGTTGCCCAAGAGGCGTGGGCGC  780
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  GAGGCGGGGGCAGTCCAGCGAAGTCTGCCGTTGCCCAAGAGGCGTGGGCGC  780

Qy   781  TGCCCCTGAGCCGGACGCGGCCGGTTGGCAGGGTCTGGCAGGTCACCTGGTGTCTGTGTGGTCACCTGCACCTCACCTCACC  840
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TGCCCCTGAGCCGGACGCGGCCGGTTGGCAGGGTCTGGCAGGTCACCTGGTGTCTGTGTGGTCACCTGCACCTCACCTCACC  840

Qy   841  GCGTGGACCGAGTGCCGTGGTTTCTGTGTGTCACCTGCACCGCGCCACCATCCGTGGGCGCCCA  900
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GCGTGGACCGAGTGCCGTGGTTTCTGTGTGTCACCTGCACCGCGCCACCATCCGTGGGCGCCCA  900

Qy   901  CACCTCTTTGGAGGTGCGCTCGCGCTCCATCCACACGTCCCTGGACACGCCTTGTCC  960
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CACCTCTTTGGAGGTGCGCTCGCGCTCCATCCACACGTCCCTGGACACGCCTTGTCC  960

Qy   961  GCCACCACGCGGGGCGCGGCCCCCATCCACACGCGGCCCGCGGCACTTCCTCTACTCCTCAGGCGACCAAGGACCAGTGCG  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  GCCACCACGCGGGGCGCGGCCCCCATCCACACGCGGCCCGCGGCACTTCCTCTACTCCTCAGGCGACGACAAGGAGCAGTGCG  1020

Qy  1021  CCCGGTGTACGCGGCACCAAGCACTTCCTCTACTCCTCAGGGCCCGACTGGCGCTCGGCTCGTGA  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  CCCGGTGTACGCGGCACGACCAAGCACTTCCTCTACTCCTCAGGCCCGACTGGCGCTCGGCTCGCGG  1080

Qy  1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCCACCGCGCTTCCGGAGGCTCGTGA  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCCAGCCTGACTGGCTCGAGGCTCGTGA  1140

Qy  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCGCAGGACTCCCGCAGGTTGCCCCGCCT  1200
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Qy  3481  GAGCAGACACCAGCAGCCCTGTCACGCCGACACGCCCTCTACGTGCCCAGGAGGAGGGGGCGGCC  3540
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Db  3481  GAGCAGACACCAGCAGCCCTGTCACGCCGACACGCCCTCTACGTGCCCAGGAGGAGGGGGCGGCC  3540

Qy  3541  CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCTGTGAGGCTGAGTGAGTGTTTGGGCCGGAGGCCTG  3600
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCTGTGAGGCTGAGTGAGTGTTTGGGCCGGAGGCCTG  3600

Qy  3601  CATGTCCGGCTGAGGCTGAGCCGGCTCGCCGCTGAGGGCTGAGCCGGCGTCCAGCCAAGGGCT  3660
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  CATGTCCGGCTGAGGCTGAGCCGGCTCGCCGCTGAGGGCTGAGCCGGCGTCCAGCCAAGGGCT  3660

Qy  3661  GAGTGTCCAGCACACTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA  3720
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  ACGGCGTCCAGCACACTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA  3720

Qy  3721  GGGCCAGCTTTCCTCACCAGGAGACCCGGCTTCCACTCCCCACATAGGAATAGTAGTCCATCC  3780
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  GGGCCAGCTTTCCTCACCAGGAGACCCGGCTTCCACTCCCCACATAGGAATAGTAGTCCATCC  3780

Qy  3781  CCAGATTCGCCATTGTTCACCCCTCGCCCTCCGCCCTGCCTTCCACCCCCACCATCC  3840
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  CCAGATTCGCCATTGTTCACCCCTCGCCCTCCGCCCTGCCTTCCACCCCCACCATCC  3840

Qy  3841  AGGTGAGAGACCCTGAGAAGGACCCTGGGAGTCTGGGAATTTGGAGTGAGGACCAAAGGTGTG  3900
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  AGGTGGAGACCCTGAGAAGGACCCTGGGAGTCTGGGAATTTGGAGTGAGGACCAAAGGTGTG  3900

Qy  3901  CCCTGTACACAGGCGGAGGACCCTGCACCTGGGAGTCTGGATGGGGGTCCTGTGGGTCAAATTGGGGG  3960
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901  CCCTGTACACAGGCGGAGGACCCTGCACCTGGGAGTCTGGATGGGGGTCCTGTGGGTCAAATTGGGGG  3960

Qy  3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA  4015
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Db  3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA  4015
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RESULT 7

US-09-675-321-1

; Sequence 1, Application US/09675321

; Patent No. 6440735

; GENERAL INFORMATION:

;   APPLICANT: Gaeta, Federico C.A.

;   APPLICANT: Geron Corporation

;   TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune

;   TITLE OF INVENTION: Response to a Telomerase Antigen

;   FILE REFERENCE: 015389-003500PC

;   CURRENT APPLICATION NUMBER: US/09/675,321

;   CURRENT FILING DATE: 2000-09-28

;   PRIOR APPLICATION NUMBER: US 60/112,006

;   PRIOR FILING DATE: 1998-03-31

;   PRIOR APPLICATION NUMBER: WO PCT/US99/06898

;   PRIOR FILING DATE: 1999-03-30

;   NUMBER OF SEQ ID NOS: 2

;   SOFTWARE: PatentIn Ver. 2.0

;   SEQ ID NO 1

;   LENGTH: 4015

;   TYPE: DNA

;   ORGANISM: Homo sapiens

;   FEATURE:

;   NAME/KEY: CDS

;   LOCATION: (56)..(3454)

;   OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)

US-09-675-321-1

Query Match   100.0%; Score 4015; DB 4; Length 4015;
Best Local Similarity   100.0%;
Matches 4015; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     1  GCAGGCCTGCCTGCCTGCCGCAGTGGGGAGCCCTGGCCCACCCCCGCCCACCCCCGCGATGCC  60
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  GCAGGCCTGCCTGCCTGCCGCAGTGGGGAGCCCTGGCCCACCCCCGCCCACCCCCGCGATGCC  60
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Db  1141  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1200
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Qy  1201  GCCCCAGCGCTACTGGCAAATGCGGCCCCGTGTTCTGGAGCTGCTTGAGGCTGCCCGCGCA  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  GCCCCAGCGCTACTGGCAAATGCGGCCCCGTGTTCTGGAGCTGCTTGAGGCTGCCCGCCGCA  1260

Qy  1261  GTGCCCCTACGGGGTGTCCTCAAGACCCACTGCCGCCGCTGCGAGCTGCGGTCACCCCAGC  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  GTGCCCCTACGGGGTGTCCTCAAGACCCACTGCCGCCGCTGCGAGCTGCGGTCACCCCAGC  1320

Qy  1321  AGCCGGTGTCTGTGCCCGGGAGAAGCCCAGGGCTCGTGCCGGCGCCCGAGGAGGAGGA  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  AGCCGGTGTCTGTGCCCGGGAGAAGCCCAGGGCTCGTGCCGGCGCCCGAGGAGGAGGA  1380

Qy  1381  CACAGACCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGTA  1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CACAGACCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGGCGTCTGTA  1440

Qy  1441  CGGCTTCGTGCGGGGGCCCTGGCGTGCGGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGCA  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  CGGCTTCGTGCGGGGGCCCTGGCGTGCGGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGCA  1500

Qy  1501  CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560

Qy  1561  GCTCTCGCTGCAGGAGCTGACGTGCAGGATGAGCGTGCCGCTTGCGTTGGAGGATCCTGGC  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  GCTCTCGCTGCAGGAGCTGACGTGCAGGATGAGCGTGCCGCTTGCGTTGGAGGATCCTGGC  1620

Qy  1621  GAGCCCAGGGTTGGCTGTGTTCCGGCCGCAGACACCGTGCGCGTGGAGGATCCTGGC  1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  GAGCCCAGGGTTGGCTGTGTTCCGGCCGCAGACACCGTGCGCGTGGAGGATCCTGGC  1680

Qy  1681  CAAGTTCCTGCACTGGCTGGATGAGTGTGTACGTCGTCAGTCTTCTCTTTA  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  CAAGTTCCTGCACTGGCTGGATGAGTGTGTACGTCGTCAGTCTTCTCTTTA  1740

Qy  1741  TGTTCACGGAGACCACGTTCAAAAGACAGGCTCTCTTTTCTACCGGAAGAGTGTCTGGAG  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  TGTTCACGGAGACCACGTTCAAAAGACAGGCTCTCTTTTCTACCGGAAGAGTGTCTGGAG  1800

Qy  1801  CAAGTTGCAAAGCATTGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGTCGCGGAGCTGTC  1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  CAAGTTGCAAAGCATTGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGTCGCGGAGCTGTC  1860

Qy  1861  GGAAGCAGAGGTCAGGCAGCAGCATCGGGAAGCCGCGCGGCGGCCGGCTGCGACTTCCG  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  GGAAGCAGAGGTCAGGCAGCAGCATCGGGAAGCCGCGCGGCGGCCGGCTGCGACTTCCG  1920

Qy  1921  CTTCATCCCCAAGCCTGGACGGGCTCGGCGGCCGGATTGTGAACATGGACTCGTGGGAGC  1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CTTCATCCCCAAGCCTGGACGGGCTCGGCGGCCGGATTGTGAACATGGACTCGTGGGAGC  1980

Qy  1981  CAGAACGTTCCGCAGAGAAAAGAGGGTGAAGGCCGCTCACCTGAAGGCACTGTT  2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAGAAACGTTCCGCAGAGAAAAGAGGGTGAAGGCCGCTCACCTGAAGGCACTGTT  2040

Qy  2041  CAGCGTGCTCAACTACGAGCGGGCGGCGGCCGGCACCTTGGGCGCCTCTGTGCTGTGGG  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CAGCGTGCTCAACTACGAGCGGGCGGCGGCCGGCACCTTGGGCGCCTCTGTGCTGTGGG  2100

Qy  2101  CCTGGACGATATCCACACAGGGCCACCTTGCTGCGTCGTCGGGGGCCCCAGGACCC  2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTGGACGATATCCACACAGGGCCACCTTGCTGCGTCGTCGGGGGCCCCAGGACCC  2160

Qy  2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGACATGGACGGGCGCTACGACACCATCCCCA  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGACATGGACGGGCGCTACGACACCATCCCCA  2220

Qy  2221  GGACAGGCTCACGGAGGTCATCGCGCCAGCAATCATCAAACCCAGAACACGTACTGCGTGCG  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGACAGGCTCACGGAGGTCATCGCGCCAGCAATCATCAAACCCAGAACACGTACTGCGTGCG  2280

Qy  2281  TCGGTATGCCGTGGTGTCCAGAGTTCGACGTCCGGCTTCGTGGCTCACCTGCAGGA  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCGGTATGCCGTGGTGTCCAGAGTTCGACGTCCGGCTTCGTGGCTCACCTGCAGGA  2340

Qy  2341  CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCCGACAGTTCGTGGCTCACCTGCAGGA  2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCCGACAGTTCGTGGCTCACCTGCAGGA  2400

Qy  2401  GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCACGAGCAGAGCTCCTCCTGAATGAGGCCAG  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCACGAGCAGAGCTCCTCCTGAATGAGGCCAG  2460

Qy  2461  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCGTGCCACCAGGGGG  2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCGTGCCACCAGGGGG  2520

Qy  2521  CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCCAGGGCCTCCTCATCCTCTCCACGCGTGCTCTG  2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCCAGGGCCTCCTCATCCTCTCCACGCGTGCTCTG  2580

Qy  2581  CAGCCTGTGCTACGGCGACATGATGAGAACAAGCTGTTTGGTGACACCTCACCTCACCGCGGGGCT  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CAGCCTGTGCTACGGCGACATGATGAGAACAAGCTGTTTGGTGACACCTCACCTCACCGCGGGGCT  2640

Qy  2641  GCTCTCGCTTGTGTGATGATTTCTTGTTGGTGACACCTCACCTCACCGCGCGAAAAC  2700
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Db  2641  GCTCTCGCTTGTGTGATGATTTCTTGTTGGTGACACCTCACCTCACCGCGCGAAAAC  2700

Qy  2701  CTTCCTCAGGACCCTGGTCCGAGTGTCCCGAGTATGGCTGCGTGGTGGTGAACTTGCGGAA  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CTTCCTCAGGACCCTGGTCCGAGTGTCCCGAGTATGGCTGCGTGGTGGTGAACTTGCGGAA  2760

Qy  2761  GACACAGTGGTGAACTTCCCTGTAGAAGACAGAGGCCCTGGCTGCACGGCTTTGTTCAGAT  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  GACACAGTGGTGAACTTCCCTGTAGAAGACAGAGGCCCTGGCTGCACGGCTTTGTTCAGAT  2820

Qy  2821  GCCGGCCCACGGCTATTCCCCTGCTGCGCGGCCTCGCTGCTGGATACCCGGACCCTGGAGGT  2880
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Db  2821  GCCGGCCCACGGCTATTCCCCTGCTGCGCGGCCTCGCTGCTGGATACCCGGACCCTGGAGGT  2880

Qy  2881  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCATCAGAGCCAGTCTCACCTTCAACCG  2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCATCAGAGCCAGTCTCACCTTCAACCG  2940

Qy  2941  CGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGGGCTGCGAAGTG  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  CGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGGGCTGCGAAGTG  3000

Qy  3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCGAACAGCTGTGCACCAACATCTA  3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCGAACAGCTGTGCACCAACATCTA  3060

Qy  3061  CAAGATCCTCCTGCTGCAGCGGTACACAGGTTCACGCATGTGTGTGCTGCAGCTCCATTTCA  3120
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Db  3061  CAAGATCCTCCTGCTGCAGCGGTACACAGGTTCACGCATGTGTGTGCTGCAGCTCCATTTCA  3120

Qy  3121  TCAGCAAGTTGGAAGAACCCACATTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT  3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  TCAGCAAGTTGGAAGAACCCACATTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT  3180

Qy  3181  CTGCTACTCCATCCTGAAAGCTGAAAGCCAGGCCAAGAACCCAGGGGGCGCCAAGGGCGCGGC  3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  CTGCTACTCCATCCTGAAAGCTGAAAGCCAGGCCAAGAACCCAGGGGGCGCCAAGGGCGCGGC  3240

Qy  3241  CGGCCCTCGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  CGGCCCTCGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT  3300

Qy  3301  GACTCGACACCGTGTCACCTCACGTGCCACTCGGGTCACTCAGGACAGCCCAGACGCGCA  3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  GACTCGACACCGTGTCACCTCACGTGCCACTCGGGTCACTCAGGACAGCCCAGACGCGCA  3360
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Qy   3361  GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAACCCGGC  3420
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Db   3361  GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAACCCGGC  3420

Qy   3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGGCCACAGCCAGGCCGA  3480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGGCCACAGCCAGGCCGA  3480

Qy   3481  GAGCAGACACCAGCAGCCCTGTCACGCCGGCTCTACGTCCCAGGGAGGGAGGGGCGGCC  3540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  GAGCAGACACCAGCAGCCCTGTCACGCCGGCTCTACGTCCCAGGGAGGGAGGGGCGGCC  3540

Qy   3541  CACACCCAGGCCCGCACCCGGAGTCGAGGCCTGAGTGAGTGTTGGCCGAGGCCTG  3600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  CACACCCAGGCCCGCACCCGGAGTCGAGGCCTGAGTGAGTGTTGGCCGAGGCCTG  3600

Qy   3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGGCT  3660
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Db   3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGGCT  3660

Qy   3661  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA  3720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA  3720

Qy   3721  GGGCCAGCTTTTCCTCACCAGGACGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC  3780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  GGGCCAGCTTTTCCTCACCAGGACGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC  3780

Qy   3781  CCAGATTCGCCATTGTTCACCCCTCCTTGCCTTCCACCCCACCATCC  3840
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781  CCAGATTCGCCATTGTTCACCCCTCCTTGCCTTCCACCCCACCATCC  3840

Qy   3841  AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG  3900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841  AGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTG  3900

Qy   3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGGGGTCAAATTGGGGG  3960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGGGGTCAAATTGGGGG  3960

Qy   3961  GAGGTGCTGTGGGAGTAAAATACTGAAATATGAGTTTTCAGTTTTGAAAAAAA  4015
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961  GAGGTGCTGTGGGAGTAAAATACTGAAATATGAGTTTTCAGTTTTGAAAAAAA  4015
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Query Match               100.0%;  Score 4015;  DB 4;  Length 4015;
Best Local Similarity     100.0%;  Pred. No. 0;
Matches 4015;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1  GCAGCGCTGCGTCCTGCTGCGCACGTGGGACAGCCTGGAAGCCCTGCACCCCGGCCACCCCGCGATGCC   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  GCAGCGCTGCGTCCTGCTGCGCACGTGGGACAGCCTGGAAGCCCTGCACCCCGGCCACCCCGCGATGCC   60

Qy   61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  120
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Qy   121 GCCGCTGCCACGTTCTGCGCGCCTGGGCGCGCCTGGGCGCTGGTCTGGTGTCAGCGGCGG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCCGCTGCCACGTTCTGCGCGCCTGGGCGCGCCTGGGCGCTGGTCTGGTGTCAGCGGCGG 180

Qy   181 GGACCCGGCGGCTTTCCGCGCCGCGCCCCCCGCGCCCGTGGTGGCCGTGGTGCCTGCCTGTGTGCCTGCCGCCTGGGACGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACCCGGCGGCTTTCCGCGCCGCGCCCCCCGCGCCCGTGGTGGCCGTGGTGCCTGCCTGTGTGCCTGCCGCCTGGGACGC 240

Qy   241 ACGGGCCGCCGCCGCCCCCGCCCCCCCTCCTTCCGCGCCGCGCCCCCTCCTTCCGCGGTGTCCTCGAAGGAGCTGGTGGC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACGGGCCGCCGCCGCCCCCGCCCCCCCTCCTTCCGCGCCGCGCCCCCTCCTTCCGCGGTGTCCTCGAAGGAGCTGGTGGC 300

Qy   301 CCGAGTGCTGCAGAGGCTGTGCGAGCCGCGGCGCGAAGAACGTGCTGCGCCTTCGGCTTCGC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGAGTGCTGCAGAGGCTGTGCGAGCCGCGGCGCGAAGAACGTGCTGCGCCTTCGGCTTCGC 360

Qy   361 GCTGCTGGACGGGGCCCGGGGGGGCCCCCCGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCTGCTGGACGGGGCCCGGGGGGGCCCCCCGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA 420

Qy   421 CCTGCCCAACACGGTGACGACGACGTGCTCGCGGGGAGCGGGGGGCGTGGGGGCTGTCTGCGG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTGCCCAACACGGTGACGACGACGTGCTCGCGGGGAGCGGGGGGCGTGGGGGCTGTCTGCGG 480

Qy   481 CCGGGTGGGCGACGACGTGCTTGGTTCACCTGGCGCGGCGCTCTTTGTGTCTGGT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCGCGTGGGCGACGACGTGCTTGGTTCACCTGGCGCGGCGCTCTTTGTGTCTGGT 540

Qy   541 GGCTCCCAGCTGCGCGCTACCAGGTGTGCGGGCGCCGCGAAGTCTGCGCGTGCCTGCCAC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCTCCCAGCTGCGCGCTACCAGGTGTGCGGGCGCCGCGAAGTCTGCGCGTGCCTGCCAC 600

Qy   601 TCAGGGCCCGGGCCCCCCCGCCCGTGGACCCCGAAGGCGTCTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCAGGGCCCGGGCCCCCCCGCCCGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC 660

Qy   661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCGGTCCCCAGCCCCGGGTGCGAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCGCGTCTCTGGCACGCGCCCACTGGGTGCGAG 720

Qy   721 GAGGGCCGGGGGCAGTGCCAGCGGAAGTCTGCGCGTGCCCGTTGCCCGTGCCGGAGTCTGCGCCAGCCGTGGCGCGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GAGGGCCGGGGGCAGTGCCAGCGGAAGTCTGCGCGTGCCCGTTGCCCGTGCCGGAGTCTGCGCCAGCCGTGGCGCGC 780

Qy   781 TGCCCCTGAGCCGGAGCCGGACGCCCGTTGGGCAGGGTCTCGGTCACCTCCCACCCGGTGGGCCCGCCA 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGCCCCTGAGCCGGAGCCGGACGCCCGTTGGGCAGGGTCTCGGTCACCTCCCACCCGGTGGGCCCGCCA 840

Qy   841 GCGTGGACGAGTGACGTGCTCAGCGGGGGTGTTCTGTGTGTGGTCACCTGGTGTGTGGTCACCTCCCAGAGGCCCACCCGGCCGGCGCCAGAAAGC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCGTGGACGAGTGACGTGCTCAGCGGGGGTGTTCTGTGTGTGGTCACCTGGTGTGTGGTCACCTCCCAGAGGCCCACCCGGCCGGCGCCAGAAAGC 900

Qy   901 CACCTCTTTGGAGGGTGTCGCGTCTCTGGCACGCGCCACTCCCACCCGCCACCATCCCGTGGGCCGCCA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CACCTCTTTGGAGGGTGTCGCGTCTCTGGCACGCGCCACTCCCACCCGCCACCATCCCGTGGGCCGCCA 960

Qy   961 GCACCACGCGGGGCCCCCATCCACATCGCGGCCACCACGTCCCGGACACGGCCTTGTCC 1020
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Db   961 GCACCACGCGGGGCCCCCATCCACATCCACATCGCGGCCACCACGTCCCGGACACGGCCTTGTCC 1020

Qy   1021 CCCGGTGTACGGCGACCAAGCACTTCCTCTACTCCTGGCAGGCCCGACAAGGAGCAGCTGCG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCCGGTGTACGGCGACCAAGCACTTCCTCTACTCCTGGCAGGCCCGACAAGGAGCAGCTGCG 1080

Qy   1081 GCCCTCCTTCTACTCAGCTCTCGAGGGCCTGACTGGCGCTCGGAGGTTCGTGGTCGTGGA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCCCTCCTTCTACTCAGCTCTCGAGGGCCTGACTGGCGCTCGGAGGTTCGTGGTCGTGGA 1140

Qy   1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGGGTTCCCCGCCT 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGGGTTCCCCGCCT 1200

Qy   1201 GCCCCAGCGCTACTGCCAAATGCGGCTACTGGGGTGCTTTGGGACTGCTTGGGACTGCCTGCTCACCCCAGC 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GCCCCAGCGCTACTGGGGTGCTTTGGGACTGCTTGGGACTGCCTGCTCACCCCAGC 1260

Qy   1261 GTGCCCCTACGGGGTGCTCCTCCTGGGGAGAAGCCACTGCCGCCGCGAGCTGCGGTGCGCTGGGACGC 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGCCCCTACGGGGTGCTCCTCCTGGGGAGAAGCCACTGCCGCCGCGAGCTGCGGTGCGCTGGGACGC 1320

Qy   1321 AGCCGGTGTCGTGCCCGGGAGAAGCCTCTGTGCCCCCGGGGCTCTGTGCGGGAAGCATGCCAA 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGCCGGTGTCGTGCCCGGGAGAAGCCTCTGTGCCCCCGGGGCTCTGTGCGGGAAGCATGCCAA 1380

Qy   1381 CACAGACCCCGTCGCCTGCTCCGCCAGCTGCTGCAGCAGAGCAGCAGCCCCTGGCAGGTGTA 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CACAGACCCCGTCGCCTGCTCCGCCAGCACAGCAGAGCACAGCAGCCCCTGGCAGGTGTA 1440

Qy   1441 CGGCTTCGTGCGCGGCCTGGTGCCCTGGTGCCCCAGGCCTCCTGGGGCTCCAGGCA 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CGGCTTCGTGCGCGGCCTGGTGCCCTGGTGCCCCAGGCCTCCTGGGGCTCCAGGCA 1500

Qy   1501 CAACGAACGCCGCTTCCTCCTCAGGAACACCACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CAACGAACGCCGCTTCCTCCTCAGGAACACCACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

Qy   1561 GCTCTCGCTGCCAGGAGCTGGAAGATGAGCGTGCGGGACTGCGCGCTTGGCTGCGCGCAG 1620
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Db   1561 GCTCTCGCTGCCAGGAGCTGGAAGATGAGCGTGCGGGACTGCGCGGTGGCGTGGCGCGCAG 1620

Qy   1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCGCGTCTGCGCAGAGCACCGTCTGCGCAGAGCACCGTCTGCGCTCTGCC 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCGCGTCTGCGCAGAGCACCGTCTGCGCAGAGCACCGTCTGCGCTCTGCC 1680

Qy   1681 CAAGTTCCTCACTCGGCTGCTGATGAGTGTGTACGTCGTCGTCGTCTCAGCTCTTTTTCTTTA 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CAAGTTCCTCACTCGGCTGCTGATGAGTGTGTACGTCGTCGTGATCTCAGCTCTTTTCTTTA 1740

Qy   1741 TGTCACGGAGACCACGTTTCAAAAGAACACAGGCTCTTTTTCTTACCGGAAGAGTGTCTGGAG 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 TGTCACGGAGACCACGTTTCAAAAGAACACAGGCTCTTTTTCTTACCGGAAGAGTGTCTGGAG 1800

Qy   1801 CAAGTTGCAAAGCATTGAATACAGAGTCGCGGGTGCAGGGTGCAGCTCACTTGAAGAGGGTCGAGCTGTC 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAAGTTGCAAAGCATTGAATACAGAGTCGCGGGTGCAGCTCACTTGAAGAGGGTCGAGCTGTC 1860

Qy   1861 GGAAGCAGAGGTCAGGCAGCAGCATCGGGAAGCCCGGCCAGGCCCGAGGGTGAAGCAGACTCCG 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 GGAAGCAGAGGTCAGGCAGCAGCATCGGGAAGCCCGGCCAGGCCCGAGGGTGAAGCAGACTCCG 1920

Qy   1921 CTTCATCCCCAAGCCTCGACGGCTGCGGCCGATTGTGAACATGGACTACGTCTGGGAGC 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTTCATCCCCAAGCCTCGACGGCTGCGGCCGATTGTGAACATGGACTACGTCTGGGAGC 1980

Qy   1981 CAGAACGTTCCGCAGAAAAGAGGCGGGGCGGCGCCGCGCCCTCTGCGCGGGAGC 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAGAACGTTCCGCAGAAGAAAGAGGCGGGGCGGCGCCGCGCCCTCTGCGCGGGAGC 2040

Qy   2041 CAGCCGTGCTCAACTACCAGCCTGGGACAAGCCTTGTCC 2100
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Db   2041 CAGCCGTGCTCAACTACCAGCCTGGGACAAGCCTTGTCC 2100

Qy   2101 CCTGGACGATATCCACAGGGCCCTGCGTCGTTCGTGCGCCCACCTTCGTGCGTGCGCCCAGGACCC 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTGGACGATATCCACAGGGCCCTGCGTCGTTCGTGCGCCCACCTTCGTGCGTGCGCCCAGGACCC 2160

Qy   2161 GCCGGCCTGAGCGTGTACTTTGTCAAGGTGGATGTGACGTGACGGGCGCCGCTACGACACCATCCCCCA 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCCGGCCTGAGCGTGTACTTTGTCAAGGTGGATGTGACGTGACGGGCGCTACGACACCATCCCCCA 2220

Qy   2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAAACGTACTGCCGTGCG 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAAACCCAGAAACGTACTGCCGTGCG 2280

Qy   2281 TCGGTATGCGTCGGTTGGTCCGAGGCCGCACGTCCGCAGTGCTTCGGAGCTGCTTCAAGAGCCA 2340
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Db   2281  TCGGTATGCCGTGGTCCAGAAGGCCCCATGGGACGTCCGCAAGGCCTTCAAGAGCCA   2340

Qy   2341  CGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA   2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  CGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA   2400

Qy   2401  GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCGAATGAGGCCAG   2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCGAATGAGGCCAG   2460

Qy   2461  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG   2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG   2520

Qy   2521  CAAGTCCTACGTCCAGTGCCAGGGGATCCCCCAGGGCTCCATCCTCTCCACGCTGCTCTG   2580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  CAAGTCCTACGTCCAGTGCCAGGGGATCCCCCAGGGCTCCATCCTCTCCACGCTGCTCTG   2580

Qy   2581  CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT   2640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT   2640

Qy   2641  GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCCTCACCTCACCGCACGGAAAAC   2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCCTCACCTCACCGCACGGAAAAC   2700

Qy   2701  CTTCCTCAGGACCCCGGTCGTCCCGAGTGTCCGTGGTGTGAGTATGCCGTGGTGCGGGAA   2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  CTTCCTCAGGACCCCGGTCGTCCCGAGTGTCCGTGGTGTGAGTATGCCGTGGTGCGGGAA   2760

Qy   2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCGTTTTGTTCAGAT   2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCGTTTTGTTCAGAT   2820

Qy   2821  GCCGGCCCACGGCCTATTCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGT   2880
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Db   2821  GCCGGCCCACGGCCTATTCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGT   2880

Qy   2881  GCAGAGCGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGACCAGTCTCACCTTCAACCG   2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  GCAGAGCGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGACCAGTCTCACCTTCAACCG   2940

Qy   2941  CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG   3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG   3000

Qy   3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGGCCTCCAACAGCGTGTGCACCAACATCTA   3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGGCCTCCAACAGCGTGTGCACCAACATCTA   3060

Qy   3061  CAAGATCCTTCTGCTGCAGGCGTACAGGTTTCACGCCATGTGCGTCGCAGCTCCCATTTCA   3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  CAAGATCCTTCTGCTGCAGGCGTACAGGTTTCACGCCATGTGCGTCGCAGCTCCCATTTCA   3120

Qy   3121  TCAGCAAGTTTGGAAGAACCCCACATTTTTCTCGCGCGTCATCTCTGACACGGCCTCCCT   3180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  TCAGCAAGTTTGGAAGAACCCCACATTTTTCTCGCGCGTCATCTCTGACACGGCCTCCCT   3180

Qy   3181  CTGCTACTCCATCCTGAAAGCTGAAACCGTGCGCAGGATGTCCGCTGGGGCGTGCAACATCTA   3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  CTGCTACTCCATCCTGAAAGCTGAAACCGTGCGCAGGATGTCCGCTGGGGCGTGCAACATCTA   3240

Qy   3241  CGGCCCCTGCGCCCTCCGAGCCGTGCAGTGCGTGCCGCACCAAGCATTCCTGCTCAAGCT   3300
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Db   3241  CGGCCCCTGCGCCCTCCGAGCCGTGCAGTGCGTGCCGCACCAAGCATTCCTGCTCAAGCT   3300

Qy   3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTCGGGTCAGCTCAGGACACGCCAGCGCA   3360
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Db   3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTCGGGTCAGCTCAGGACACGCCAGCGCA   3360

Qy   3361  GCTGAGTCGGAAGCTCCCGGGACGCACGCTGACTCGGGCTGCCCTGCGACTGCTCCGGC   3420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361  GCTGAGTCGGAAGCTCCCGGGACGCACGCTGACTCGGGCTGCCCTGCGACTGCTCCGGC   3420
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Qy   3421  ACTGCCCTCAGACTTCAAGAGACCATCCTGGACTGTGATGGCCACCACCGCCCACAGCCAGGCCGA   3480
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Db   3421  ACTGCCCTCAGACTTCAAGAGACCATCCTGGACTGTGATGGCCACCACCGCCCACAGCCAGGCCGA   3480

Qy   3481  GAGCAGACACCAGCAGCCCTGTCACGGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCC   3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  GAGCAGACACCAGCAGCCCTGTCACGGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCC   3540

Qy   3541  CACACCCAGGCCGCCGCCACCGGTCTGGGAGTCTGAGCGCCTGAGTGAGTGTTTGGCCAGGCTG   3600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  CACACCCAGGCCGCCGCCACCGGTCTGGGAGTCTGAGCGCCTGAGTGAGTGTTTGGCCAGGCTG   3600

Qy   3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGTGTCCGCTGAGGCCTGAGGCCTGAGGCCTCAGCCAAGGGCT   3660
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Db   3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGTGTCCGCTGAGGCCTGAGGCCTGAGGCCTCAGCCAAGGGCT   3660

Qy   3661  GAGTGTCCAGCACACCTGCGTCTTCACTTCCGTCTTCACTTCCCACAGGATAGAATAGTCCATCC   3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  GAGTGTCCAGCACACCTGCGTCTTCACTTCCGTCTTCACTTCCCACAGGATAGAATAGTCCATCC   3720

Qy   3721  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACTCCCCACCATCC   3780
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACTCCCCACCATCC   3780

Qy   3781  CCAGATTCGCCATTGTTCACCCCTGCCTTCCTTGCCTTCCTTGCCTTCCACCCCACCATCC   3840
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Qy   3841  AGTGGAGACCCCTGAGAAGGACCCTGGGAGCTCTGGGAGTTGGAATTGGACCAAAGGTGTG   3900
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Db   3841  AGTGGAGACCCCTGAGAAGGACCCTGGGAGCTCTGGGAGTTGGAATTGGACCAAAGGTGTG   3900

Qy   3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGGTCCTGTGGGTCAAATTGGGGG   3960
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Db   3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGGTCCTGTGGGTCAAATTGGGGG   3960

Qy   3961  GAGGTGCTGTGGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA   4015
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Db   3961  GAGGTGCTGTGGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA   4015
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PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 08/854,050
    FILING DATE:  09-MAY-1997
    CLASSIFICATION:  435
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 08/851,843
    FILING DATE:  06-MAY-1997
    CLASSIFICATION:  435
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 08/846,017
    FILING DATE:  25-APR-1997
    CLASSIFICATION:  435
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 08/844,419
    FILING DATE:  18-APR-1997
    CLASSIFICATION:  435
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  US 08/724,643
    FILING DATE:  01-OCT-1996
    CLASSIFICATION:  435
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    TELEPHONE:  (415) 576-0200
    TELEFAX:  (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
    LENGTH:  4015 base pairs
    TYPE:  nucleic acid
    STRANDEDNESS:  single
    TOPOLOGY:  linear
MOLECULE TYPE:  cDNA
FEATURE:
    NAME/KEY:  CDS
    LOCATION:  56..3454
    OTHER INFORMATION:  /product= "hTRT"
    OTHER INFORMATION:  /note= "human telomerase reverse
    OTHER INFORMATION:  transcriptase (hTRT) catalytic protein
    OTHER INFORMATION:  component"
US-08-912-951-1
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Query Match      100.0%;  Score 4015;  DB 4;  Length 4015;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 4015;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1  GCAGGCTGGCTGCCTGCTGCCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGGCGATGCC   60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GCAGGCTGGCTGCCTGCTGCCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGGCGATGCC   60

Qy     61  GCGCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGCGAGGTGCT  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GCGCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGCGAGGTGCT  120

Qy    121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCGCCCAGGGCTGGCGGCGTGCAGCGCGGCGG  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCGCCCAGGGCTGGCGGCGTGCAGCGCGGCGG  180

Qy    181  GGACCCGGCGGCTTCCGGCGCGCTGCCCTGGGGCGTGCGTGGTGCGGCCCAGTGCCCGGACGC  240
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Db    181  GGACCCGGCGGCTTCCGGCGCGCTGCCCTGGGGCGTGCGTGGTGCGGCCCAGTGCCCGGACGC  240

Qy    241  ACGGGCCGCTCCCGAGAGGCTGTGCCAGAGCTGCTCTGGCGCGGCCGGAAGAACGTGCTCGGCTTCGC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ACGGGCCGCTCCCGAGAGGCTGTGCCAGAGCTGCTCTGGCGCGGCCGGAAGAACGTGCTCGGCTTCGC  300

Qy    301  CCGAGTGCTGCAGAGGCTTCACCACCAGCGTGCGCAGCTA  360
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Db    301  CCGAGTGCTGCAGAGGCTTCACCACCAGCGTGCGCAGCTA  360
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Qy    361  GCTGCTGACGGGGCCGCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGGCAGCTA  420
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Db    361  GCTGCTGACGGGGCCGCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGGCAGCTA  420

Qy    421  CCTGCCCAACACGTGACGACGCACTGCGGGGGAGCCGGGGCGGGGGGCTGGGGGGCTGCTCGTCTGCG  480
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Qy    481  CGGCGTGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGGCGCGCTCTTTGTGCTGGT  540
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Db    481  CGGCGTGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGGCGCGCTCTTTGTGCTGGT  540

Qy    541  GGCTCCCAGCTGCGGCTACCAGTGTGGGGGCCGGCCGCCGCCGCCGTGTACCAGCTGCGAACGGGC  600
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Db    541  GGCTCCCAGCTGCGGCTACCAGTGTGGGGGCCGGCCGCCGCCGCCGTGTACCAGCTGCGAACGGGC  600

Qy    601  TCAGGCCCCGGCCCCACACGCTAGTGCCACACGCGTGGGACCCCGAAGGCGTCTGGGATGCGAACGGGC  660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TCAGGCCCCGGCCCCACACGCTAGTGCCACACGCGTGGGACCCCGAAGGCGTCTGGGATGCGAACGGGC  660

Qy    661  CTGGAACCATAGCGTCAGGGAGGCCGGGGGTCCCCTGGGCGTTGCCCAAGAGGCCCAGGCCGTGGCGC  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTGGAACCATAGCGTCAGGGAGGCCGGGGGTCCCCTGGGCGTTGCCCAAGAGGCCCAGGCCGTGGCGC  720

Qy    721  GAGGGCGCGGGGCAGTGCCAGCGCCGAAGTCTGCCGTTGCGAGGGTCTGGGCAGGGTCCACCCGGCAGGAC  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GAGGGCGCGGGGCAGTGCCAGCGCCGAAGTCTGCCGTTGCGAGGGTCTGGGCAGGGTCCACCCGGCAGGAC  780

Qy    781  TGCCCCTGAGCCCGAGCGACGCCCGTTGGGCAGGGTGTCACCTGGTGTCACCTGCCAGACCCGCCGAAGAGC  840
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Db    781  TGCCCCTGAGCCCGAGCGACGCCCGTTGGGCAGGGTGTCACCTGGTGTCACCTGCCAGACCCGCCGAAGAGC  840

Qy    841  GGTGGACCGAGTGACCGTGGTTTCGTTGTGTCGTTGTGTCACTCCGCAGACCCGCCGAAGAGC  900
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Db    841  GGTGGACCGAGTGACCGTGGTTTCGTTGTGTCGTTGTGTCACTCCGCAGACCCGCCGAAGAGC  900

Qy    901  CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGGCCCACTCCCACCATCCGTGGGCCGCCA  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGGCCCACTCCCACCATCCGTGGGCCGCCA  960

Qy    961  GCACCACGCGGGCCCCCATCCACATCGCGGCCACCAGTCCCTGGACACGCCTTGTCC  1020
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCCTCGGAGGCTCGTGGA  1140
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Qy   1141  GACCATCTTTCTGGGTTTCGGGGTTCCGGCAGCCAGGTGTCCTCGCGCAGAGGCTGGAGGTGCT  1200
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Qy   1201  GCCCCAGCGCTACTGGCAAATGCGGGCCCCGTGTTCTGGAGCTGCTTGGGAACCACGCGCA  1260
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Qy   1261  GTGCCCCTACGGGGCTTTCCGGCGCGCGTGGTGCCCAGTGCCAGTGCCACTGCTCCCGGTGTGCCTGGGACGC  1320
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Db   1261  GTGCCCCTACGGGGCTTTCCGGCGCGCGTGGTGCCCAGTGCCAGTGCCACTGCTCCCGGTGTGCCTGGGACGC  1320

Qy   1321  AGCGGTGTCTGTGCCCCGGGAGAAGCCTCGTGCCTGAAGGAGGCTGGTGGC  1380
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Db   1321  AGCGGTGTCTGTGCCCCGGGAGAAGCCTCGTGCCTGAAGGAGGCTGGTGGC  1380

Qy   1381  CACAGACCCCGTGGTGCCGCTGGTGCAGCTGCTCCCGCCGCACAGCAGCCCTGCCAGGTGTA  1440
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Db   1381  CACAGACCCCGTGGTGCCGCTGGTGCAGCTGCTCCCGCCGCACAGCAGCCCTGCCAGGTGTA  1440

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Db   1441  CGGCTTCGTGCGGGGCCTGCCGCTGCCGCGGCGCTGGTTGCCCGCGCTGGTTCCAGGCA  1500
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Qy   1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
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Db   1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

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Qy   1861 GGAAGCAGAGGTCAGGCAGCAGTCATCGGGAGAATCAGCAGCACTTCGGGAGAGGGTGCGCAGCTGCCAGACTCCG 1920
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Db   1861 GGAAGCAGAGGTCAGGCAGCAGTCATCGGGAGAATCAGCAGCACTTCGGGAGAGGGTGCGCAGCTGCCAGACTCCG 1920

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Db   1921 CTTCATCCCCAAGCCTGACGGCTGCGGCGATTGTGAACATCAGCACTTGAACAGGGGTGGGGAGC 1980

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Db   2041 CAGCGGCTGCTCAACTACGAGGGGCGCGGCGGCGGGCGGCCCGGGCCCTGTGCTGCGGG 2100

Qy   2101 CCTGGACGATATCCCACAGGGCCTGGCCGCCTTCGTGCGTGCGCGGCGACCC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTGGACGATATCCCACAGGGCCTGGCCGCCTTCGTGCGTGCGCGGCGACCC 2160

Qy   2161 GCCGCCTGAGCTGTACTTTGTCAAGTGGATGGACGGGCGTACGACACCATCCCCCA 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGACAACGTACTGCGTGCG 2280
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Db   2581 CAGCCCTGTGCTACGGCGACATGAGAACAAAGTCTGTTTGCGGGGATTCGGCGGCGGGGACGGGCT 2640

Qy   2641 GCTCCTGCGTTGTGGATGATTCTTGTTGGTGACACCTCACCTCACCCACCGCGAAAAC 2700
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Qy   2701 CTTCCTCAGGACCCTGGTCTCCGAGTGTATGCCTGGTGAACTTGCGGAA 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CTTCCTCAGGACCCTGGTCTCCGAGTGTATGCCTGGTGAACTTGCGGAA 2760

Qy   2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCGTTTTGTTCAGAT 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCGTTTTGTTCAGAT 2820

Qy   2821 GCCGGGCCACGGGCCTATTCCCCTGCTGCGCCCTGCTCGTGGATACCCGGAGT 2880
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Db   2821 GCCGGGCCACGGGCCTATTCCCCTGCTGCGCCCTGCTCGTGGATACCCGGAGT 2880

Qy   2881 GCAGAGGCACTACTCCAGCTATGCCCGGACCTCTCCATCAGACCCAGTCTCCACCTCAACCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCAGAGGCACTACTCCAGCTATGCCCGGACCTCTCCATCAGACCCAGTCTCCACCTCAACCG 2940

Qy   2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGTGAAGTG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3001 TCACAGCCTGTTTCTGGATTTGCAGGTGCAACATGGACTACGTCGTGGGAGC 3060

Qy   3061 CAAGATCCTCCTGCTGCCCTCCGAGGCCGAGCGTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3121 TCAGCAAGTTTGGAAGAACCCCACATTTTCCTGCGCGTCATCTCTGACACGGCCTCCT 3180

Qy   3181 CTGCTACTTCCATCTCCTGAAAGCCAAGAACGCCAGGATGTCGCTGCTGGGGGCCGGC 3240
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Db   3181 CTGCTACTTCCATCTCCTGAAAGCCAAGAACGCCAGGATGTCGCTGCTGGGGGCCGGC 3240

Qy   3241 CGGCCCTCGCCCTCCGAGGCCGTGCAGTGGCCGTCGTGCCACCAAGCATTCTGCTCAAGCT 3300
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Db   3421 ACTGCCCTCAGACTTCAAGACCATCCTGACTGATGCCCAGCGTGTCACCTGCAGGA 3480

Qy   3481 GAGCAGCACCAGGCGCCGCCGCCCAGGGCTCTACGTCCCAGGGGGCGGGCCGCC 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3541 CACACCCAGGCCGCCGCCCACCCGGCCTCCCCAGGTGAGTGTTGGCCGGAGGCCTG 3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CACACCCAGGCCGCCGCCCACCCGGCCTCCCCAGGTGAGTGAGTGTTTGGCCGGAGGCCTG 3600

Qy   3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGTCTCAGCCAGGGCT 3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3661 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3721 GGGCCAGCTTTTCCTCCACCAGGAGCCCGGCGTTCCACTCCCCACATAGGAATAGTCCATCC 3780
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Qy   3781 CCAGATTCGCCATTGTTCACCCCGCTCCTGCCTTCCACCCCACCATCC 3840
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Db   3901 CCCTGTACACAGGCGAGGACCCTGGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG 3960

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RESULT 10
US-09-733-294A-3
; Sequence 3, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-733-294A-3

  Query Match   100.0%; Score 4015; DB 4; Length 4015;
  Best Local Similarity   100.0%;
  Matches 4015; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      1 GCAGCGCTGCGCTCCTGCTGCGCTGCGCACGTGGGAAGCCCTGGCCCCCGGATGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAGCGCTGCGCTCCTGCTGCGCTGCGCACGTGGGAAGCCCCACCCCCGGATGCC 60

Qy     61 GGCGGCTCCCCGTCCCGCGGCGGCGCCGTGCGCTCCCTGCTCGCAGCCACTACCGCGAGGTGCT 120
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Db    241 ACGGGCGTGTCTGCGCGGCCCCGCCCCTTCCGCGCCCCGCCCCGCGCCGGCGGC 300
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Qy    301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGGCGCGGAAGAACGTGCTGGCCTTCGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGGCGCGGAAGAACGTGCTGGCCTTCGC 360

Qy    361 GCTGCTGGACGGGGCCCGGCCGGGGGGCCCCCGGGGCCCCGGGCCGGCGCCAGCTA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTGCTGGACGGGGCCCGGCCGGGGGGCCCCCGGGGCCCCGGGCCGGCGCCAGCTA 420

Qy    421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGCGTGGGGGCGTGCTGGCTGCTGCG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGCGTGGGGGCGTGCTGGCTGCTGCG 480

Qy    481 CCCGGTGGCGACGACGTGCTGGTTCACCTGGCACGCTGCGCGCCGCCGCTCTTTGTGCTGGT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCCGGTGGCGACGACGTGCTGGTTCACCTGGCACGCTGCGCGCCGCCGCTCTTTGTGCTGGT 540

Qy    541 GGCTCCCAGCTGCGCCTACCAGTGTGCGGGCGCCGCGCCGTGTACCAGCTCGGCGCTGCCAC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCTCCCAGCTGCGCCTACCAGTGTGCGGGCGCCGCGCCGTGTACCAGCTCGGCGCTGCCAC 600

Qy    601 TCAGGCCCGCCCGCCCCGCCACACGTAGTGACCCGAAGGCGTCTGGGATGCGAACGGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TCAGGCCCGCCCGCCCCGCCACACGTAGTGACCCGAAGGCGTCTGGGATGCGAACGGGC 660

Qy    661 CTGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGCCTGGAGGGCCCAGCCCGGGTGCGAG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGCCTGGAGGGCCCAGCCCGGGTGCGAG 720

Qy    721 GAGGCGCGGGGCAGTGCCGCGAAGTCTGCCGTTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GAGGCGCGGGGCAGTGCCGCGAAGTCTGCCGTTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGC 780

Qy    781 TGCCCCTGAGCCGGAGCGGACGCCGGTTGGGCAGGGCGTCTGGGCAGGGGTCCCACCCGGCAGGAC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TGCCCCTGAGCCGGAGCGGACGCCGGTTGGGCAGGGCGTCTGGGCAGGGGTCCCACCCGGCAGGAC 840

Qy    841 GCGTGGACCGAGTGACCGTGGTTTCGTGGTGTCGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCGTGGACCGAGTGACCGTGGTTTCGTGGTGTCGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC 900

Qy    901 CACCTCTTTGGAGGTGCGCTCGCTCCTGGCACGCACGGCCACTCCCACCATCGTGGGGCCGCCA 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACCTCTTTGGAGGTGCGCTCGCTCCTGGCACGCACGGCCACTCCCACCATCGTGGGGCCGCCA 960

Qy    961 GCACCACGCGGGCGCCCCCCATCCACATCGCGGCCACATCCGGCACTCCGGGACACGCCCTTGTCC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GCACCACGCGGGCGCCCCCCATCCACATCGCGGCCACATCCGGCACTCCGGGACACGCCCTTGTCC 1020

Qy   1021 CCCGGTGTACGCCGAGACCACTTCCTCTACTTCCTACTCCCAGGCGACAAGGAGCAGCTGCG 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCCGGTGTACGCCGAGACCACTTCCTCTACTTCCTACTCCCAGGCGACAAGGAGCAGCTGCG 1080

Qy   1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCTGACTGCGGAGGCTCGGACTCGTCGGA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCTGACTGCGGAGGCTCGGACTCGTCGGA 1140

Qy   1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCCCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCCCT 1200

Qy   1201 GCCCCAGCCGCTACTGGCAAATGCGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GCCCCAGCCGCTACTGGCAAATGCGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260

Qy   1261 GTGCCCCTACGGGGTGCTCCTCAAGACGACTCCGGCTCGTGGTCGGTGCAGCCCAGC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGCCCCTACGGGGTGCTCCTCAAGACGACTCCGGCTCGTGGTCGGTGCAGCCCAGC 1320

Qy   1321 AGCGGGTGTCGTGCCCGGAAGCCCTGCTCCGGTCGCAGGGGTCTGGGGC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGCGGGTGTCGTGCCCGGGAGAAGCCCAGGGGTCTGTGGCGGCCCCGAGGAGGAGGA 1380

Qy   1381 CACAGACCCCCGTCGCTGCTGGTGCAGCTGCTCCCGCCAGCAGCAGCCCCCTGGCAGGTGTA 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG 2520
                                                                  2520
Qy  2461 CAAGTCCTACGTCCAGTGCCAGTCCAGGGGATCCCAGGGGTCCATCCTCTCCACGCTGCTCTG 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAAGTCCTACGTCCAGTGCCAGTCCAGGGGATCCCAGGGGTCCATCCTCTCCACGCTGCTCTG 2580

Qy  2521                                                              2580
Db  2521 CAGCCTGTCTACGGCGACATGAGAACAAGTGTGTTGCGGCGGACACGGGCT 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 CAGCCTGTCTACGGCGACATGAGAACAAGTGTGTTGCGGCGGACACGGGCT 2640

Qy  2641 GCTCCTGCGTTTGGTGGATGATTCTTGTTGGTGACACCTCACTCACCCACCGCGAAAAC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 GCTCCTGCGTTTGGTGGATGATTCTTGTTGGTGACACCTCACTCACCCACCGCGAAAAC 2700

Qy  2701 CTTCCTCAGGACCCTGGTCCGAGTGTCCGAGTATGGCTGCTGGTGGTGAACTTGCGGAA 2760
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Db  2701 CTTCCTCAGGACCCTGGTCCGAGTGTCCGAGTATGGCTGCTGGTGGTGAACTTGCGGAA 2760

Qy  2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGTGGCCACGGGCTTTGTTGTTCAGAT 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGTGGCCACGGGCTTTGTTGTTCAGAT 2820

Qy  2821 GCCGGGCCACGCGGCCTATTCCCCTGTGCGCGGCCTGCTGCGTGGACCCTGGAGT 2880
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Db  2821 GCCGGGCCACGCGGCCTATTCCCCTGTGCGCGGCCTGCTGCGTGGACCCTGGAGT 2880

Qy  2881 GCAGAGGCGACTACTCCAGCTCCATCAGACCAGTCTCACCTTCAACCG 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 GCAGAGGCGACTACTCCAGCTCCATCAGACCAGTCTCACCTTCAACCG 2940

Qy  2941 CGGCTTCAAGGTGTGGAGGGAACATGCGCTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 CGGCTTCAAGGTGTGGAGGGAACATGCGCTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000

Qy  3001 TCACAGCCTGTTTCTGGATTTGCAGGCGTACAGGTTTCACGCATGTGTCTGCAGCTCCCATTCTA 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 TCACAGCCTGTTTCTGGATTTGCAGGCGTACAGGTTTCACGCATGTGTCTGCAGCTCCCATTCTA 3060

Qy  3061 CAAGATCCTCCTGCTCGCAGGCGTCACCTCGAGGTGAAGGCACTGTT 3120
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Db  3061 CAAGATCCTCCTGCTCGCAGGCGTCACCTCGAGGTGAAGGCACTGTT 3120

Qy  3121 TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCTCCCT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCTCCCT 3180

Qy  3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGAGATGTCGCTCGGGGCGCGGCCGCGCGC 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGAGATGTCGCTCGGGGCGCGGCCGCGCGC 3240

Qy  3241 CGGCCCTGCCCCTCGGAGCCGTCGAGTGGCGTGCCGTACGACACCATCCTGCTCAAGCT 3300
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Db  3241 CGGCCCTGCCCCTCGGAGCCGTCGAGTGGCGTGCCGTACGACACCATCCTGCTCAAGCT 3300

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Db  3301 GACTCGACACCGTGTCCAACTCCTGGGGTCACTCAGGACGGCCCAGACGCA 3360

Qy  3361 GCTGAGTCGGAAGCTCCTGAGTCGGGGACGCCTGCCCTGACGCCTTCAAGAGCCAACCCGGC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 GCTGAGTCGGAAGCTCCTGAGTCGGGGACGCCTGCCCTGACGCCTTCAAGAGCCAACCCGGC 3420

Qy  3421 ACTGCCCCCAGACTTCAAGACCATCCTGGCTCGTTCGTGCTCACCTGATGGCCAGGCCGA 3480
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Db  3421 ACTGCCCCCAGACTTCAAGACCATCCTGGCTCGTTCGTGCTCACCTGATGGCCAGGCCGA 3480

Qy  3481 GAGCAGCAACCACCAGCCCTCCTCCCAGGAGGGGCGGCTCCTACGTCACGCGGGGAGGGGGCC 3540
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Db  3481 GAGCAGCAACCACCAGCCCTCCTCCCAGGAGGGGCGGCTCCTACGTCACGCGGGGAGGGGGCC 3540

Qy  3541 CACACCCAGCCCCCACCCGTGCCACCACGCCACCCGCCGGGCCTG 3600
         ||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CACACCCAGCCCCCACCCGTGCCACCACGCCACCCGCCGGGCCTG 3600
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Db  1381                                                              1440
Qy  1381 CACAGACCCCCGCTCGCCGCCTGGTGCAGCTGCACGAGCAGCCACGGCCCTGGGGCTGTA 1440
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Qy  1441 CGGCTTCGTGCGGGGCCTGCGCCGGGGCGTGGTGCCCCCAGGGCCTGGTGCCCCCAGGGCCTGGGGCGCCTGGGGCGCCTCCAGGCA 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CGGCTTCGTGCGGGGCCTGCGCCGGGGCGTGGTGCCCCCAGGGCCTGGTGCCCCCAGGGCCTGGGGCGCCTCCAGGCA 1500

Qy  1501 CAACGAACGCGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAATGCCAA 1560
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Db  1501 CAACGAACGCGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAATGCCAA 1560

Qy  1561 GCTCTCGCTGCAGGAGCTGACCTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCGAG 1620
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Db  1561 GCTCTCGCTGCAGGAGCTGACCTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCGAG 1620

Qy  1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGTCTGCGTGAGCTGCTCAGGTCTTCTTTTA 1680
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Db  1621 GAGCCCAGGGGTTGGCTGTGTTCCGGCCGTCTGCGTGAGCTGCTCAGGTCTTCTTTTA 1680

Qy  1681 CAAGTTCCTGCACTGGCTGCGTGATGAGTGTGTACGTGCGTCGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CAAGTTCCTGCACTGGCTGCGTGATGAGTGTGTACGTGCGTCGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1740

Qy  1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800

Qy  1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTC 1860
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Db  1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTC 1860

Qy  1861 GGAAGCAGAGGTCAGGCAGCAGTCAGGGAAGCCAGGCGGCCCGCCCTGCTGCGAGTCTCCG 1920
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Db  1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCTGCGCGCCGCCGCGATTGTGAACATGTCGTCGTGGGAGC 1980

Qy  1981 CAGAAACGTTCCGACAGAGAAAAGAGGGCCGAGCGTTCACCTCGAGGTGAAGGCACTGTT 2040
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Db  1981 CAGAAACGTTCCGACAGAGAAAAGAGGGCCGAGCGTTCACCTCGAGGTGAAGGCACTGTT 2040

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Db  2041 CAGCGGCTGCTCAACTGCTCACGGAGGTCACGAGCGGGCGCGGGGCGCGGCCCTCTGTGCTGCTGGG 2100

Qy  2101 CCTGGACGATATCCCACAGGGGCCGCCACCTTCGTGCTGCGTGCGGTGCGCCCAGGACCCC 2160
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Db  2101 CCTGGACGATATCCCACAGGGGCCGCCACCTTCGTGCTGCGTGCGGTGCGCCCAGGACCCC 2160

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Db  2161 GCCGGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGTACGACACCATCCCCCA 2220

Qy  2221 GGACAGGCTCACGGAGGTCATCGACGAGGTCATCGACCAGCATCATCAAAACCCAGAACACGTACTGCGGTGCG 2280
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Db  2221 GGACAGGCTCACGGAGGTCATCGACGAGGTCATCGACCAGCATCATCAAAACCCAGAACACGTACTGCGGTGCG 2280

Qy  2281 TCGGTATGCCGTGGTCCAGAGGCACGTCCGGCACGTCCGGCACGTCCGGCACGTTCAAGAGCCAAGGCCTTCAAGAGCCA 2340
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Db  2281 TCGGTATGCCGTGGTCCAGAGGCACGTCCGGCACGTCCGGCACGTTCAAGAGCCAAGGCCTTCAAGAGCCA 2340

Qy  2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTTGGCTCACCTGCCAGGA 2400
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Db  2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTTGGCTCACCTGCCAGGA 2400

Qy  2401 GACCAGCCCGCTGAGGGATGCCGTGCTCATCGAGCAGCAGTGTCCTCCTCCCTGAATGAGGCCAG 2460
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Db  2401 GACCAGCCCGCTGAGGGATGCCGTGCTCATCGAGCAGCAGTGTCCTCCTCCCTGAATGAGGCCAG 2460

Qy  2461 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3601  CATGTCCGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT  3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  CATGTCCGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT  3660

Qy   3661  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCACAGGCTGGCGCTCGGCTCCACCCCA  3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCACAGGCTGGCGCTCGGCTCCACCCCA  3720

Qy   3721  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGAGAATAGTCCATCC  3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGAGAATAGTCCATCC  3780

Qy   3781  CCAGATTCGCCATTGTTCACCCCTGGGAGCTCTGGGAATTCGAGTGACCAAAGGTGTG  3840
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Qy   3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTCACCTGGATGGGGGTCCCTGTCAAATTGGGGG  3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901  CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTCACCTGGATGGGGGTCCCTGTCAAATTGGGGG  3960

Qy   3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA  4015
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```

RESULT 11

US-08-974-549A-343

; Sequence 343, Application US/08974549A

; Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:
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CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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INFORMATION FOR SEQ ID NO: 343:

SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note= "refined sequence of hTRT cDNA"

US-08-974-549A-343

Query Match   99.8%; Score 4008.6;   DB 3;   Length 4037;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 4008; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Qy    1  GCAGCGGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGGCGATGCC   60
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Db    1  GCAGCGGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGGCGATGCC   60

Qy   61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  120

Qy  121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG  180

Qy  181  GGACCCGGCGGTTTCCGGCGCGTGGTGCGGCCCAGTGCCTGGTTGCGTGCGTGCGGACGC  240
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Db  181  GGACCCGGCGGTTTCCGGCGCGTGGTGCGGCCCAGTGCCTGGTTGCGTGCGTGCGGACGC  240

Qy  241  ACGCGCCGCGCCCCCGCCGCCCCTCCTTCCGCGCGGCGCCCCTCCTTCCGCGTGCTGGGC  300
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Db  241  ACGCGCCGCGCCCCCGCCGCCCCTCCTTCCGCGCGGCGCCCCTCCTTCCGCGTGCTGGGC  300

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Qy  361  GCTGCTGGACGGGGCCCCGGGGGCCTTCACCACCAGCGTGCCAGCTA  420
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  GCTGCTGGACGGGGCCCCGGGGGCCTTCACCACCAGCGTGCCAGCTA  420

Qy  421  CCTGCCCAACACGTGACCGACCTGCGGGGGGCGGGGGCGGGGGGCTGTGCTGCG  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  CCTGCCCAACACGTGACCGACCTGCGGGGGGCGGGGGCGGGGGGCTGTGCTGCG  480
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Qy    481 CCGGCGTGGGCGACGACGTGCTGGTTCACCTGCTGCACGCTGCGCGCTCTTCTTGTCGTCTGGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCGGCGTGGGCGACGACGTGCTGGTTCACCTGCTGCACGCTGCGCGCTCTTCTTGTCGTCTGGT  540

Qy    541 GGCTCCCAGGTGCCGCCTACCAGGTGTGCGGAGGCCGGGACCCCCACACGCTCGGCGCTGCCAC  600
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Db    541 GGCTCCCAGGTGCCGCCTACCAGGTGTGCGGAGGCCGGGACCCCCACACGCTCGGCGCTGCCAC  600

Qy    601 TCAGGCCCGGCCCCCCGCCCACACGCTAGTGGACGGCGTCTGGATGCGAACGGGC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TCAGGCCCGGCCCCCCGCCCACACGCTAGTGGACGGCGTCTGGATGCGAACGGGC  660

Qy    661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGGCTCCCAGCCCCGGGTGCGAG  720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGGCTCCCAGCCCCGGGTGCGAG  720

Qy    721 GAGGGCGGGGGCAGTGCCAGCGGAGTCTGCCGGAAGTCGCCGGTGCCCAAGAGAGCCCAGGCGTGGCGGC  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GAGGGCGGGGGCAGTGCCAGCGGAGTCTGCCGGAAGTCGCCGGTGCCCAAGAGAGCCCAGGCGTGGCGGC  780

Qy    781 TGCCCCTGAGCCGGAGCGGACGGCGCCCGTTGGGCAGGGGTCTCGGGGCCCAGGGCCAGGAC  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TGCCCCTGAGCCGGAGCGGACGGCGCCCCGTTGGGCAGGGGTCTCGGGGCCCAGGGCCAGGAC  840

Qy    841 GCGTGGACCGAGTGACCGTGTTCTGTGTGTGTCACCTGCCAGTCGGCGGAGGAAGC  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCGTGGACCGAGTGACCGTGTTCTGTGTGTGTCACCTGCCAGTCGGCGGAGGAAGC  900

Qy    901 CACCCTTTGGAGGGTGCGCTCTGGCACGCGGCCCACTCCCACCCCATCCGTGGGGCCCCCA  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACCCTTTGGAGGGTGCGCTCTGGCACGCGGCCCACTCCCACCCCATCCGTGGGGCCCCCA  960

Qy    961 GCCACACGCGGGGCCCCCCATCCACATCGCGGCCACTTCCTCTACTCGCGGCCCAGCGCTGCG  1020
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Db    961 GCCACACGCGGGGCCCCCCATCCACATCGCGGCCACTTCCTCTACTCGCGGCCCAGCGCTGCG  1020

Qy   1021 CCCGGTGTACGGCCGAGACCAAGCACTTCCTCTACTCGCTGAGGGCCCTGACTGGCGTCGGAGGCTCGTGGA  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCCGGTGTACGGCCGAGACCAAGCACTTCCTCTACTCGCTGAGGGCCCTGACTGGCGTCGGAGGCTCGTGGA  1080

Qy   1081 GCCCTCCTCCTCAGCTCTCTGAGGCCCAGCCTGGATGCCAGGGGACTCCCCCAGGTTGCCCCGGCCT  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCCCTCCTCCTCAGCTCTCTGAGGCCCAGCCTGGATGCCAGGGGACTCCCCCAGGTTGCCCCGGCCT  1140

Qy   1141 GACCATCTTTCTGGGTTCCAGGCCCTGGAATGCCAGGGCCCTGGGAGCTGTCCCCGGGTGCCCCGCCCT  1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GACCATCTTTCTGGGTTCCAGGCCCTGGAATGCCAGGGCCCTGGGAGCTGTCCCCGGGTGCCCCGCCCT  1200

Qy   1201 GCCCAGGCTACTGGCAAATGCCGCCCCCGTGTTCTGGGAACCAGCGCA  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GCCCAGGCTACTGGCAAATGCCGCCCCCGTGTTCTGGGAACCAGCGCA  1260

Qy   1261 GTGCCCCTACGGGGTGCTCCAAGACGCACTGGCGTGGGTGCGGCGCACCCCAGC  1320
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Db   1261 GTGCCCCTACGGGGTGTCTGTGCCGAGCACTGGCGTGGGTGCGGCGCACCCCAGC  1320

Qy   1321 AGCCCGTGTCTGTGCCCGGGAGAAGCCCAGGGCTCTGTGGCGGCTCTCGGAGGA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGCCCGTGTCTGTGCCCGGGAGAAGCCCAGGGCTCTGTGGCGGCTCTCGGAGGA  1380

Qy   1381 CACAGACCCCGCGGGGGCCCCCAGGGCTCGGCTCGCCGGCCTCGTGCCCGTGCTGGTGCAGTGTA  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CACAGACCCCGCGGGGGCCCCCAGGGCTCGGCTCGCCGGCCTCGTGCCCGTGCTGGTGCAGTGTA  1440

Qy   1441 CGGCTTCGTGCAGTCGTGCCGCCGGCCGCTGCCTCGGGCTCTCCCGGGGCTCGGGCCTCCAGGCA  1500
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Db   1441 CGGCTTCGTGCAGTCGTGCCGCCGGCCGCTGCCTCGGGCTCTCCCGGGGCTCGGGCCTCCAGGCA  1500

Qy   1501 CAACGAACGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CAACGAACGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560

Qy   1561 GCTCCTGCGCTTGTGTGATGATTCTTGTTGGTGACACCTCACCTCACCTGGCTGCGCAG  1620
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Db   1561 ... GCTCTCGCTGCAGGAGGTGACGTGACGCTGGGAAGATGAGCGTGGGGACTGCGGTGGGCTTGCCGGC  1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   1621 GAGCCCAGGGGTTGGCTGTGTCCCAGAGCACCGTCTGCGTGGAGGACACCTGGC  1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGCCCAGGGGTTGGCTGTGTCCCAGAGCACCGTCTGCGTGGAGGAGATCCTGC  1680

Qy   1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGTCTTTCTTTTA  1740
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Db   1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGTCTTTCTTTTA  1740

Qy   1741 TGTCACGGAGACCACGTTCAAAAGAACAGAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG  1800
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Db   1741 TGTCACGGAGACCACGTTCAAAAGAACAGAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG  1800

Qy   1801 CAAGTTGCAAAGCATTGAAATCAGACGCACTTGAAGAGGGTGCAGCTGCGCGGGAGCTGTC  1860
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Db   1801 CAAGTTGCAAAGCATTGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGCGGGAGCTGTC  1860

Qy   1861 GGAAGCAGAGGTCAGGGAAGCCATCGGGAAGCCAGGCCCCGCCCGCCCTGCTGACGTGACTCCG  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 GGAAGCAGAGGTCAGGGAAGCCATCGGGAAGCCAGGCCCCGCCCGCCCTGCTGACGTGACTCCG  1920

Qy   1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGGATTGTGAACATGACTACGTCGTGGGAGC  1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGGATTGTGAACATGACTACGTCGTGGGAGC  1980

Qy   1981 CAGAAACGTTCCCGACAGAAAAGAGGGCGGCGGGGCCCGAGCGTTCACCTCGAAGGTGAAGGCACTCGTT  2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAGAAACGTTCCCGACAGAAAAGAGGGCGGCGGGGCCCGAGCGTTCACCTCGAAGGTGAAGGCACTCGTT  2040

Qy   2041 CCTGGACGATATCCACAGGGCCTGGCGCGTTCGTGCTCCTGGGCCTCGTGCTGGG  2100
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Db   2041 CCTGGACGATATCCACAGGGCCTGGCGCGTTCGTGCTCCTGGGCGTGTGCTGGGG  2100

Qy   2101 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACCACCATCCCCCCA  2160
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Db   2101 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACCACCATCCCCCCC  2160

Qy   2161 GGACAGGCTCACGGAGGTCATCGGAGGTCATCGCCAGCATCATCAAACCCCGGCACGTCGTGCG  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GGACAGGCTCACGGAGGTCATCGGAGGTCATCGCCAGCATCATCAAACCCCGGCACGTCGTGCG  2220

Qy   2221 TCGGTATGCGGTGTCCAGAAGGCCGCCATGGGCACGTCCCAGAAGGCCGTTCAAGAGCCA  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCGGTATGCCGGTGTCCAGAAGGCCGCCATGGGCACGTCCCAGAAGGCCGTTCAAGAGCCA  2280

Qy   2281 CGTCTCTACCTTGACAGACCTCAGCGCTGCACAGTTCGTGGCTCCACGTCGCAGA  2340
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Db   2281 CGTCTCTACCTTGACAGACCTCAGCGCTGCACAGTTCGTGGCTCCACGTCGCAGA  2340

Qy   2341 GACCAGCCCGCTCGTGCTGCTGAGGATGCCGTCGTCATCGAGCAGAGCTCCCGAATGAGGAGGCAG  2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 GACCAGCCCGCTCGTGCTGCTGAGGATGCCGTCGTCATCGAGCAGAGCTCCTGAATGAGGAGCCAG  2400

Qy   2401 CACAGACCCCGCTCGTGCTGCCCGGCCTCTCCATCCGCAGGGCTCTGCTGGGCCGTGTGCGCATCAGGGG  2460
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Db   2401 CACAGACCCCGCTCGTGCTGCCCGGCCTCTCCATCCGCAGGGCTCTGCTGGGCCGTGTGCGCATCAGGGG  2460

Qy   2461 CGGCTTCGTGCAGTCGTCCAGTGCAGGGCTCCAGGGCTCTGGGGAATTCGGCGGACGGGCTCTG  2520
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Db   2461 CGGCTTCGTGCAGTCGTCCAGTGCAGGGCTCCAGGGCTCTGGGGAATTCGGCGGACGGGCTCTG  2520

Qy   2521 CAGCCTGCGCTTCCTCAGGAACAAGCTGTTTGCGGGGATTCGGCGGACGGGCT  2580
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Db   2521 CAGCCTGTGTCACGGCGACATGGGAAGAACAAAGCTGTTTGCGGGGACGGGCT  2580

Qy   2581 GCTCCTGCGTTTGTGGTGACACCTCACCTTGGCTGCGCAG  2640
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Db   2641  GCTCCTGCGTTTGGTGTGGATGATTTCTTGTTGGTGACACCTCACCCACGCGCGAAAAC  2700

Qy   2701  CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAACTTGCGGAA  2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAACTTGCGGAA  2760

Qy   2761  GACAGTGGTGAACTTCCCTGTAGAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCGAGAT  2820
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Db   2761  GACAGTGGTGAACTTCCCTGTAGAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCGAGAT  2820

Qy   2821  GCCGGCCACGGCCTATTCCCCTGGTGCGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGT  2880
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Db   2821  GCCGGCCACGGCCTATTCCCCTGGTGCGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGT  2880

Qy   2881  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG  2940
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Db   2881  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTGTCACCTTCAACCG  2940

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Db   2941  CGGCTTCAAGGCTGGGAGGAACATGCTGCTGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG  3000

Qy   3001  TCACAGCCCTGTTTCTGGATTTGCAGGTGAACAGCTCCAGACGGTGTGCACCAACATCTA  3060
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Db   3001  TCACAGCCCTGTTTCTGGATTTGCAGGTGAACAGCTCCAGACGGTGTGCACCAACATCTA  3060

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Db   3061  CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGGCATGTGTGCTGCAGCTCCCATTTCA  3120

Qy   3121  TCAGCAAGTTGGAAGAACCCCACATTTTCTCTGCGCGGTCATCTCTGACACGGCCTCCCT  3180
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Db   3121  TCAGCAAGTTGGAAGAACCCCACATTTTCTCTGCGCGGTCATCTCTGACACGGCCTCCCT  3180

Qy   3181  CTGCTACTCCATCCTGAAAGCCAAGAACCAGCAGGGATGTCGCTGGGGCCCAAGGGCGCGC  3240
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Db   3181  CTGCTACTCCATCCTGAAAGCCAAGAACCAGCAGGGATGTCGCTGGGGCCCAAGGGCGCGC  3240

Qy   3241  CGGCCCCTCTGCCCTCCGAGGCCGTGTGCGCACCAAGCATTCCTGCTCAAGCT  3300
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Db   3241  CGGCCCCTCTGCCCTCCGAGGCCGTGTGCGCACCAAGCATTCCTGCTCAAGCT  3300

Qy   3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACACAGCCCAGACGCA  3360
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Db   3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACACAGCCCAGAGCA  3360

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Db   3361  GCTGAGTCGGAAGCTCCCGGGGACGACCTGACTCCCTGGAGGCCGAGCCAACCCGGC  3420

Qy   3421  ACTGCCCTTCAGACTTCAAGACCATCCTGGACTTGATGGCCACCCGCACCAGCAGGCCA  3480
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Db   3421  ACTGCCCTTCAGACTTCAAGACCATCCTGGACTTGATGGCCACCCGCACCAGCAGGCCGA  3480

Qy   3481  GAGCAGACACCAGCAGCCCGTTCACCGTCTACGTCCCAGGAGGAGGGGGCCGGCC  3540
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Db   3481  GAGCAGACACCAGCAGCCCGTTCACCGTCTACGTCCCAGGAGGAGGGGGCCGGGC  3540

Qy   3541  CACACCCAGGCCCGCCACCCGTGGAGTCTGAGGCTGAGTGAGTGTTTGGCCGAGGCCTG  3600
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Db   3541  CACACCCAGGCCCGCCACCCGTGGAGTCTGAGGCTGAGTGAGTGTTTGGCCGAGGCCTG  3600

Qy   3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCAAGGGCT  3660
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Db   3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCAAGGGCT  3660

Qy   3661  GAGTGTCCAGCACACACCTGCCGCTCTTCACTTCCCCCACCAGCTGCGGCCTGCTCCACCCCA  3720
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Db   3661  GAGTGTCCAGCACACACCTGCCGCTCTTCACTTCCCCCACCAGCTGCGGCCTGCTCCACCCCA  3720

Qy   3721  GGGCCAGCTTTTCCTCACCAGGAGACCCCGGGCCCGCTCTTCCCCACTCCCCACATAGGAATAGTCCATCC  3780
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Db   3721  GGGCCCAGCTTTTTCYTCACCAGGAGACCCCGGGCCCGCTGCTTCCCCACTCCCCACATAGGAATAGTCCATCC  3780
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Qy   3781  CCAGATTCGCCATTGTTCACCCCTGCCCTCCTTGCCTTCACCCCACCCCACCATCC  3840
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Db   3781  CCAGATTCGCCATTGTTCACCCYTCGCCCYTCGCCTTCGCCTTCCACCCCACCATCC  3840

Qy   3841  AGGTGGAGACCCTGAGAAGGACCCTGGGAATTGGAGTTGACCAAAGGTGTG  3900
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Qy   3901  CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGGTCAAATTGGGG  3960
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Db   3901  CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGGTCAAATTGGGG  3960

Qy   3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAAA  4015
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RESULT 12
US-08-851-843A-173
; Sequence 173, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
;   APPLICANT: Cech, Thomas R.
;   APPLICANT: Lingner, Joachim
;   APPLICANT: Nakamura, Toru
;   APPLICANT: Chapman, Karen B.
;   APPLICANT: Morin, Gregg B.
;   APPLICANT: Harley, Calvin
;   APPLICANT: Andrews, William H.
;   TITLE OF INVENTION: No. 6093809el Telomerase
;   NUMBER OF SEQUENCES: 225
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, 8th Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: United States of America
;   ZIP: 94111
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/851,843A
;   FILING DATE: 06-MAY-1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph T.
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-002930US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4029 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear

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;     MOLECULE TYPE: cDNA
;     FEATURE:
;       NAME/KEY:
;       LOCATION:  1..4029
;     OTHER INFORMATION:  /note= "preliminary sequence for
;     OTHER INFORMATION:  human TRT cDNA insert of
;     OTHER INFORMATION:  plasmid pGRN121"
US-08-851-843A-173

Query Match        95.9%;   Score 3849.2;   DB 3;   Length 4029;
Best Local Similarity 98.5%;   Pred. No. 0;
Matches 3955   Conservative 0;   Mismatches 53;   Indels 9;   Gaps 8;
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Qy      1  GCAGGGCTGCGCTCGCGCACGTGGGAAGCCCTGGCCCCGGCCCACCCCGGCGATGCC     60
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Db      1  GCAGGCTGCGCTCGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCCACCCCGGCGATGCC     60

Qy     61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCCCGGAGGTGCT   120
           ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCCACTACCCCGGAGGTGCT   120

Qy    121  GCCGCTGGCCACGTTCGTGCGCGCCTGGGCCCAGGGCTGGCCGGCTGGTGCAGCGCGG   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCCGCTGGCCACGTTCGTGCGCGCCTGGGCCCAGGGCTGGCCGGCTGGTGCAGCGCGG   180

Qy    181  GGACCCGGCGGCTTCCGGCGCTGCGTGTCCAGTGCCTGTCGTGTGCGTGCCTGGGACGGC   240
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Db    181  GGACCCGGCGGCTTCCGCGCNTGGTGCGCCANTGCNTGGTGTGCCTGCCTGCGGGANGN   240

Qy    241  ACGGGTCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGC   300
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Db    241  ANGGCNGCCCCGCCGCCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAANGANCTGGTGGC   300

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Db    301  CCGAGTGCTGCANANCGTGGCGACGACGTGGTGGCGGCGGGCGGAANACTGCTGGCCTTCGT   360

Qy    361  GCTGCTGGACGGGGCGGCCCCCCGAGGGCCTTCACCACCAGCGTGCCAGCTA   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GCTGCTGGACGGGGCGGCCCCCGAGGGCCTTCACCACCAGCGTGCCAGCTA   420

Qy    421  CCTGCCCAACACGTGACCGACGCACTGCGGGGCGTGGGGCGTGGGGCGTGCTGCGG   480
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Qy    481  CCGGTGGGGACGACGTGCTGGTTCACCTGCTGGCACGTGCGCGCCTCTTGTCTGTGGT   540
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Qy    541  GGCTCCCAGTGCTGCGCCTACCAGGTGTGCGGGGCGGCCCCGCGCCGCTGTACCAGCTCGGCGCTGCCAC   600
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||| | | | | |
Db    541  GGNTCCCAGTGCTGCGCCTACCANGTGTGCGGGGCGGCCCCGCGCCGCTGTACCAGCTCGGCGCTGCCNAC   600

Qy    601  TCAGGCCCCGGAGCCGGACGCGCCCCGTTGGGCAGGCGCTAGTGACGCCCAAGGCGTCTGGGATGCGAACGGGC   660
           ||||||||||||||||||||||||||| ||| ||||||||||| |
Db    601  TCAGGCCCCGGAGCCGGACGCCCCGTTGGGCAGGCGCTANTGGA-CCCGAANGCGTCTGGGAT-CCAACGGGC   658

Qy    661  CTGGAACCATAGCGTCAGGAGGCCGCAGTGCCAGCCCGAAGTCTGCCCGGTTGCCCAAGAGGCCCCAGGCCGTGGCGC   720
           |||||||||||||||||||||||||||||||||||||||||||||| | |||||||||||||||||
Db    659  CTGGAACCATAGCGTCAGGAGGCCGCAGTGCCAGCCCGAAGTCTGCCCGGTTGCCCAAGAGGCTCT-CGGCCCCTGGG   717

Qy    721  GAGGGCCGGGGAGTCTGCCAGCCGAGTCTGCCCGTTGCCCAAGAGGCCCCAGGCCGTGGCGC   780
           |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    718  GAGGGCCGGGGAGTCTGCCAGCCGAGTCTGCCCGTTGCCCAAGAGGCCCCAGGCCGTGGCGC   777

Qy    781  TGCCCCTGAGCCGGAGCGGACGGCCCGTTGTTCTGTGTGTTGTCACCTGCTGGTGTTCGTTCACCTGCTGGTGC   840
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Db    778  TGCCCCTGAGCCGGAGCGGACGGCCCGTTGTTTCTGTGTGTTGTCACCTGCTGGTGTTCGTTCACCTGCTGGTGC   837

Qy    841  GGTGACCCAGTGACCGTCGTTTCTGGTGTGTCTGTTCCAGACCCCGCTGCCAGACCCGCCAGAAGC   900
           ||||||||||||||||||||||| ||||||||||||||| |||||||||||||||||||||||||||
Db    838  GCTTCATCCCCAAGCCTGACGGCCTGACCGCTGACTGCCTGCCCAGACCCGCCGCCCGAAGAAGC   897
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Qy    901  CACCTCTTTGGAGGGTGCGCTCTCTGCCACGGCGGCCACTCCCACCATCCGTGGCCCCCA   960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898  CACCTCTTTGGAGGGTGCGCTCTCTGCGGCGGCCACTCCCACCATCCGTGGCCCCCA   957

Qy    961  GCACCAGCGGCGGGCCCCCCATCCACATCGCGGCCGGCCACCACCACCAGCGGCCACCACCACCGTTGTCC   1020
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Db    958  GCACCAGCGGCGGGCCCCCCATCCACATCGCGGCCGGCCACCAC-CCTGGGACACGGCCCTTGTCC   1016

Qy   1021  CCGGGTGTACGGCCGAGACCAAGACACTTCCTCTACTCCTCAGGGGCACAAGGAGCAGCTCGG   1080
           ||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   1017  CCGGGTGTACGGCCGAGACCAAGACACTTCCTCTACTCCTCAGGGGACAGNA--CACTCGCG   1074

Qy   1081  GCCCTCCTTCCTACTC-AGCTCTCTGAGGCCCAGCCTGACTGGCCGCTCGGAGGCTCGTGG   1139
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Db   1075  NCCCTCCTTCCTCCTACTCAATATATCGGGAGGCCCAGCCTGACTGGCGGTTCGGGAGTTCGTG   1134

Qy   1140  AGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGGCTCTCGGACGTTGCCCCGCC   1199
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Db   1135  GAGACANTCTTTCTGGTTCCAGGCCTTGGATGCCA-GGAATTCCCCGGCA-GGAATTGCCCCGCCCC   1193

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Qy   1260  AGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGGGTGCGGTGCAGCCCAG   1319
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Db   1254  AGTGCCCCTACGGGGTGTTCCTCAAGACGCACTGCCCGCTGCGGGTGCGGTGCAGCCCAG   1313

Qy   1320  CAGCCGGTGTCTGTGCCCGGCTCGTGGGGCCCCCGAGGAGGAGG   1379
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Db   1314  CAGCCGGTGTCTGTGCCCGGCTCGTGGGGCGCCCCGAGGAGGAGG   1373

Qy   1380  -ACACAGACCCCGTGCGCTGGTCAGCTGCCGGGCGGGAGATGCGGGACTGCCAGGTG   1438
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Qy   1439  TACGGGCTTCGTGCGGCCTGCCTGCCGCTGGTGCCCCCAGGCCTTCACCACCAGCCCCAGG   1498
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Db   1434  TACGGCCTTCGTGCGGCCTGCCTGCCGCTGCCGCTGGTGCCCCCAGGCCTTCACCACCAGCCCCAGG   1493

Qy   1499  CACAACGAACGCCGCTTCCTCAGGAACAACCAAGAAGTTCATCTCCTGGGGAAGCATGCC   1558
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Db   1494  CACAACGAACGCCGCTTCCTCAGGAACAACCAAGAAGTTCATCTCCTGGGGAAGCATGCC   1553

Qy   1559  AAGCTCTCGCTGCGAGGAGCTGACGTGGAAGATGAGCGTGCCGGACTGCGTTGCGCGC   1618
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Db   1554  AAGCTCTCGCTGCGAGGAGCTGACGTGGAAGATGAGCGTGCCGNTNTTGTGCCTGGT   1613

Qy   1619  AGGAGCCCAGGGGTGGCTGTGTTCCGGCGCGTGCGCGAGAGCTGCTGTGCGGAGATCCTG   1678
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Db   1614  AGGAGCCCAGGGGTTGGCTGTGTTCCGGCGCGTGCGCGAGAGCTGCTGTGCGGAGATCCTG   1673

Qy   1679  GCCAAGTCCTGCACTCGGCTGCTGCTGGTACGGTCGTGCGAGCTGTCTTCTT   1738
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Db   1674  GCCAAGTTCCTGCACTCGGCTGCTGCTGGTACGGTCGTGCGAGCTGTCTTTCTTT   1733

Qy   1739  TATGTCACGGAGACCACGTTCAAAAGACAGGCTCTTTTTCACCGGAAGAGTGTCTGG   1798
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1734  TATGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTTCACCGGAAGAGTGTCGG   1793

Qy   1799  AGCAAGTTGCAAAGCAATTGGAATCAGACAGATCAGACACTTGAAGAGGTGCAGCTGCGGGGAGTG   1858
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Qy   1859  TCGGAACGAGAGTTCAGGCGACGCATCGGGAGAGCCCGGCCTGGAGAGCCGCCAGGAC   1918
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Qy   1919  CGCTTCATCCCCAAGCCTGACGGTCTTCTGTGTGTGTCACCTGCTGCCAGACCCCGCCGCAAGAAGC   1978
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Db   1914  CGCTTCATCCCCAAGCCTGACGGCCTGACCGCTGACATTGGCAAACATGGCATTGGACTACGTCGTGGGA   1973

Qy   1979  GCCAGAACGTTCCGCAGAGAAAAGAGAGGGCCGAGCGTCTCCACCTCGACCTGAAGGGTGAAGGCACTG   2038
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RESULT 13
US-08-974-549A-292
; Sequence 292, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.

```
;  APPLICANT:  Harley, Calvin B.
;  APPLICANT:  Andrews, William H.
;  TITLE OF INVENTION:  Human Telomerase Catalytic Subunit
;  NUMBER OF SEQUENCES:  727
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  Townsend and Townsend and Crew LLP
;    STREET:  Two Embarcadero Center, Eighth Floor
;    CITY:  San Francisco
;    STATE:  California
;    COUNTRY:  USA
;    ZIP:  94111-3834
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE:  Floppy disk
;    COMPUTER:  IBM PC compatible
;    OPERATING SYSTEM:  PC-DOS/MS-DOS
;    SOFTWARE:  PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/08/974,549A
;    FILING DATE:  19-NOV-1997
;    CLASSIFICATION:  536
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/724,643
;    FILING DATE:  01-OCT-1996
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/844,419
;    FILING DATE:  18-APR-1997
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/846,017
;    FILING DATE:  25-APR-1997
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/851,843
;    FILING DATE:  06-MAY-1997
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/854,050
;    FILING DATE:  09-MAY-1997
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/911,312
;    FILING DATE:  14-AUG-1997
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/912,951
;    FILING DATE:  14-AUG-1997
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/915,503
;    FILING DATE:  14-AUG-1997
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  WO PCT/US97/17618
;    FILING DATE:  01-OCT-1997
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  WO PCT/US97/17885
;    FILING DATE:  01-OCT-1997
;  ATTORNEY/AGENT INFORMATION:
;    NAME:  Apple, Randolph Ted
;    REGISTRATION NUMBER:  36,429
;    REFERENCE/DOCKET NUMBER:  015389-002610US
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  (415) 576-0200
;    TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 292:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4029 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..4029
;    OTHER INFORMATION:  /note= "preliminary sequence for
;    OTHER INFORMATION:  human TRT cDNA insert of
;    OTHER INFORMATION:  plasmid pGRN121"

US-08-974-549A-292
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Query Match   95.9%;   Score 3849.2;   DB 3;   Length 4029;

Best Local Similarity   98.5%;   Pred. NO: 0;
Matches 3955;   Conservative 0;   Mismatches 53;   Indels 9;   Gaps 8;

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Qy      1  GCAGCGCTGCGGTCCTGCTGCGCACGTGGAAGCCCTGCCCCGGCCACCCCCGCGATGCC    60
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Db      1  GCAGCGCTGCGGTCCTGCTGCGCACGTGGAAGCCCTGCCCCGGCCACCCCCGCGATGCC    60

Qy     61  GGGGGCTCCCGCTGCCAGCCGCTGCGCTCCCTGCCCGCGCAGGCCACTACCGGCGAGGTGCT   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GGGGGCTCCCGCTGCCAGCCGCTGCGCTCCCTGCCCGCGCAGGCCACTACCGGCGAGGTGCT   120

Qy    121  GCCGCTGCCACAGTTCGTGCGGCGCCTCGGCGCCCAGGCTGGCGGCTGGTGCAGCGCGCGG   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCCGCTGCCACAGTTCGTGCGGCGCCTCGGCGCCCAGGCTGGCGGCTGGTGCAGCGCGCGG   180

Qy    181  GGACCCGGCGGCTTTCGCGCCGCTGGTGGCCCAGTGCTGGTGTGCCCTGGGACGC   240
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Db    181  GGACCCGGCGGCTTTCCGCGCGNTGGTGCGCCANTGCNTGGTGTGCGGTGCCCTGGGANGN   240

Qy    241  ACGGCGCCCCCGCCCCGCCCTCCTTCCGCCCAGGTGTCCTGCCCAGGTGTCCTGGCCTTCCGCCTTCCGC   300
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Db    241  ANGGCNGCCCCCGCCCCGCCCCTCCTTCCGCCCAGGTGTCCTGCCCAGGTGTCCTGGCCTTCCGC   300

Qy    301  CCGAGTGCTGCAGAGGCGTGTGCGAGCGCGCGGGCGGCGGAGAAACGTGCTGGCCTTCGCCTTCGC   360
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Db    301  CCGAGTGCTGCANANGCTGTGCGANCCGCGGCGGCGGAANAACGTGCTGGCCTTCGCCTTCGC   360

Qy    361  GCTGCTGGACGGGCCCGCGGGGCCTTCACCACCAGCGTGCGCAGCTA   420
           |||||||||||||||||||||||||||||||||||||||||||
Db    361  GCTGCTGGACGGGCCCGCGGGGCCTTCACCACCAGCGTGCGCAGCTA   420

Qy    421  CCTGCCCAACAGGTGACCGAGCGTGCTGGTTCACCTGCTGCTGCGCG   480
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Qy    481  CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGTTGTGCTGGT   540
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Db    481  CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGCGCGNTNTTGTGCTGGT   540

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Db    601  TCAGGCCCGGCGTCGGGGTCTGGGATGCGAACGGGC   658

Qy    661  CTGGAACCATAGCGTCAGGGAGGCCCGGGTGCCCCCCCGGTGCGGCAG   720
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Db    659  CTGGAACCATAGCGTCAGGGAGGCCCGGGTCCCCCCCGGG -CTGCCAGCCCCGGGTGCGGCAG   717

Qy    721  GAGGCGCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAGGAGGCCGTGGCGC   780
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Db    718  GAGGCGCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAGGAGGCCGTGGCGC   777

Qy    781  TGCCCCTGAGCCGGACGGCCCCCACCGGGTCCTGGGCCCCACCGGGCCAGGAC   840
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Db    838  GCCTGGACCGAGTGACCGTGGTTTCTGTGTGTCACCTGCCAGAAGAAGC   897

Qy    901  CACCTCTTTGGAGGGTGCGCTCTCGGCACACGGGCCACTCCACCACCCGGGCCGCCA   960
           ||||||||||||||||||||||||||||||||||||||||||||||
Db    898  CACCTCTTTGGAGGGTGCGCTCTCGGCACACGGGCCACTCCACCACCCGGGCCGCCA   957

Qy    961  GCACCACGCGGGCCCCCCCATCCACAGTCCCTGGGACACGCCTTGTCC   1020
           |||||||||||||||||||||||||||||| -||||||||||||||
Db    958  GCACCACGCGGGCCCCCATCCACATCCGGCGCCACCACCT -CCTGGGACACGCCTTGTCC   1016

Qy   1021  CCCGGTGTACGCCCGAGACCAAGCACTTCCTCTACTCCTTCAGGCGACAAGGACAGCAGTGCG   1080
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Qy  2159  CCGCCGCCTGAGCTGTACTTGTCAAGGTGGATGTGACGGCGGCGTACGACACCATCCCC  2218
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Db  2154  CCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGGCGCTACGACACCATCCCCC  2213

Qy  2219  CAGGACAGGCTCACGGAGGTCATCCCAGCATCATCAAACCCAGAACACGTACTGCGTG  2278
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Db  2214  CAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTG  2273

Qy  2279  CGTCGGTATGCCGTGGTCCAGAAGGCCGGCCCATGGCACGTCCCAAGGCCTTCAAGAGC  2338
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2274  CGTCGGTATGCCGTGGTCCAGAAGGCCGGCCCATGGCACGTCCCAAGGCCTTCAAGAGC  2333

Qy  2339  CACGTCTCTACCTTGACAGACCTCCAGCGTCGTCATGCGACAGTCGTGGCTCACCTGCAG  2398
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Db  2334  CACGTCTCTACCTTGACAGACCTCCAGCGTCGTCATGCCACAGTCGTGGCTCACCTGCAG  2393

Qy  2399  GAGACCAGCCCGCTGAGGGATGCCGTGCTCATCGAGCAGAGCTCCTCCTGAATGAGGCC  2458
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Db  2394  GANAACAGCCCGCTGAGGGATGCCGTCATCGAGCAGAGCTCCTCCTGAATGAGGCC  2453

Qy  2459  AGCAGTGGCCTCTTCGACGTCTTCCTACCGCTTCATGTGCCACCACGCCGTGCCGATCAGG  2518
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Db  2454  AGCAGTGGCCTCTTCGACGTCTTCCTACCGCTTCATGTGCCACCACGCCGTGCCGATCAGG  2513

Qy  2519  GGCAAGTCCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTC  2578
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Db  2994  TGTCACAGGCCTGTTTCTGCAGGTGTCACGGTTGAACAGCCTTCCAGCACGTGTGCACCAACATC  3053

Qy  3059  TACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTCAGCTCCCATTT  3118
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Db  3054  TACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTCAGCTCCCATTT  3113

Qy  3119  CATCAGCAAGTTTGGAAGAACCCCACCATTTTTCCTGCTGCGCTCATCCTCTGACACGGCCTCTG  3178
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Db  3114  CATCAGCAAGTTTGGAAGAACCCCACCATTTTTCCTGCTGCGCTCATCCTCTGACACGGCCTCC  3173

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Db  3174  CTCTGCTACTCCATCCTGAAAGCCTGAAAGCCGAGGAGATGTCGCTGGGGGCCAAGGGCGCC  3233
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Db  1135  GAGACANTCTTTCGGGTTCCAGGCCTTCGGATGCCA-GGATTCCCCGCAGGTTGCCCCCCC  1193

Qy  1200  TGCCCCAGCGCTACTGGCGAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGC  1259
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Qy  1260  AGTGCCCCTACGGGGTCTCCTCAAGACGCACTGCCCCTGCCCAGCTCGGTCGCGGTCACCCCAG  1319
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Qy  1439  TACGGCTTCGTGCGGGCCTGCCTGCGCCCGGCTGGTGCCCCCAGGCCTTCTGGGGCTCCAGG  1498
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Db  1434  TACGGCTTCGTGCGGGCCTGCCTGCGCCCGGCTGGTGCCCCCCAGGCCTTCTGGGGCTCCAGG  1493

Qy  1499  CACAACGAACGCGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCC  1558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1494  CACAACGAACGCGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCC  1553

Qy  1559  AAGCTCTCGCTGCGAGGAGCTGACGTGGAAGAGCGTGCGGGGACTGCGCGTGGCGTCGCGC  1618
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Db  1554  AAGCTCTCGCTGCGAGGAGCTGACGTGGAAGAGCGTGCGGGGACTGCGCGTGGCGTCGCGC  1613

Qy  1619  AGGAGCCCCAGGGGTTGGCTGTGTTCCGGCCCAGAGCGTCTGCGTGAGGAGATCCTG  1678
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Db  1614  AGGAGCCCCAGGGGTTGGCTGTGTTCCGGCCCAGAGGGTCTGCGTGAGGAGATCCTG  1673

Qy  1679  GCCAAGTTCCTGCACTGGCTCAGTGGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTT  1738
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Db  1674  GCCAAGTTCCTGCACTGGCTCAGTGGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTT  1733

Qy  1739  TATGTCACGGAGACCACGTTTCAAAAGACAGCTCTCTTTTCTACCGGAAGAGTGTCTCGG  1798
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Qy  1859  TCGGAAGCAGAGGTCAGGCAGCATCGGAAGCCCGGCCCTGCGCGCCCTCCCCGGCGGCCTCC  1918
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Db  3414  GCACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCC  3473

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Db  3474  GAGAGCAGACAGCACCAGCAGCCCTGTCACGCCGGCTCTACGTCCCAGGAGGAGGGGCGG  3533

Qy  3539  CCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGCGCTGAGTGTTTGGCCGAGGCC  3598
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Db  3594  TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGTGTCCGGCTGAGCGAGTGTCCAGCCAAGGG  3653

Qy  3659  CTGAGTGTCTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGCGCCTCGGCTCCACCC  3718
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 14
US-08-854-050-173
; Sequence 173, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
;   APPLICANT: Cech, Thomas R.
;   APPLICANT: Lingner, Joachim
;   APPLICANT: Nakamura, Toru
;   APPLICANT: Chapman, Karen B.
;   APPLICANT: Morin, Gregg B.
;   APPLICANT: Harley, Calvin
;   APPLICANT: Andrews, William H.
;   TITLE OF INVENTION: No. 6261836el Telomerase
;   NUMBER OF SEQUENCES: 225
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Center, 8th Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: United States of America
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;     ZIP: 94111
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/854,050
;     FILING DATE: 09-MAY-1997
;     CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/851,843
;     FILING DATE: 06-MAY-1997
;     CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/846,017
;     FILING DATE: 25-APR-1997
;     CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/844,419
;     FILING DATE: 18-APR-1997
;     CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/724,643
;     FILING DATE: 01-OCT-1996
;     CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Apple, Randolph T.
;     REGISTRATION NUMBER: 36,429
;     REFERENCE/DOCKET NUMBER: 015389-002930US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 576-0200
;     TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 4029 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY:
;     LOCATION: 1..4029
;     OTHER INFORMATION: /note= "preliminary sequence for
;     OTHER INFORMATION: human TRT cDNA insert of
;     OTHER INFORMATION: plasmid pGRN121"
US-08-854-050-173

Query Match       95.9%;   Score 3849.2;   DB 3;   Length 4029;
Best Local Similarity 98.5%;   Pred. No. 0;
Matches 3955;   Conservative  0;   Mismatches  53;   Indels   9;   Gaps   8;
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Qy    1  GCAGCCGCTGCGTCCTGCTGCGCACGTGGGAAGCCTGGCCCCGCCACCCCGCGATGCC   60
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Qy  241  ACGGGCCGGCCCCCGCCCCCGCCCCCGCCCCGCCCCTCCTTCCTCCGCCAGTGTCCTGGTCAAATTGGGGC  300
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Db     718 GAGGCGGGGGAGCAGTGCCAGCCCGGAAGTCTGCCGTTGCCCGAGAGGCGGCCGGTGCGC 777                                Db    1794 AGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGGAGCTG 1853
Qy     781 TGCCCCTGAGCCCGGAGCCGGACGGACGTCTTGGGCAGGGTGCTGGGGCCCCACCCGGGCAGGAC 840                           Qy    1859 TCGGAAGCAGAGGTCAGGCAGCATCGGGGAGGCCAGGCCCGCCCGCCCTGCTGACGTCCAGACTC 1918
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Db     838 GCGTGGACGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCACGCCCACTGCCCCACCCTGGGGCC 897                         Db    1914 CGCTTCATCCCCCAGACCTGACGCGTGCGGCTGCGGCCGATTGTGAACATGGACTACGTGCTGTGGA 1973
Qy     901 CACCTCTTGGAGGGTCGCGCTCTCTGCGGCCGCCCCATCACATCGGGCCACCACCAGTCCCTGGCCGCCA 960                      Qy    1979 GCCAGAAGCGTTCCGCAGAGAAAAGAGCGGGGCGCGTCGCAGCGTCGAGGGGTGAAGGCACTG 2038
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Db   3954 GGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTTGAAAAAA 4010

RESULT 15
US-09-430-323-173
; Sequence 173, Application US/09430323
; Patent No. 6309867
GENERAL INFORMATION:
  APPLICANT: Cech, Thomas R.
             Lingner, Joachim
             Nakamura, Toru
             Chapman, Karen B.
             Morin, Gregg B.
             Harley, Calvin
             Andrews, William H.
  TITLE OF INVENTION: No. 6309867el Telomerase
  NUMBER OF SEQUENCES: 225
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, 8th Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: United States of America
    ZIP: 94111
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/430,323
    FILING DATE: 29-Oct-1999
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/854,050
    FILING DATE: 09-MAY-1997
    APPLICATION NUMBER: US 08/851,843
    FILING DATE: 06-MAY-1997
    APPLICATION NUMBER: US 08/846,017
    FILING DATE: 25-APR-1997
    APPLICATION NUMBER: US 08/844,419
    FILING DATE: 18-APR-1997
    APPLICATION NUMBER: US 08/724,643
    FILING DATE: 01-OCT-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Apple, Randolph T.
    REGISTRATION NUMBER: 36,429

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Qy   2579 TGCAGCCGTGCTACGGCGACATGGAGAACAAGCTGTTGCGGGGATTCGGCGGACGGG 2638
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Db   2574 TGCAGCCGTGCTACGGCGACATGGAGAACAAGCTGTTGCGGGGATTCGGCGGACGGG 2633

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Qy   3299 CTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACG 3358
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Qy   3359 CAGCTGAGTCGGAAGCTCCCGGGGGACAGCGCTGACGTGCCCTGGAGGCCGCAGCCAACCCG 3418
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REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 4029 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    MOLECULE TYPE: cDNA
    FEATURE:
        NAME/KEY:
        LOCATION: 1..4029
        OTHER INFORMATION: /note= "preliminary sequence for
        human TRT cDNA insert of
        plasmid pGRN121"
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US-09-430-323-173:
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Query Match          95.9%;   Score 3849.2;   DB 4;   Length 4029;
Best Local Similarity 98.5%;   Pred. No. 0;
Matches 3955;   Conservative 0;   Mismatches 53;   Indels 9;   Gaps 8;
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Qy      1 GCAGCGCTGCGTCCTTGCTGCCGACGTGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCC GATGCGC 60
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Db      1 GCAGCGCTGCGTCCTTGCTGCCGACGTGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCCGATGCGC 60

Qy     61 GCGCGCTCCCCGCTTGCCGAGCCGTGCGTGCCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
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Qy    121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCTG CCCAGGGCTGGCGGCTGGTGTGCAGCGCGC 180
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCTGCCCAGGGCTGGCGGCTGGTGTGCAGCGCGG 180

Qy    181 GGACCCCGGGCGGCGGCTTCCCAGTGCTGGCGCCGGCGCTGGTGGTGTGCGTGCCCTGGGACGC 240
          |||||||||||||||||||||||||||||||||| ||  |||||||||||||||||||||||||
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Qy    241 ACGGCCCCGCCCCGCCCGCCCCCTCCTTCCGCGCCAGTGTCCTGCCTGAAGGAGCTGGTGGC 300
          |   | |||||||||||||||||||||||||||||||||| ||  ||||||||||||||||||
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Qy    361 GCTGCTGGACGGGGCCCCGCCGGGGGCCCCCGAGGGCCTTCACCACCAGCGTGCCGCAGCTA 420
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Db    718 GAGGGCCGGGGGGCAGTGCCAGCGGAGTCTGCCGTTGCCGACGAGAGGCCCAGGCGTGGCGC 777

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Qy    841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAGACCGCCGAGAAGC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838 GCCTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAGACCGCCGAGAAGC 897

Qy    901 CACCTCTTTGGAGGGTGCGCTCTTCTGCACGCGCCACTCCACCCATCCGTGGGCGGCGCCA 960
          |||||||||||||||||||||||||||||||||||| |||
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Qy    961 GCACCACGCGGGGCCCCCATCCACATCCACATCGCGGCCACCACAGTCCCTGGGACACGCCTTGTCC 1020
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Qy   1320 CAGCGGCCGGTCTGTGTGCCCGGGAGAAGCCGTCTCGGCAGCAGCACACAGCCCTGCCAGGAGG 1379
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Qy   1380 -ACACAGACCCCCGTCGCGCTGGTGCGACGCCGCGGCGAAGAACGTGCTGGCCTTCGGCCTTCGC 1438
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Db  2874 GTGCAGCAGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTCTCACCTTCAAC 2933
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Qy  2939 CGCGGCCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGTCTTCGGGCTGCGAAG 2998
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us-10-054-295-224.rni

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Job time : 241 secs

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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	4015	100.0	4015	10	US-09-990-080-1	Sequence 1, Appl
3	4015	100.0	4015	10	US-09-843-676-224 ⌄	Sequence 224, App
4	4015	100.0	4015	10	US-09-953-052-1	Sequence 1, Appl
5	4015	100.0	4015	14	US-10-053-758-224 ✓	Sequence 224, App
6	4015	100.0	4015	14	US-10-208-243-1	Sequence 1, Appl
7	4015	100.0	4015	14	US-10-054-295-224	Sequence 224, App
8	4015	100.0	4015	14	US-10-054-611-224 ✓	Sequence 224, App
9	4015	100.0	4015	14	US-10-105-963-1	Sequence 1, Appl
10	4015	100.0	4015	14	US-10-044-692-1	Sequence 1, Appl
11	4015	100.0	4015	14	US-10-044-539-1 ✓	Sequence 1, Appl
12	3849.2	95.9	4029	10	US-09-843-676-173	Sequence 173, App
13	3849.2	95.9	4029	11	US-09-438-486-173	Sequence 173, App
14	3849.2	95.9	4029	14	US-10-053-758-173	Sequence 173, App
15	3849.2	95.9	4029	14	US-10-054-295-173	Sequence 173, App
16	3849.2	95.9	4029	14	US-10-054-611-173	Sequence 173, App

17	3641	90.7	3855	14	US-10-044-692-4	Sequence 4, Appl
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45	385.8	9.6	389	10	US-09-843-676-62	Sequence 62, Appl

ALIGNMENTS

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; Patent No. US20020045588A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: William Gaarde
;  APPLICANT: Susan M. Freier
;  APPLICANT: Edward V. Wancewicz
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
;  FILE REFERENCE: ISPH-0527
;  CURRENT APPLICATION NUMBER: US/09/733,294A
;  CURRENT FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: 09/572,423
;  PRIOR FILING DATE: 2000-05-16
;  NUMBER OF SEQ ID NOS: 108
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;  LENGTH: 4015
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;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (56)...(3454)
US-09-733-294A-3

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Qy   2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCGTTTTGTTCAGAT 2820
Db   2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCGTTTTGTTCAGAT 2820

Qy   2821 GCCGGCCACGGCCTATTCCCCGGTGCGGCCTGCTGCTGATACCCGGACCCTGGAGGT 2880
Db   2821 GCCGGCCACGGCCTATTCCCCGGTGCGGCCTGCTGCTGATACCCGGACCCTGGAGGT 2880

Qy   2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCAGTCGCCAGTCTCCATCAGAGCCAGTCTCAACCG 2940
Db   2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCAGTCGCCAGTCTCCATCAGAGCCAGTCTCAACCG 2940

Qy   2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCCAAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000
Db   2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGCCAAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000

Qy   3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCGTCCAGACGCGTGCACCAACATCTA 3060
Db   3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCGTCCAGACGCGTGCACCAACATCTA 3060

Qy   3061 CAAGATCCTCCTGCTGCAGGCTACAGGTTTCACCGCATGTGTGCTGCAGCTCCCATTTCA 3120
Db   3061 CAAGATCCTCCTGCTGCAGGCTACAGGTTTCACCGCATGTGTGCTGCAGCTCCCATTTCA 3120

Qy   3121 TCAGCAAGTTTGGAAGAACCCACATTTTCCTGCGCCGTCATCTCTGACACGGCCTCCCT 3180
Db   3121 TCAGCAAGTTTGGAAGAACCCACATTTTCCTGCGCCGTCATCTCTGACACGGCCTCCCT 3180

Qy   3181 CTGCTACTCCATCCTGAAAGCCTGAAGCCAGGAGGTCGCTGGGGCCAAGGCGCCGC 3240
Db   3181 CTGCTACTCCATCCTGAAAGCCTGAAGCCAGGAGGTCGCTGGGGCCAAGGGGCCGC 3240

Qy   3241 CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGCGCGTGCTGCCACCAAGCATTCCTGCTCAAGCT 3300
Db   3241 CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGCGCGTGCTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy   3301 GACTCGACACCGTGTCACCTACGTGCCACTCGGGGACGCTGACTCGCTGGGGACGCTGACT 3360
Db   3301 GACTCGACACCGTGTCACCTACGTGCCACTCGGGGACGCTGACTCGCTGGGGACGCTGACT 3360

Qy   3361 GCTGAGTCGGAAGCTCGGAGGGCTCCCGGACGCGCTGACTGCCCTGAGGCCGCAGCCAACCCGGC 3420
Db   3361 GCTGAGTCGGAAGCTCGGAGGGCTCCCGGACGCGCTGACTGCCCTGAGGCCGCAGCCAACCCGGC 3420

Qy   3421 ACTGCCCTCAGACTTCAAGACCACCATCCTGACTGATGGCCACCCGCCCACAGCCAGGCCGA 3480
Db   3421 ACTGCCCTCAGACTTCAAGACCACCATCCTGACTGATGGCCACCCGCCCACAGCCAGGCCGA 3480

Qy   3481 GAGCAGACCACCAGCACCCCGTCTACGCCGGTCTACGTGTCCCCAGGAGGGAGGGGCGGCC 3540
Db   3481 GAGCAGACCACCAGCACCCCGTCTACGCCGGTCTACGTGTCCCCAGGAGGGAGGGGCGGGC 3540

Qy   3541 CACACCCAGGCCCCGCCACCCCTGGGAGTCGAGTGCTGAGGCCCTGAGTGAGTGTTTGGCCGAGGCCCTG 3600
Db   3541 CACACCCAGGCCCCGCCACCCCTGGGAGTCGAGTGCTGAGGCCCTGAGTGAGTGTTTGGCCGAGGCCTG 3600

Qy   3601 CATGTCCGGCTGAAGGCTGTAGTGTCCGGCTGGAGGCCTGAGGCCTGAGCCTGCTGAGCCCAAGGGCT 3660
Db   3601 CATGTCCGGCTGAAGGCTGTAGTGTCCGGCTGGAGGCCTGAGGCCTGAGCCTGCTGAGCCCAAGGGCT 3660

Qy   3661 GAGTGTCCAGCACACCTGCCGTCTCACTTCACTCCCCACCAGGCTGCGGCTCGGCTCGGCTCCACCCCA 3720
Db   3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCACTCCCCACCAGGCTGCGGCTCGGCTCGGCTCCACCCCA 3720

Qy   3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGCTTCCCACTCCCCCACACATAGGAATAGTCCATCC 3780
Db   3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGCTTCCCACTCCCCCACATAGGAATAGTCCATCC 3780

Qy   3781 CCAGATTCCGCCATTGTTCACCCTCGTCCCCTTCGCCTTCCACCCACCATCC 3840
Db   3781 CCAGATTCGCCATTGTTCACCCTCGTCCCCTTGCCTTCCACCCACCATCC 3840

Qy   3841 AGTGGGAGACCCTGAGAAGGACCCTGGGAGTCTGGAGTTTGGAGTTGACCAAAGGTGTG 3900
Db   3841 AGTGGGAGACCCTGAGAAGGACCCTGGGAGTCTGGAGTTTGGAGTTGACCAAAGGTGTG 3900

Qy   3901 CCCTGTACACAGGCGAGGACCCCTGCACCTGGATCGGGGTCCCTGTGGGTCAAATTGGGGG 3960
Db   3901 CCCTGTACACAGGCGAGGACCCCTGCACCTGGATCGGGGTCCCTGTGGGTCAAATTGGGGG 3960

Qy   3961 GAGGTGCTGTGGGGAGTAAAATACTGAAATATATGAGTTTTCAGTTTTGAAAAAA 4015
Db   3961 GAGGTGCTGTGGGGAGTAAAAATACTGAAATATATGAGTTTTCAGTTTTGAAAAAA 4015

RESULT 2
US-09-990-080-1
; Sequence 1, Application US/09990080
; Patent No. US2002010268A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258c
; CURRENT APPLICATION NUMBER: US/09/990,080
; CURRENT FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT) cDNA
US-09-990-080-1

Query Match   100.0%;   Score 4015;   DB 10;   Length 4015;
Best Local Similarity   100.0%;   Pred. NO. 0;
Matches 4015;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GCAGCGCTCGGTCCTGCTGCCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC 60
Db   1 GCAGCGCTCGGTCCTGCTGCCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC 60

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Qy   61 GCGCGGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTCTGCGCAGCCACTACCGCGAGGTGCT   120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCGCGGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTCTGCGCAGCCACTACCGCGAGGTGCT   120

Qy  121 GCCGCTGGCCACGTTCGTCGGCGCGCTGGGGCGCCTGGGCGGCCTGGTGCGTGCCCTGGACGC   180
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Db  121 GCCGCTGGCCACGTTCGTCGGCGCGCTGGGGCGCCTGGGCGGCCTGGTGCGTGCCCTGGACGC   180

Qy  181 GGACCCGCGGCGCCCCCGCGCGCCCCCGCGCCCCCGCGCGGGG                       240
        |||||||||||||||||||||||||||||||||||||||||||
Db  181 GGACCCGCGGCGCCCCCGCGCGCCCCCGCGCCCCCGCGCGGGG                       240

Qy  241 ACGGCCGCCGCCCACCGGTGACCGACGTGCGGTGCCTGAAGGAGTGCCTGGTGGC           300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ACGGCCGCCGCCCACCGGTGTCCTGCAGGTGTCCTGCCTGAAGGAGTGCCTGGTGGC           300

Qy  301 CCGAGTGCTGCAGAGGCGTGCGACGACGTGCCTGCCTCGCAGGCGCGGGGCTGCTCGGCTTCGC   360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CCGAGTGCTGCGACGACGTGCGACGACGTGCCTGCCTCGCAGGCGCGGGGCTGCTCGGCTTCGC   360

Qy  361 GCTGCTGGACGCGGGCCCCGGGGGCCCCGGGGCCTTCACCACCAGCGTGCGCAGCTA           420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GCTGCTGGACGCGGGCCCCGGGGGCCCCGGGGCCTTCACCACCAGCGTGCGCAGCTA           420

Qy  421 CCTGCCCAACACGGTGACCGACGTGCTGCGGGGGGAGCGGGGCTGCTGCGTGCG           480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CCTGCCCAACACGGTGACCGACGTGCTGCGGGGGGAGCGGGGCTGCTGCGTGCG           480

Qy  481 CCCGCTGGGCCGACCAGCACTGCTCGTGTTCACCTGCACGCTGCGCGCCGCTCTTCTTTGTCGGT   540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 CCCGCTGGGCCGACGACGTGCTGTTCACCTGCACGCTGCGCGCCGCTCTTCTTTGTCGGT   540

Qy  541 GGCTCCCAGCTGCGCCTACCAGTGTGCGGGCCCCGTGTACCAGCTCGGCCGCCTGCCAC           600
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Db  541 GGCTCCCAGCTGCGCCTACCAGTGTGCGGGCCCCGTGTACCAGCTCGGCCGCCTGCCAC           600

Qy  601 TCAGGGCCCGGCCCCGCCACAGGTGGACCCCGCTAGTGAGGCGTCTGGGATGCCGGAACGGGC           660
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Db  601 TCAGGGCCCGGCCCCGCCACAGGTGGACCCCGCTAGTGAGGCGTCTGGGATGCCGGAACGGGC           660

Qy  661 CTGGAACCATAGCGTCAGGGAGGTGCGCCTCTCCTGGGCCTGGCCAGCCCAGGGGTGCGAG           720
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Db  661 CTGGAACCATAGCGTCAGGGAGGTGCGCCGGCCGGGTGCCCCGCTGCCCAGCCCAGGGTGCGGAG           720

Qy  721 GAGGCGGGGAGCCCGGGACGCCCGTTGGCAGGGGTCCTGGCACCACCCCGGGACGCCTTGTCC          780
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Db  721 GAGGCGGGGAGCCCGGGACGCCCGTTGGCAGGGGTCCTGGCACCACCCCGGGACGCCTTGTCC          780

Qy  781 TGCCCCTGAGCCGGAGCCGTGGTTTCTGTGTGTCACCTGGTGTCACGCTGGGATGCCGAAGAGGC     840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 TGCCCCTGAGCCGGAGCCGTGGTTTCTGTGTGTCACCTGGTGTCACGCTGGGATGCCGAAGAGGC     840

Qy  841 GGCTGGACCGGACGTGACCGTGGTTTCTGGTGTGCACCTCTCCAGAGAGAGCCCGCGTGGGGCCGCA     900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GGCTGGACCGAGTGACCGTGGTTTCTGGTGTGCACCTCTCCAGAGAGCCCGCCAGAGAGCCCGCCAGAAGAGC     900

Qy  901 CACCTGTTTGAGGGTGCGCCTCCTCTGGCACGCGCCCACTCCCCACCACGTCCCTGGGACACGCCTTGTCC   1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 CACCTGTTTGAGGGTGCGCCTCCTCTGGCACGCGCCCACTCCCCACCACGTCCCTGGGACACGCCTTGTCC   1020

Qy  961 GACCACGCGGGCCCCCCGAGACCACTCCCTGCGGCCACCGGTCCCTCAGGCGCGACAAGGAGCAGCTCGCG   1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 GCACCACGCGGGCCCCCCGAGACCACTCCCTGCGGCCACCGGTCCCTCAGGCGCGACAAGGAGCAGCTCGCG   1080

Qy 1021 CCCGGTGTACGCGGGCCCCTGGGACGTCTCGAGGCCTGGCGCTGGCTGCGGAGGCCTCGGAGGCCTCGTGA   1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 CCCGGTGTACGCGGGCCCCTGGGACGTCTCGAGGCCTGGCGCTGGCTGCGGAGGCCTCGGAGGCCTCGTGA   1140

Qy 1081 GCCCTCCTTCCTACTCAGCTCTCTCAGGCCCTGAGGGACTGCCCCGCAGGTTGCCCCGCCT           1200
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 GCCCTCCTTCCTACTCAGCTCTCTCAGGCCCTGAGGGACTGCCCCGCAGGTTGCCCCGCCT           1200
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Qy 1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT   1200
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Db 1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT   1200

Qy 1201 GCCCCAGCGCTACTGGCAAATGCGGCCACTGCCCCGTTCTGGAGCTGCTGGGAGCTGGTGAGCTCGGTCACCCAGC   1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 GCCCCAGCGCTACTGGCAAATGCGGCCACTGCCCCGTTCTGGAGCTGCTGGGAGCTGGTGAGCTCGGTCACCCAGC   1260

Qy 1261 GTGCCCCTACGGGGTGCTCCTCAAGACCACTCGCCGCCGCTGCCGAGCTGCGGGCTGCGGCCCCGAGGAGGAGA   1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 GTGCCCCTACGGGGTGCTCCTCAAGACCACTCGCCGCCGCTGCCGAGCTGCGGGCTGCGGCCCCGAGGAGGAGA   1320

Qy 1321 AGCCGGTGTCTGTGCCGCGCCCCTCTTCCGGGAGAGCCCAGGGCTCTGTGCCGCGCCCCTCTTCCGGGAGAGC   1380
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 AGCCGGTGTCTGTGCCGCGCCCCTCTTCCGGGAGAGCCCAGGGCTCTGTGCCGCGCCCCTCTTCCGGGAGAGC   1380

Qy 1381 CACAGACCCCCGTCGCGCCTGGTGCAGCTGCTCCGCCAGCACAGCCCTGGCAGGTGTA   1440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 CACAGACCCCCGTCGCGCCTGGTGCAGCTGCTCCGCCAGCACAGCCCTGGCAGGTGTA   1440

Qy 1441 CGGCTTCGTCGTGCGGGCCTGCCTGCCGGTGCCCCGGGGCCTCGTGGGGCTCCAGGCA   1500
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 CGGCTTCGTCGTGCGGGCCTGCCTGCCGGTGCCCCGGGGCCTCGTGGGGCTCCAGGCA   1500

Qy 1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA   1560
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501 CAACGAACGCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA   1560

Qy 1561 GCTCTCGCTGCGCAGGAGCTGACGTGGAAGATGAGCGTGGCGGACTGCGGTTGGCTGCGCAG   1620
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1561 GCTCTCGCTGCGCAGGAGCTGACGTGGAAGATGAGCGTGGCGGACTGCGGTTGGCTGCGCAG   1620

Qy 1621 GAGCCCAGGGGTTGGCTGGTGTTCCGGCCCAGAGCACCGTGCGCGAGCTGCTGCTCTCGAGCTCCTGGC   1680
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1621 GAGCCCAGGGGTTGGCTGGTGTTCCGGCCCAGAGCACCGTGCGCGAGCTGCTGCTCTCGAGCTCCTGGC   1680

Qy 1681 CAAGTTCCTGCACTGGCTGGCTGGCTGGCTGATGAGTGTGACGTGTACGTCGTCTCAGGTCTTTCTTTA   1740
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681 CAAGTTCCTGCACTGGCTGGCTGGCTGGCTGATGAGTGTGACGTGTACGTCGTCTCAGGTCTTTCTTTA   1740

Qy 1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTTCTACCCGGAAGAGTGTCTGGAG   1800
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741 TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTTCTACCCGGAAGAGTGTCTGGAG   1800

Qy 1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACACTTGAAGAGGTGCAGCTGCGGGAGCTGTGTC   1860
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACACTTGAAGAGGTGCAGCTGCGGGAGCTGTGTC   1860

Qy 1861 GGAAGCAGAGGTCAGGCAGCATCGGGGAAGCCAGCCCGCCCGCTGCTGACGTCCAGACTCCG   1920
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1861 GGAAGCAGAGGTCAGGCAGCATCGGGGAAGCCAGCCCGCCCGCTGCTGACGTCCAGACTCCG   1920

Qy 1921 CTTCATCCCCAAGCCTGACGCCTGCGGCGCTGACCGATTGTGAACATGTGAACATGTCGTGGGAGC   1980
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921 CTTCATCCCCAAGCCTGACGCCTGCGGCGCTGACCGATTGTGAACATGTGAACATGTCGTGGGAGC   1980

Qy 1981 CAGAACGTTCCGCAGAGAAAAGAGAGGCCGAGCGTCACCTGAGGGTGAAGGCACTGTT   2040
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1981 CAGAACGTTCCGCAGAGAAAAGAGAGGCCGAGCGTCACCTGAGGGTGAAGGCACTGTT   2040

Qy 2041 CAGGCCTGCTCAACTACGAGCGAGCAGGGCCTCTGTGCCGCCTCCTCGTGTGCTGGG   2100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2041 CAGGCCTGCTCAACTACGAGCGAGCAGGGCCTCTGTGCCGCCTCCTCGTGTGCTGGG   2100

Qy 2101 CCTGACGATATCCCAAGGCCTCGCACCTTCGTGCGTCGTGTGCGCCCAGGACCCC   2160
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2101 CCTGACGATATCCCAAGGCCTCGCACCTTCGTGCGTCGTGTGCGCCCAGGACCCC   2160

Qy 2161 GCCCCCTGAGCTGTACTTTGTCAAGGTGACTGGATGTGACGTCGGGCCGCGTACGACACCATCCCCCA   2220
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2161 GCCCCCTGAGCTGTACTTTGTCAAGGTGACTGGATGTGACGTCGGGCCGCGTACGACACCATCCCCCA   2220

Qy 2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG   2280
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG   2280
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Db   2221  GGACAGGCTCACGGAGTCATCGCCAGCATCATCAAACCCCAGAAGACACGTACTGCGTGCG  2280

Qy   2281  TCGGTATGCCGTGGTCCAGAGAGGCCGCCATGGCACGTCCCAAGGCCTTCAAGAGCCA    2340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  TCGGTATGCCGTGGTCCAGAGAGGCCGCCATGGCACGTCCCAAGGCCTTCAAGAGCCA    2340

Qy   2341  CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACCAGTTCGTGGCTCACCTGCAGGA  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACCAGTTCGTGGCTCACCTGCAGGA  2400

Qy   2401  GACCAGCCGCGTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG    2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  GACCAGCCGCGTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG    2460

Qy   2461  CAGTGGCCTCTTCGACGTCTTCCTACCGCTTCATGTGCCACCACGCCGTGCGCATCAGGG   2520
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Db   2461  CAGTGGCCTCTTCGACGTCTTCCTACCGCTTCATGTGCCACCACGCCGTGCGCATCAGGG   2520

Qy   2521  CAAGTCCTACGTCCAGTGCCACGGGGATCCCCAGGGCTCCACCTCTCTCCACGCTGCTCTG  2580
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Db   2521  CAAGTCCTACGTCCAGTGCCACGGGGATCCCCAGGGCTCCACCTCTCTCCACGCTGCTCTG  2580

Qy   2581  CAGCCTGTCTACGGGCACATGGAGAACAAGCTGTTTGTGGTGACACCTCACCTCACGCGGGGCT  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  CAGCCTGTCTACGGGCACATGGAGAACAAGCTGTTTGTGGTGACACCTCACCTCACGCGGGGCT  2640

Qy   2641  GCTCCTCGCGTTTGGTGATGATTTCTTGTTCGTTGGTGACAACTCACCTCACCGCGAAAAC  2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  GCTCCTCGCGTTTGGTGATGATTTCTTGTTCGTTGGTGACAACTCACCTCACCGCGAAAAC  2700

Qy   2701  CTTCCTCAGGACACCTGGTCCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGGTGAACTGCCGAA  2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  CTTCCTCAGGACACCTGGTCCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGGTGAACTGCCGAA  2760

Qy   2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGCCACGGCTTTTGTTGTTCAGAT   2820
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGCCACGGCTTTTGTTGTTCAGAT   2820

Qy   2821  GCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGAGGT            2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  GCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGAGGT            2880

Qy   2881  GCAGAGGCGACTACTCCAGCTATGCCCCGGACCTCCATCAGAGCCAGTCTCACCTTCACCCG   2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  GCAGAGGCGACTACTCCAGCTATGCCCCGGACCTCCATCAGAGCCAGTCTCACCTTCACCCG   2940

Qy   2941  CGGCTTCAAGGCTGGGAGGAACATGCCTGCCAAACTCTTTGGGTCTTGCGGCTGAGTG     3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  CGGCTTCAAGGCTGGGAGGAACATGCCTGCCAAACTCTTTGGGTCTTGCGGCTGAGTG     3000

Qy   3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGCGTGCACCAACATCTA    3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGCGTGCACCAACATCTA    3060

Qy   3061  CAAGATCCTCCTGCTCCGAGGCTACAGTGTGTCTCGCAGCTCCCATTTCA              3120
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  CAAGATCCTCCTGCTCCGAGGCTACAGTGTGTCTCGCAGCTCCCATTTCA              3120

Qy   3121  TCAGCAAGTTTGGAAGAACCCACAATTTTTCCTGCTGGCGTCATCTCTGACACGGCCTCCCT  3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121  TCAGCAAGTTTGGAAGAACCCACAATTTTTCCTGCTGGCGTCATCTCTGACACGGCCTCCCT  3180

Qy   3181  CTGCTACTCCATCCTGAAAGCCAAGACGCAGGGCTGGGGCGCCAAGGGCGCCGGC        3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181  CTGCTACTCCATCCTGAAAGCCAAGACGCAGGGCTGGGGCGCCAAGGGCGCCGGC        3240

Qy   3241  CGGCCCTGCCCTCCGAGGCCGTGCAGTGCGCTGTGCCAAGCATTCCTGCTCAAGCT       3300
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Db   3241  CGGCCCTGCCCTCCGAGGCCGTGCAGTGCGCTGTGCCAAGCATTCCTGCTCAAGCT       3300

Qy   3301  GACTCGACACCGTGTCACCTACGTGCCACTCGTTGGGGTCACTCAGGACAGCCCAGACGCA   3360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301  GACTCGACACCGTGTCACCTACGTGCCACTCGTTGGGGTCACTCAGGACAGCCCAGACCCA   3360
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Db   3361  GCTGAGTCGGAAGCTCCCGGGGACGACGCGTCGACTGCCCTGACTGCCCTGCCCGCAGCCCCAGCCGC  3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3361  GCTGAGTCGGAAGCTCCCGGGGACGACGCGTCGACTGCCCTGACTGCCCTGCCCGCAGCCCCAGCCGC  3420

Qy   3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGCGATGAGCCACACCCCAGCCGGA     3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGCGATGAGCCACACAGCCCACAGGCCGA     3480

Qy   3481  GAGCAGACACCAGCAGCCCTGTCACGGGCTCTACGTCCCAGGGAGGAGGGGCGGCC      3540
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Db   3481  GAGCAGACACCAGCAGCCCTGTCACGCCCGGCTCTACGTCCCACGGGAGGAGGGGCGGGCC      3540

Qy   3541  CACACCCAGGCCCGCCACCCGGGAGTCTGAGGCTGGGAGTGAGTGTTTGGCCGAGGCCTG    3600
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Db   3541  CACACCCAGGCCCGCCACCCGGGAGTCTGAGGCTGGGAGTGAGTGTTTGGCCGAGGCCTG    3600

Qy   3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCGCTGAGCGAGTGTCCACCCCA    3660
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APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph T.
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 4015 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 56..3454
    OTHER INFORMATION: /product= "hTRT"
      /note= "human telomerase reverse
      transcriptase (hTRT) catalytic protein
      component"
  SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-843-676-224
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Query Match      100.0%;    Score 4015;   DB 10;   Length 4015;
Best Local Similarity  100.0%;    Pred. NO. 0;
Matches 4015;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;
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Qy    1 GCAGCGCTGCGTCCTGCTGCACGTGGGAAGCCTGGCCCCGCCACCCCGCGGATGCC
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Db    1 GCAGCGCTGCGTCCTGCTGCACGTGGGAAGCCTGGCCCCGCCACCCCGCGGATGCC   60

Qy   61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCGTCCCCTGCTGCGCCGGT
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  121 GCGCCCTGGCCACGTTCGTGCGGCCCCCAGGGCCCCAGGGCTGTCGGTCGCAGCCGGG
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GCGCCCTGGCCACGTTCGTGCGGCCCCCAGGGCCCCAGGGCTGTCGGTCGCAGCCGGG  180

Qy  181 GGACCCGGCGGCTTCCCGCGCGCCCCGCCCCCTCCTTCCGCGAGGCGGCGGCCTTCGC
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Db  181 GGACCCGGCGGCTTCCCGCGCGCCCCGCCCCCTCCTTCCGCGAGGCGGCGGCCTTCGC  240

Qy  241 ACGGCGCGCCCCGCGCGCCCCGCCCCCCTCCTTCCGCGAGGTGTCCTGCCCAGTGTCC
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ACGGCGCGCCCCGCGCGCCCCGCCCCCCTCCTTCCGCGAGGTGTCCTGCCCAGTGTCC  300

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        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  421 CCTGCCCAACACCGTGACCGACGCACTGCCGGGGGAGCGGGGGCGTGGGGGCTGCTGCG
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Db  481 CCCGCTGGGGCGACCACGTGCTGGTTCACCTGCTGGTTCACCTGCTCTTTGTGCTGGT  540

Qy  541 GGCTCCCAGCTGCGGCCTGCGGGCCGCCTACCAGTCCGCGCTGCCCAC
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Db  601 TCAGGGCCGGCCCCCCACACGCGTCTAGTGGACCCGAAGGCGTCTGGGATGCGAACGGGC  660

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Db  661 CTGGAACCATAGCGTCAGGAGGACCGGGTCCCGGGCCTGGGCCCCCGGGGTGCGAG  720

Qy  721 GAGGCGCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCGTGCCGTGCCCAGGCGTGGCGC
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Db  721 GAGGCGCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCGTGCCGTGCCCAGGCGTGGCGC  780

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Qy  841 GCGTGGACCGAGTGACCGTGTTTCTGTGTCACCTGCCAGACCCGCCGAAGAAGC
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Qy  961 GCACCACGCGGCCCCCCATCCACATGCGGCCACCAGCGTCCCTGGGACACGCCTTGTCC
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Db 1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGCGGACCAAGGAGCAGCTGCG  1080

Qy 1081 GCCCTCCTCCTACTCAGCTCTCTGAGGCCCAGCTGACTGGCGTCGAGGCTCGTGGA
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Db 1201 GCCCCAGCGCTACTGCAAATGCGGCCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA  1260

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Db   2041 CAGCCGTGCTCAACTACGAGCGGCGCGGCGCCCCGTGTGCTGGG 2100

Qy   2101 CCTGGACGATATCCCACAGGCCTGGCGCCACCTTCGTGCTGCGGCCCCAGGACCC 2160
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Db   2941 CGGCTTCAAGGCTGGGAGGAACATGGTCGTGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000

Qy   3001 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGTGTGCACCAACACTCTA 3060
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Qy   3061 CAAGATCCTCCTGCTCAGGCGTACAGGTTCACGCATGTGCTGCAGCTCCCATTTCA 3120
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Qy   3121 TCAGCAAGTTGGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGGCCTCCCT 3180
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Db   3181 CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGCTGGGGTCACTCAGGCT 3240

Qy   3241 CGGGCCCTGCTCTCCGAGGCCGTCAGTGGCGTCGTGCTCATCGTGACAGGCCTCCCT 3300
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Qy   3721 GGGCCAGTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCACATAGGAATAGTCCATCC 3780
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Qy   3781  CCAGATTGCCATTGTTCACCCCTGCCCTCCTTGCCTTCCACCCCACCATCC   3840
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Db   3781  CCAGATTGCCATTGTTCACCCCTGCCCTCCTTGCCTTCCACCCCACCATCC   3840

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RESULT 4
US-09-953-052-1
; Sequence 1, Application US/09953052
; Patent No. US2002017347GA1
; GENERAL INFORMATION:
;   APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin B.
;   Andrews, William H.
;   TITLE OF INVENTION: Antisense Compositions for Detecting and
;   Inhibiting Telomerase Reverse Transcriptase
;   NUMBER OF SEQUENCES: 72
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/953,052
;   FILING DATE: 14-Sep-2001
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/052,919
;   FILING DATE: <Unknown>
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997
;   APPLICATION NUMBER: US 08/854,050
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: US 08/911,312
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/912,951
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/915,503
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/974,549
;   FILING DATE: 19-NOV-1997
;   APPLICATION NUMBER: US 08/974,584
;   FILING DATE: 19-NOV-1997
;   APPLICATION NUMBER: WO PCT/US97/17618
;   FILING DATE: 01-OCT-1997
;   APPLICATION NUMBER: WO PCT/US97/17885
;   FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
;   NAME: Parent, Annette S.
;   REGISTRATION NUMBER: 42.058
;   REFERENCE/DOCKET NUMBER: 015389-003600US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4015 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 56..3454
;   OTHER INFORMATION: /product= "human telomerase reverse
;   transcriptase (hTRT)"
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-953-052-1

Query Match   100.0%;   Score 4015;   DB 10;   Length 4015;
Best Local Similarity   100.0%;
Matches 4015;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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RESULT 5
US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1
GENERAL INFORMATION:
  APPLICANT: Cech, Thomas R.
             Lingner, Joachim
             Nakamura, Toru
             Chapman, Karen B.
             Morin, Gregg B.
             Harley, Calvin
             Andrews, William H.
  TITLE OF INVENTION: No. US20030032075A1e1 Telomerase
  NUMBER OF SEQUENCES: 225
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, 8th Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: United States of America
    ZIP: 94111
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/053,758
    FILING DATE: 18-Jan-2002
    CLASSIFICATION: 536
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/854,050
    FILING DATE: 09-MAY-1997
    APPLICATION NUMBER: US 08/851,843
    FILING DATE: 06-MAY-1997
    APPLICATION NUMBER: US 08/846,017
    FILING DATE: 25-APR-1997
    APPLICATION NUMBER: US 08/844,419
    FILING DATE: 18-APR-1997
    APPLICATION NUMBER: US 08/724,643
    FILING DATE: 01-OCT-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Apple, Randolph T.
    REGISTRATION NUMBER: 36,429
    REFERENCE/DOCKET NUMBER: 015389-002930US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 576-0200
    TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 4015 base pairs
    TYPE: nucleic acid
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Query Match   100.0%;   Score 4015; DB 14;   Length 4015;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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   121     GCGGCTGCCGGGCGGCTTCGTGCGGCCGCCTGGGCGCTGGTGTGCCTGGGACGC          180
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   181     GGACCCGGCGGCTTCCCGGCCGTGGTGCCCGCCTGGTGGCCTGGTGCGCTGGGACGC       240
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   181     GGACCCGGCGGCTTCCCGGCCGTGGTGCCCGCCTGGTGGCCTGGTGCGCTGGGACGC       240
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Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   1081    GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTGCGACTGGAGGCTCGTGGA      1140
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   1141    GACCATCTTTCTGGGTTCCAGGCCTGATGCCAGGACTCCCCGCAGGTTGCCCCGCCT      1200
Db         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   1141    GACCATCTTTCTGGGTTCCAGGCCTGATGCCAGGACTCCCCGCAGGTTGCCCCGCCT      1200
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(DNA sequence alignment; Query (Qy) and Database (Db) sequences, positions 1–1140 and 1081–2220, shown as a gapless match alignment.)

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Qy  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCTGCG  2280
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Db  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCTGCG  2280

Qy  2281  TCGGTATGCCGTGGTCCAGAGAGGCGCCGCCCAGGGCGTTCCGCAAGGGCCTTCAAGAGCCA  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCGGTATGCCGTGGTCCAGAGAGGCGCCGCCCAGGGCCGTTCCGCAAGGGCCTTCAAGAGCCA  2340

Qy  2341  CGTCTCTACCTTGACAGACCTCCAGCCGCTACATGCGACAGTTCGTGGCTCACCTGCAGGA  2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGTCTCTACCTTGACAGACCTCCAGCCGCTACATGCGACAGTTCGTGGCTCACCTGCAGGA  2400

Qy  2401  GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGTCCTCCCTGAATGAGGCCAG  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGTCCTCCCTGAATGAGGCCAG  2460

Qy  2461  CAGTGGCCGTCTTCGACGTCTTCCTCATGTCGCCACCACGCCGTGCGCATCAGGGG  2520
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Db  2461  CAGTGGCCGTCTTCGACGTCTTCCTCATGTCGCCACCACGCCGTGCGCATCAGGGG  2520

Qy  2521  CAAGTCCTACGTCCAGTGCCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCGTGCTCTG  2580
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CAAGTCCTACGTCCAGTGCCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCGTGCTCTG  2580

Qy  2581  CAGCCGTGCTACGGCGACATGAGGAGAACAAGCTGTTTGTGTGACACCTCACCTCCACGGGCGGCT  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CAGCCGTGCTACGGCGACATGAGGAGAACAAGCTGTTTGTGTGACACCTCACCTCCACGGGCGGCT  2640

Qy  2641  GCTCCTCGTTTGGTGATGATTCTTGTTGTGACACCTCACCTCCACGCGGACGGGCT  2700
          ||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCTCCTCGTTTGGTGATGATTCTTGTTGTGACACCTCACCTCCACGCGGACGGGCT  2700

Qy  2701  CTTCCTCAGGACCCTGGTCCCGGAGGTGTCCCTGAGTATGGCTGCGTGGTGGTGAACTTGCGGAA  2760
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Db  2701  CTTCCTCAGGACCCTGGTCCCGGAGGTGTCCCTGAGTATGGCTGCGTGGTGGTGAACTTGCGGAA  2760

Qy  2761  GACAGTTGGTGAACTTCCCTGTAGAGACGAGGCCCTGGGTGGTGCACGCTTTGTTCAGAT  2820
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Db  2761  GACAGTTGGTGAACTTCCCTGTAGAGACGAGGCCCTGGGTGGTGCACGCTTTGTTCAGAT  2820

Qy  2821  GCCGGCCCACGCGTCCCTATTCCCCTGGTGCGCCTGCTGCTGCTGCTCGTGACCCCTGGAGGT  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  GCCGGCCCACGCGTCCCTATTCCCCTGGTGCGCCTGCTGCTGCTGCTCGTGACCCCTGGAGGT  2880

Qy  2881  GCAGAGCGACTACTCCAGCTATGCCCCGGACTCCATCAGAGCCAGTCTCACCTTCAACCG  2940
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Db  2881  GCAGAGCGACTACTCCAGCTATGCCCCGGACTCCATCAGAGCCAGTCTCACCTTCAACCG  2940

Qy  2941  CGGCTTCAAGGCTGGGAGGAACAATGCGTCGCAAACTCTTTGGGGTCTTTGCGGCTGAAGTG  3000
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  CGGCTTCAAGGCTGGGAGGAACAATGCGTCGCAAACTCTTTGGGGTCTTTGCGGCTGAAGTG  3000

Qy  3001  TCACAGCCGTGTTTCTGGATTTGCAGTGAACAGCGTCCAGACGGTTGCACCAACATCTA  3060
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  TCACAGCCGTGTTTCTGGATTTGCAGTGAACAGCGTCCAGACGGTTGCACCAACATCTA  3060

Qy  3061  CAAGATCCTCTGCTGCCAGGCTACACGTTCACGCATGTGTGCTGCAGCTCCCATTTCA  3120
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  CAAGATCCTCTGCTGCCAGGCTACACGTTCACGCATGTGTGCTGCAGCTCCCATTTCA  3120

Qy  3121  TCAGCAAGTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCCTGACACGGCCTCCCT  3180
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  TCAGCAAGTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCCTGACACGGCCTCCCT  3180

Qy  3181  CTGCTACTCCATCCTGAAACCCGAAAGCCAAGAACGCAGGGATGTCGCGTCGGGGGCCGCGC  3240
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Db  3181  CTGCTACTCCATCCTGAAAGCCGAAAGCCAAGAACGCAGGGATGTCGCGTCGGGGGCCGCGC  3240

Qy  3241  CGGCCCCTGCCCTCCGCCCGGCCCTCCCAGGCCCGCTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT  3300
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  CGGCCCCTGCCCTCCGCCCGGCCCTCCCAGGCCCGCTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT  3300
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Qy  3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA  3360
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA  3360

Qy  3361  GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCCAGCCAACCCGGC  3420
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Db  3361  GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCCAGCCAACCCGGC  3420

Qy  3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA  3480
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Db  3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA  3480

Qy  3481  GAGCAGACACCAGCAGCCCTGTCACGCCCGGCTCTACGCCCGGAGGAGGGGACGGGGCC  3540
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  GAGCAGACACCAGCAGCCCTGTCACGCCCGGCTCTACGCCCGGAGGAGGGGACGGGGCC  3540

Qy  3541  CACACCCAGGCCCGCACCGCTGGGAGTCGGAGGCCTGAGGGTGTTTGGCCGAGGCCTG  3600
          ||||||||||||||||||||||||||||||||||||||||||||
Db  3541  CACACCCAGGCCCGCACCGCTGGGAGTCGGAGGCCTGAGGGTGTTTGGCCGAGGCCTG  3600

Qy  3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGGCCTGAGCCAGCCAAGGGCT  3660
          |||||||||||||||||||||||||||||||||||||||||||
Db  3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGGCCTGAGCCAGCCAAGGGCT  3660

Qy  3661  GAGTGTCCAGCACACCTGCGCGTCCTTCACTTCCCACAGGCTGGCGCGTCCCACCCCA  3720
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  GAGTGTCCAGCACACCTGCGCGTCCTTCACTTCCCACAGGCTGGCGCGTCCCACCCCA  3720

Qy  3721  GGGCCAGCTTTCCTCACCAGGAGCGCCGGCTTCCCACTCCCCACATAGGAGAATAGTCCATCC  3780
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Db  3721  GGGCCAGCTTTCCTCACCAGGAGCGCCGGCTTCCCACTCCCCACATAGGAGAATAGTCCATCC  3780

Qy  3781  CCAGATTGCCATTGTTCACCCTGCCTCCTTGCCTTCACCCCCACCATCC  3840
          |||||||||||||||||||||||||||||||||||||
Db  3781  CCAGATTGCCATTGTTCACCCTGCCTCCTTGCCTTCACCCCCACCATCC  3840

Qy  3841  AGGTGGAGACCCTGAGAAGGACACCCTGGGAGCTCTGGAATTTGGAGTGACCAAAGGTGTG  3900
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  AGGTGGAGACCCTGAGAAGGACACCCTGGGAGCTCTGGAATTTGGAGTGACCAAAGGTGTG  3900

Qy  3901  CCCTGTACCAGGCGAGGACCCTGCCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG  3960
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  3901  CCCTGTACCAGGCGAGGACCCTGCCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG  3960

Qy  3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAA  4015
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Db  3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAA  4015
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;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (56)..(3454)
;   OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
US-10-208-243-1

Query Match        100.0%;   Score 4015;   DB 14;   Length 4015;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 4015   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy      1  GCAGGCGTGGTGCTGCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCCCGCGATGCC  60
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Db      1  GCAGGCGTGGTGCTGCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCCCGCGATGCC  60

Qy     61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  120

Qy    121  GCCGGTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGGCTGGCCGGCTGGTCAGCGCGG  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCCGGTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGGCTGGCCGGCTGGTCAGCGCGG  180

Qy    181  GGACCCGGCGCTTCCGCGCCGCGCTGTGTGCCCAGTGCCTGGTGTGCGTCCCTGGGACGC  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GGACCCGGCGCTTCCGCGCCGCGCTGTGTGCCCAGTGCCTGGTGTGCGTCCCTGGGACGC  240

Qy    241  ACGGGCGCCCCCGCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ACGGGCGCCCCCGCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGC  300

Qy    301  CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGGCGGCCCCCCAGGGCGTGGGGCTTCGC  360
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Db    301  CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGGCGGCCCCCCAGGGCGTGGGGCTTCGC  360

Qy    361  GCTGCTGGACGGGGCCCGCGGGGGCCCCCCAGAGGCCGTTCACCACCAGCGTGCGCAGCTA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GCTGCTGGACGGGGCCCGCGGGGGCCCCCCAGAGGCCGTTCACCACCAGCGTGCGCAGCTA  420

Qy    421  CCTGCCCAACACGGTGACCGACGCGCTGCGGGGCAGCGGGGCGTGGGGCGCTGCGCG  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  CCTGCCCAACACGGTGACCGACGCGCTGCGGGGCAGCGGGGCGTGGGGCGCTGCGCG  480

Qy    481  CCGGCGTGGGCGACGACGCTGGTGGTTCACCTGCCCTCTTTGTGCTGGT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CCGGCGTGGGCGACGACGCTGGTGGTTCACCTGCCCTCTTTGTGCTGGT  540

Qy    541  GGCTCCCAGTGCCGCCTACCAGGTGGCGGCCCCACGCTAGTGGACCCCCACACGGGC  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GGCTCCCAGTGCCGCCTACCAGGTGGCGGCCCCACGCTAGTGGACCCCCACACGGGC  600

Qy    601  TCAGGCCCGGCCCCCGCCGCACCACAGGGTCTGGGATGCCAGGGCCCGGGGTCGCGAG  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TCAGGCCCGGCCCCCGCCGCACCACAGGGTCTGGGATGCCAGGGCCCGGGGTCGCGAG  660

Qy    661  CTGGAACCATAGCGTCAGGAGAGCCGGGGTCCCCGGCCAGCCCGGGGTGCGAG  720
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Qy    721  GAGGGCCGGGGGCAGTGCGCAGGCCCGAAGTCTCCGTTGCCAGGAGGCGGTGGCGC  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  GAGGGCCGGGGGCAGTGCGCAGGCCCGAAGTCTCCGTTGCCAGGAGGCGGTGGCGC  780

Qy    781  TGCCCCTGAGCCGGACGCCCGTTGGGCGGGACGCCCCGTTGGGCAGGGGTCCTGGGCGGGAGGAGGCAGGAC  840
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Db    841  GCGTGACCGAGTGACCTGTTTCTGTGTGTCACCTGTCACCTGCCAGACCCGCCGCAGAAGC  900

Qy    901  CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACCATCCGTGGGCCGCCA  960
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Db    901  CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACCATCCGTGGGCCGCCA  960

Qy    961  GCACCACCCGGCGGCCCCATCCACATCCGGCGGCCACCAGTCCCTGGGACACGCCTTGTCC  1020
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Db    961  GCACCACCGGGCGGCCCCCATCCACATCCACATCCGGCGGCCACCAGTCCCTGGGACACGCCTTGTCC  1020

Qy   1021  CCGGTGTACGCCGAGACCAAGACCACTCCTCTACTCCTCAGGCCACAAGGAGCAGCTGCGG  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  CCGGTGTACGCCGAGACCAAGACCACTCCTCTACTCCTCAGGCCACAAGGAGCAGCTGCGG  1080

Qy   1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGGCGCTGGGGCTCGGTGA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGGCGCTGGGGCTCGGTGA  1140

Qy   1141  GACCATCTTTCTGGGTTCCAGGCCCTGGCAGCCACTACCGCGAGGTGCT  1200
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Db   1141  GACCATCTTTCTGGGTTCCAGGCCCTGGCAGCCACTACCGCGAGGTGCT  1200

Qy   1201  GCCCAGGCTACTGGCAAATGCGCCCTGTTTCTGGAGCTGCGTTGGGAACCACGCGCCA  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  GCCCCAGGCTACTGGCAAATGCGCCCTGTTTCTGGAGCTGCGTTGGGAACCACGCGCCA  1260

Qy   1261  GTGCCCCTACGGGGTGCTCTCCTCAAGACCGCACTGCCCGTGCGGAGCGGTGCGGGTCACCCCAGC  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  GTGCCCCTACGGGGTGCTCTCCTCAAGACCGCACTGCCCGTGCGGAGCGGTGCGGGTCACCCCAGC  1320

Qy   1321  AGCCGGTGCTGTGCCCGGGGAGAGCCTCGTGTGGCGGCCCCCGAGGAGGAGGA  1380
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Db   1321  AGCCGGTGCTGTGCCCGGGGAGAGCCTCGTGTGGCGGCCCCCGAGGAGGAGGA  1380

Qy   1381  CACAGACCCCCGTGCGCCTGCTCGTGCAGCTGCGCGAGAACGTGCTCGGCCTTCGGCTGTA  1440
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Db   1381  CACAGACCCCCGTGCGCCTGCTCGTGCAGCTGCGCGAGAACGTGCTCGGCCTTCGGCTGTA  1440

Qy   1441  CGGCTTCGTGCGGGGCCTGCTTCCTCAGGAGGACGCGGGGCGTGGGGGAAGTCATCTCCCAGGCA  1500
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Qy   1501  CAACGAACGGCCGCTTCATCAGGAGGTGGAGATGAGGTCGCCGTTGGCTGCGCAA  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  CAACGAACGGCCGCTTCATCAGGAGGTGGAGATGAGGTCGCCGTTGGCTGCGCAA  1560

Qy   1561  GCTCTCGCTGCTGCAGGAGCTGCACGTGGAAGATCAGACAGCAGCACTTGAAGAGGGTGCGCGACTCCTGCGCAG  1620
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Qy   1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC  1680
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Db   1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC  1680

Qy   1681  CAAGTTCCTGCACTGGCTGATGAGTGTCTGATGAGTGTGTACCGGCTGCTTTCTTTTA  1740
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Db   1681  CAAGTTCCTGCACTGGCTGATGAGTGTCTGATGAGTGTGTACCGGAGATCCTGGCTCTTTTCTTTTA  1740

Qy   1741  TGTCACGGAGACCACGTTCAGGGGTCTTCAAAAGAACAGGCTCTTTTTTTCACCGGAAGAGTGCTGGAG  1800
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Db   1741  TGTCACGGAGACCACGTTCAGGGGTCTTCAAAAGAACAGGCTCTTTTTTTCTACCGGAAGAGTGCTGGAG  1800

Qy   1801  CAAGTTGCAAAGCATTGGAATCAGAGGAGACAGCACTTGAAGAGGGTGCAGCTGCAGCTGTC  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  CAAGTTGCAAAGCATTGGAATCAGAGGAGACAGCACTTGAAGAGGGTGCAGCTGCAGCTGTC  1860

Qy   1861  GGAAGCAGAGGTCAGGCAGCATCGGAAGCCCGCGTCCAGACTCCG  1920
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Qy   1921  CTTCATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980
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Db   1921  CTTCATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980

Qy   1981  CAGAACGTTCCGCAGAGAAAAGAGGGCCCGAGCCGTCTCACCTGAAGGCACTGTT  2040
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Db   1981  CAGAACGTTCCGCAGAGAAAAGAGGGCCCGAGCCGTCTCACCTGAAGGGTCACTGTT  2040
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Nucleotide sequence alignment (Qy / Db) spanning positions 2041–4015.

NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-295-224

Query Match   100.0%;   Score 4015;   DB 14;   Length 4015;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 4015;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GCAGGCTGCGGTCCTGCGCGCTGCCGAGCCGTGCGCAGCCCTGCCCCGCACCCCGCGATGCC  60

Qy    61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120

Qy   121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTCCAGCGCGG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTCCAGCGCGG 180

Qy   181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC 240

Qy   241 ACGGCCGGTGTCTGTGCCCCGCCCTCTTCCGCCCAGGTGTCCTGCCTGAAGGAGCTGGTGGC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACGGCCGGTGTCTGTGCCCCGCCCTCTTCCGCCCAGGTGTCCTGCCTGAAGGAGCTGGTGGC 300
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Qy   301 CCGAGTCGTGCAGAGGCGTGTGCGAGCGGCGGCGGGCGCGGCGAAGAACGTGCTGGCCTTCGC 360
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Db   301 CCGAGTCGTGCAGAGGCGTGTGCGAGCGGCGGCGGGCGCGGCGAAGAACGTGCTGGCCTTCGC 360

Qy   361 GCTGCTGGACGGGGCCCGGGGCGGGGCCCCCGAGCCTTCACCACCAGCGTGCCGCAGCTA 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCTGCTGGACGGGGCCCGGGGCGGGGCCCCCGAGCCTTCACCACCAGCGTGCCGCAGCTA 420

Qy   421 CCTGCCCAACACGGTGACCGACCACTGCGGGGGCGGGGAGCCGGGGCGTGGGGGCTGCTGCCGG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTGCCCAACACGGTGACCGACCACTGCGGGGGCGGGGAGCCGGGGCGTGGGGGCTGCTGCCGG 480

Qy   481 CCGGTGGGCGGACGACGTGCTGTGGCTTCACCTGCGCACGCTGCCGCGCTCTTTGTGCTGGT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCGGTGGGCGGACGACGTGCTGTGGCTTCACCTGCGCACGCTGCCGCGCTCTTTGTGCTGGT 540

Qy   541 GGCTCCCAGCTGCCTACCAGGTGTGCGGGCGCCCGCGTACCAGCTCGGCGCTGCCAC 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCTCCCAGCTGCCTACCAGGTGTGCGGGCGCCCGCGTACCAGCTCGGCGCTGCCAC 600
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Qy   601 TCAGGCCCGGCCCCACACGCTAGTGCACCGCGTCTGGGATGCGAACCGGC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCAGGCCCGGCCCCACACGCTAGTGCACCGCGTCTGGGATGCGAACCGGC 660

Qy   661 CTGGAACCATAGCGTCAGGAGGCCGGGGTCCCCCTGGGGCCCGGGCTGCGGAG 720
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Db   661 CTGGAACCATAGCGTCAGGAGGCCGGGGTCCCCCTGGGGCCCGGGCTGCGGAG 720

Qy   721 GAGGCGCGGGGCAGTGCCGCCGAAGTCTGCCGGTGCTCGCCCAAGAGGCCGGTGGGCGGC 780
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Db   721 GAGGCGCGGGGCAGTGCCGCCGAAGTCTGCCGGTGCTCGCCCAAGAGGCCGGTGGGCGGC 780

Qy   781 TGCCCCTGAGCCCGGACGGCCGTTGGGCAGGGTCCTGGGCCCCACCCGGGCCAGAC 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGCCCCTGAGCCCGGACGGCCGTTGGGCAGGGTCCTGGGCCCCACCCGGGCCAGAC 840

Qy   841 GGCGTGGACCGAGTGACCGTGGTTTCGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGCGTGGACCGAGTGACCGTGGTTTCGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC 900
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Qy   901 CACCTCTTTGGAGGGTGCGCTCTCTGCGACGCGCCACTCCACCATCCGTGGGCGCCA 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   961 GCACCACGCGGGCCCCCCATCCACATCGCGGCCACCAGTGCCTTGGGACACGCCTTGTCC 1020

Qy  1021 CCGGTGTACGCCGGAGACCAAGCACTTCCTCTACTCCTCAGGCGGGACAAGGAGGAGCAGCTGCG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 CCGGTGTACGCCGGAGACCAAGCACTTCCTCTACTCCTCAGGCGGGACAAGGAGGAGCAGCTGCG 1080

Qy  1081 GCCCTCCTTCTCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCCTCGGAGGCTCGTGGA 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 GCCCTCCTTCTCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCCTCGGAGGCTCGTGGA 1140

Qy  1141 GACCATCTTTCTGGGTTCCAGGCCCTGATGCGGACTCCCGCGGACTTGCCCGCCCT 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GACCATCTTTCTGGGTTCCAGGCCCTGATGCGGACTCCCGCGGACTTGCCCGCCCT 1200

Qy  1201 GCCCCAGGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGGCA 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GCCCCAGGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGGCA 1260

Qy  1261 GTGCCCTACGGGGTGCTCCTCAAGAACGACTGCCTGCGAGCTGGGACGGC 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GTGCCCTACGGGGTGCTCCTCAAGAACGACTGCCTGCGAGCTGGGACGGC 1320

Qy  1321 AGCCGGTGTCTGTGCCCGGGAGAAGCGTCCTGCCTTGAAGGAGAGAGGA 1380
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Db  1321 AGCCGGTGTCTGTGCCCGGGAGAAGCGTCCTGCCTTGAAGGAGAGAGGA 1380
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Qy  1381  CACAGACCCCGTGCCTGGTCAGCTGCTCCGGCCAGCACAGCAGCCCTGGCAGGTGTA  1440        Qy  2461  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGGCGTGCGCATCAGGGG  2520
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Db  1381  CACAGACCCCGTGCCTGGTCAGCTGCTCCGGCCAGCACAGCAGCCCTGGCAGGTGTA  1440        Db  2461  CAGTCCTCACGTGCGCTTCCTACGCTTCATGTGCCACCACGGCGTGCGCATCAGGGG  2520

Qy  1441  CGGCTTCGTGCGGGCCTGCCTGCGCCGGCCTGGTGCCCTGGGGCTTCGGGGCTCCAGGCA  1500        Qy  2521  CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGGCTTCCATCGTGCCGCTGCTCCTG  2580
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Db  1441  CGGCTTCGTGCGGGGCCTGCCTGCGCCGGCCTGGTGCCCTGGGGCTTCGGGGCTCCAGGCA  1500        Db  2521  CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGGCTTCCATCGTGCCGCTGCTCTG  2580

Qy  1501  CAACGAACGCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA  1560        Qy  2581  CAGCCTGTGCTACGGCGACATGGAGAACAAGTCGTGTTTGCGGGATTCGGCGGGACGGGCT  2640
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Db  1501  CAACGAACGCCGCTTCCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA  1560        Db  2581  CAGCCTGTGCTACGGCGACATGGAGAACAAGTCGTGTTTGCGGGATTCGGCGGGACGGGCT  2640

Qy  1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGGCGTGACAGGCGTGCCGCTGGCTGCGCAG  1620        Qy  2641  GCTCCTGCGTTGGTGGTGGATGATTCTTGTTGGTGACACCTCACCTCACCACGCGGCAAAAC  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGGCGTGACAGGCGTGCCGCTGGCTGCGCAG  1620        Db  2641  GCTCCTGCGTTGGTGGTGGATGATTCTTGTTGGTGACACCTCACCTCACCACGCGGCAAAAC  2700

Qy  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCCAGCACCGTGCGTGCTGCGGAGATCCTGC  1680        Qy  2701  CTTCCTCAGGACCCTGGTCCCGAGGTGTCCCTGAGTGGCTGCGGTGGTGAACTTGCGGAA  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCCAGCACCGTGCGTGCTGCGGAGATCCTGC  1680        Db  2701  CTTCCTCAGGACCCTGGTCCCGAGGTGTCCCTGAGTGGCTGCGGTGGTGAACTTGCGGAA  2760

Qy  1681  CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGTCTCAGTCTTTCTTTTA  1740        Qy  2761  GACAGTGGTGAACTTCCCTGTAGAGACAGAGGCCCTGGCGTGGTGGCACGGCTTTGTTCAGAT  2820
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Db  1681  CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGTCTCAGTCTTTCTTTTA  1740        Db  2761  GACAGTGGTGAACTTCCCTGTAGAGACAGAGGCCCTGGCGTGGTGGCACGGCTTTGTTCAGAT  2820

Qy  1741  TGTCACGGAGACCACAGTTTCAAAAGAACAGAGCTCTTTTTCTACCGGAAGAGTGTCTGGAG  1800        Qy  2821  GCCGGCCCACGGCCTATTCCCCTGTGCGCCTGCTGCTGGATACCCGGACCCTGGAGGT  2880
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Db  1741  TGTCACGGAGACCACAGTTTCAAAAGAACAGAGCTCTTTTTCTACCGGAAGAGTGTCTGGAG  1800        Db  2821  GCCGGCCCACGGCCTATTCCCCTGTGCGCCTGCTGCTGGATACCCGGACCCTGGAGGT  2880

Qy  1801  CAAGTTGCAAAGCATTGAAATCAGAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC  1860        Qy  2881  GCAGAGGACTACTCCAGTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG  2940
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Db  1861  GGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCGCCGCCCGGCCTCCGACCTCCG  1920        Db  2941  CGGCTTCAAGGCTGGGAGGAACAATCGTCGCGGAACTCTTTGGGGTCTTCGGCGGTGAAGTG  3000

Qy  1921  CTTCATCCCAAGCCTGACGGCGTGCGGCCGATTGTGAACATGACTACGTCGTCGGGAGC  1980        Qy  3001  TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA  3060
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Db  1921  CTTCATCCCAAGCCTGACGGCGTGCGGCCGATTGTGAACATGACTACGTCGTCGGGAGC  1980        Db  3001  TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA  3060

Qy  1981  CAGAACGGTTCCGCAGAGAAAGAGGGGCGGCCGAGCGTCTCACCTGAGGGTGAAGGCACTGTT  2040        Qy  3061  CAAGATCCTCTGCTGCAGGCGTACAGGTTCACGCCATGTGTGTCGCAGTCTCCCATTCA  3120
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Db  1981  CAGAACGGTTCCGCAGAGAAAGAGGGGCGGCCGAGCGTCTCACCTGAGGGTGAAGGCACTGTT  2040        Db  3061  CAAGATCCTCTGCTGCAGGCGTACAGGTTCACGCCATGTGTGTCGCAGTCTCCCATTCA  3120

Qy  2041  CAGCCTGCTCAACTACGACGGGAGGCCTCGGCCACCTTCGTGTCTGCGTGTGCCGGACCC  2100        Qy  3121  TCAGCAAGTTGGAAGAACCCCACATTTTCCTGCGGCTCATCTCTGACACGGCTCCCT  3180
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Db  2041  CAGCCTGCTCAACTACGACGGGAGGCCTCGGCCACCTTCGTGTCTGCGTGTGCCGGACCC  2100        Db  3121  TCAGCAAGTTGGAAGAACCCCACATTTTCCTGCGGCTCATCTCTGACACGGCTCCCT  3180

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Db  2101  CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGTCTGCGTGTGCCGGACACCATCCCCCA  2160        Db  3181  CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGCTCGGCTGTGCCACCAAGCATTCCTGCTCAAGCT  3240

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Db  2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGACGGGCGCGTACGACACCATCCCCCA  2220        Db  3241  CGGCCCTCGTGCCCCTCCGAGGCCGTGCTGCCACCAAGCATTCCTGCTCAAGCT  3300

Qy  2221  GGACAGGCTGTGTCCGAGGTCATCGAGTCGTCCAGCATCATGGGCAGTCGGCGTGCG  2280        Qy  3301  GACTCGGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACGCAGACGCA  3360
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Db  2221  GGACAGGCTGTGTCCGAGGTCATCGAGTCGTCCAGCATCATGGGCAGTCGGCGTGCG  2280        Db  3301  GACTCGGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACGCAGACGCA  3360

Qy  2281  TCGGTATGCCGTGGTGTCCAGAAGGCCACTGCGGCTTCCGCAGGGCCTTCAAGAGCCA  2340        Qy  3361  GCTGAGTCGGAAGCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCCACCCGGC  3420
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Qy  2341  CGTCTCTACCTTGACAGACCTCCAGCATGCGACAGTTCGTGGCTCACCTGCAGGA  2400        Qy  3421  ACTGCCCTCAGACTTCAAGACTCATCCTGACTGATGGCCACCCGCCCACCCGGA  3480
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Db  2341  CGTCTCTACCTTGACAGACCTCCAGCATGCGACAGTTCGTGGCTCACCTGCAGGA  2400        Db  3421  ACTGCCCTCAGACTTCAAGACTCATCCTGACTGATGGCCACCCGCCCACCCGGA  3480

Qy  2401  GACCAGCCCGCTGAGGGGATGCCGTCGTCACGCAGCAGACCCTGTCACGCTCCCCTCAAATGAGGCCAG  2460        Qy  3481  GAGCAGACACCAGCAGCCCTGTCACGCTCCCCTCAAATGAGGCCGCC  3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GACCAGCCCGCTGAGGGGATGCCGTCGTCACGCAGCAGACCCTGTCACGCTCCCCTCAAATGAGGCCAG  2460        Db  3481  GAGCAGACACCAGCAGCCCTGTCACGCTCCCCTCAAATGAGGCCGCC  3540

                                                                                        Qy  3541  CACACCCAGGCCGCCACCCGTCGGGAGTCTGAGTGAGTGTTTGGCCGGAGGCCTG  3600
                                                                                                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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REFERENCE/DOCKET NUMBER: 015389-00293OUS

TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 224:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 4015 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 56..3454
    OTHER INFORMATION: /product= "hTRT"
    /note= "human telomerase reverse
    transcriptase (hTRT) catalytic protein
    component"
  SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-611-224

Query Match 100.0%; Score 4015; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCAGGCGTCCGTCCGTGCGCACGTGGGAAGCCCTGGCCCCGCCAGCCACCCCCGCGATGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAGGCGTCCGTCCGTGCGCACGTGGGAAGCCCTGGCCCCGCCAGCCACCCCCGCGATGCC 60

Qy     61 GCGCGCTCCCCGCCGCCGAGCCGTGCGCTCCCTGCGCTGCGCCAGCCACTACCGCGAGGTGCT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGCGCTCCCCGCCGCCGAGCCGTGCGCTCCCTGCGCTGCGCCAGCCACTACCGCGAGGTGCT 120

Qy    121 GCGCGTGCCAGCTTCGTGCGCGGCCCTGGGGCGCCCAGGGCTGCGCGGCTGGTGCAGCGCGG 180
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Db    121 GCGCGTGCCAGCTTCGTGCGCGGCCCTGGGGCGCCCAGGGCTGCGCGGCTGGTGCAGCGCGG 180

Qy    181 GGACCCGGCGGCTTCCGCGCTGCCCAGTGCCTGCTGTGCGTGCGCCCCGGGGACGGC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGACCCGGCGGCTTTCCGCGCTGCCCAGTGCCTGCTGTGCGTGCGCCCCGGGGACGGC 240

Qy    241 ACGGCCGCGCCCCGCCCCCGCCCCTCCTTCCGCGCGCCTTCCGCGCGCCTCCCAGGTGTGGTGGC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACGGCCGCGCCCCGCCCCCGCCCCTCCTTCCGCGCGCCTTCCGCGCGCCTCCCAGGTGTGGTGGC 300

Qy    301 CCGAGTCGTGCGAGAGGCTGTGCGAGCCGCGCGAAGAAACGTGCTGGCCTTCGGCCTTCGC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGAGTCGTGCGAGAGGCTGTGCGAGCCGCGCGAAGAAACGTGCTGGCCTTCGGCCTTCGC 360

Qy    361 GCTGCTGGACGGGCCCGCGGGGGCCCCCCCGAGGGCCTTCACCCACCGCGTGCGCAGCTA 420
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Db    361 GCTGCTGGACGGGCCCGCGGGGGCCCCCCCGAGGGCCTTCACCCACCGCGTGCGCAGCTA 420

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Qy    661 CTGGAACCATAGCGTCAGGAGGCCCGGGTCCCCGGCCTTCGGCCCTGGCCAGCCCCGGTGCGAG 720
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Db    661 CTGGAACCATAGCGTCAGGAGGCCCGGGTCCCCGGCCTTCGGCCCTGGCCAGCCCCGGTGCGAG 720
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Db   3541 CACACCCAGGCCCCGACCCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGCGCCGAGGCCTG 3600
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Qy   3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCCGAGTGTCCAGCCAAGGGCT 3660
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Qy   3661 GAGTGTCCAGCACACTGCCGTCTTCACTTCCCCACAGGCTGGCCGCTCGGCTCCACCCCA 3720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCCGCTTCCCACTCCCCACATAGGAATAGTCCATCC 3780
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Db   3721 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCCGCTTCCCACTCCCCACATAGGAATAGTCCATCC 3780

Qy   3781 CCAGATTCGCCATTGTTCACCCCTGCGCCTCCTTGCCTTCCACCCCACCATCC 3840
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Db   3841 AGGTGGAGACCCTGAGAAGGACCCTGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTG 3900

Qy   3901 CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960

Qy   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTGAAAAAA 4015
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Db   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTGAAAAAA 4015
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RESULT 8
US-10-054-611-224
; Sequence 224, Application US/10054611
; Publication No. US2003005987A1
GENERAL INFORMATION:
  APPLICANT: Cech, Thomas R.
    Lingner, Joachim
    Nakamura, Toru
    Chapman, Karen B.
    Morin, Gregg B.
    Harley, Calvin
    Andrews, William H.
  TITLE OF INVENTION: NO. US2003005987A1el Telomerase
  NUMBER OF SEQUENCES: 225
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, 8th Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: United States of America
    ZIP: 94111
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/054,611
    FILING DATE: 18-Jan-2002
    CLASSIFICATION: 536
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/854,050
    FILING DATE: <Unknown>
    APPLICATION NUMBER: US 08/846,017
    FILING DATE: 25-APR-1997
    APPLICATION NUMBER: US 08/844,419
    FILING DATE: 18-APR-1997
    APPLICATION NUMBER: US 08/724,643
    FILING DATE: 01-OCT-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Apple, Randolph T.
    REGISTRATION NUMBER: 36,429

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Qy  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAGAGGTGCAGCTGCGGGAGCTGTC  1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAGAGGTGCAGCTGCGGGAGCTGTC  1860

Qy  1861  GGAAGCAGAGGTCAGCGCAGCATCGGCAGCATCGGGAAGCCAGGACCCGCCGCTTGCTGCACGTGCGGGAGACTCCG  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  GGAAGCAGAGGTCAGCGCAGCATCGGCAGCATCGGGAAGCCAGGACCCGCCGCTTGCTGCACGTGCGGGAGACTCCG  1920

Qy  1921  CTTCATCCCCAAGCCTGACGGGCGCTGCGGGCTGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CTTCATCCCCAAGCCTGACGGGCGCTGCGGGCTGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980

Qy  1981  CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT  2040

Qy  2041  CAGCGTGCTCAACTACGAGCGGGCGGGCGGCCTCCTGGGCGCCTCTGGGGCGCTGTGTGGGG  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CAGCGTGCTCAACTACGAGCGGGCGGGCGGCCTCCTGGGCGCCTCTGGGCGTGTGTGGGG  2100

Qy  2101  CCTGACGATATCCACAGGGCCTGCTGCGTGTGCGTCGTGCGCGTACGACACACCATCCCCA  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTGACGATATCCACAGGGCCTGCTGCGTGTGCGTCGTGCGCGTACGACACACCATCCCCA  2160

Qy  2161  GCGCCTGAGCTGTACTTTGTCAAGTGGATGGAATGGACGGGGCGCGTACGACAACCCCCA  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCGCCTGAGCTGTACTTTGTCAAGTGGATGGAATGGACGGGGCGCGTACGACAACCCCCA  2220

Qy  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGACACGTACTGCGTGCG  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGACACGTACTGCGTGCG  2280

Qy  2281  TCGGTATGCCGTGGTCGTGGACCTCCATCGAGCCAGAGAGCTCCTCCCTGAATGAGGCCAG  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCGGTATGCCGTGGTCGTGGACCTCCATCGAGCCAGAGAGCTCCTCCCTGAATGAGGCCAG  2340

Qy  2341  CGTCTCTACCTTGACAGACCTCCAGCGCTGCAGTTCGTGCTCCACCTGCAGGA  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGTCTCTACCTTGACAGACCTCCAGCGCTGCAGTTCGTGCTCCACCTGCAGGA  2400

Qy  2401  GACCAGCGCCGCTGAGGGATGCCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GACCAGCGCCGCTGAGGGATGCCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG  2460

Qy  2461  CAGTGGCCTTCTTCGACGCTTCATGTGCCACCAGCCGTGCCGTCATCGGGG  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CAGTGGCCTTCTTCGACGCTTCATGTGCCACCAGCCGTGCCGTCATCGGGG  2520

Qy  2521  CAAGTCCTACGTCCAGTCCAGGGATCCCGCAGGGTCTCCATCCTCTCCACGCTGCTCTG  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CAAGTCCTACGTCCAGTCCAGGGATCCCGCAGGGTCTCCATCCTCTCCACGCTGCTCTG  2580

Qy  2581  CAGGCCTGTGCTACGGCCACTGGGATTCGGCGGGGATTCGGCGGGGACGGGGCT  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CAGGCCTGTGCTACGGCCACTGGGATTCGGCGGGGATTCGGCGGGGACGGGGCT  2640

Qy  2641  GCTCCTGCGTTGGTGGATGATTCTTGTTGGTGGACACCTCACCTCACCGCGGAAAAC  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCTCCTGCGTTGGTGGATGATTCTTGTTGGTGGACACCTCACCTCACCGCGGAAAAC  2700

Qy  2701  CTTCCTCAGGACCCTGGTCCCGAGGTGTCCCCAGGTGGTATGGCTGCGGTGGAA  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CTTCCTCAGGACCCTGGTCCCGAGGTGTCCCCAGGTGGTATGGCTGCGGTGGAA  2760

Qy  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGCACGGCTCTTTGTTCAGAT  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGCACGGCTCTTTGTTCAGAT  2820

Qy  2821  GCCGGCCCACGGCCTATTCCCCGGCTATGCCCGGACTCTCACCTTCAACCG  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  GCCGGCCCACGGCCTATTCCCCGGCTATGCCCGGACTCTCACCTTCAACCG  2880

Qy  2881  GCAGAGCGACTACTCCAGCTATGCCGGACTCTCACCTTCAACCG  2940
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Qy   721  GAGGCGCGGGGGGCAGTGCCGAGTCTGCCGTTGCCCGAAGAGGGCCCAGGCGGTGGCGC  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  GAGGCGCGGGGGGCAGTGCCGAGTCTGCCGTTGCCCGAAGAGGGCCCAGGCGGTGGCGC  780

Qy   781  TGCCCCTGAGCCGGAGCCGGACGCCCGTTGGGCAGGGGTCTGGGCGTCCAGGGCCAGGAC  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TGCCCCTGAGCCGGAGCCGGACGCCCGTTGGGCAGGGGTCTGGGCGTCCAGGGCCAGGAC  840

Qy   841  GCGTGGACCGAGTGACCGTGGTTTCTGTCGGTCACCTGCCAGACCCGCCGAAGAAGC  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GCGTGGACCGAGTGACCGTGGTTTCTGTCGGTCACCTGCCAGACCCGCCGAAGAAGC  900

Qy   901  CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCATCCGTGGGCCGCCA  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCATCCGTGGGCCGCCA  960

Qy   961  GCACCACGCGGGGCCCCATCCACCAGCTCCCTGGGACACGGCCTTGTCC  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  GCACCACGCGGGGCCCCATCCACCAGCTCCCTGGGACACGGCCTTGTCC  1020

Qy  1021  CCCGGTGTACGCCGAGACCAAGACACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  CCCGGTGTACGCCGAGACCAAGACACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1080

Qy  1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCCTCGGAGGCTCGTGA  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCCTCGGAGGCTCGTGA  1140

Qy  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCCGCCT  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCCGCCT  1200

Qy  1201  GCCCCAGCGCTACTGGCAAATGCGGCCCCGTGTTCTGGAGCTGCGCGCTGCGGGAACCACGCGCCA  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  GCCCCAGCGCTACTGGCAAATGCGGCCCCGTGTTCTGGAGCTGCGCGCTGCGGGAACCACGCGCCA  1260

Qy  1261  GTGCCCCTACGGGGTGCTGCTCCTCAAGACGCACTGCCGAGCCTGCGGCTGCGGGTCACCCAGC  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  GTGCCCCTACGGGGTGCTGCTCCTCAAGACGCACTGCCGAGCCTGCGGCTGCGGGTCACCCAGC  1320

Qy  1321  AGCCGGTGTCTGTGCCCGGGAGAGCCCAGGGCGTCTGTGGCGGCGCCCCCAGGAGGAGGA  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  AGCCGGTGTCTGTGCCCGGGAGAGCCCAGGGCGTCTGTGGCGGCGCCCCCAGGAGGAGGA  1380

Qy  1381  CACAGACCCCCGCCCTGGTCAGCGTGTGTCCGCCAGCACAGCAGCCCTGCGCAGTGTA  1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CACAGACCCCCGCCCTGGTCAGCGTGTGTCCGCCAGCACAGCAGCCCTGCGCAGTGTA  1440

Qy  1441  CGGCTTCCTGCGGGCGCCCTGCCTGGTCGCCGGCTGGTGCCCCCCAGGCCTCCAGGCA  1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  CGGCTTCCTGCGGGCGCCCTGCCTGGTCGCCGGCTGGTGCCCCCCAGGCCTCCAGGCA  1500

Qy  1501  CAACGAACGCGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  CAACGAACGCGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560

Qy  1561  GCTCTCCGCCTGCGTTTGGTGGATGATTCTTGTTGGTGGACACCTCACCTCACCGCGGAAAAC  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  GCTCTCCGCCTGCGTTTGGTGGATGATTCTTGTTGGTGGACACCTCACCTCACCGCGGAAAAC  1620

Qy  1621  GAGCCCAGGGGTGGCGTGTGTCCCGGGCCGCAGAGCTGCTGTGAGGAGGATCCTGGC  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  GAGCCCAGGGGTGGCGTGTGTCCCGGGCCGCAGAGCTGCTGTGAGGAGGATCCTGGC  1680

Qy  1681  CAAGTTCCTGCACTGGCTGTGTACGTCGTCGCAGCTGTCTTTTTCTTTTTTA  1740
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Db  1681  CAAGTTCCTGCACTGGCTGTGTACGTCGTCGCAGCTGTCTTTTTCTTTTTTA  1740

Qy  1741  TGTCACGGAGACCACGTTTCAAAGAGAACAGGCTCTTTTTCTTTTTTTACCGGAAGAGTGTCTGGAG  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  TGTCACGGAGACCACGTTTCAAAGAGAACAGGCTCTTTTTCTTTTTTTACCGGAAGAGTGTCTGGAG  1800

Qy  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAGAGGTGCAGCTGCGGGAGCTGTC  1860
```

RESULT 9
US-10-105-963-1
; Sequence 1, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
;   APPLICANT: Geron Corporation
;   APPLICANT: Denning, Chris
;   APPLICANT: Clark, A. John
;   APPLICANT: Schiff, J. Michael
;   TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
;   TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection Syst
;   TITLE OF INVENTION: Recombination
;   FILE REFERENCE: 731/002
;   CURRENT APPLICATION NUMBER: US/10/105,963
;   CURRENT FILING DATE: 2002-03-21
;   PRIOR APPLICATION NUMBER: US 60/277,811
;   PRIOR FILING DATE: 2001-03-21
;   NUMBER OF SEQ ID NOS: 40
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 4015
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (56)..(3454)
;   OTHER INFORMATION:
US-10-105-963-1

Query Match   100.0%; Score 4015; DB 14; Length 4015;
Best Local Similarity 100.0%;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCGCCACCCCGCCGGATGCC 60
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Db   1 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCGCCACCCCGCCGGATGCC 60

Qy   61 GGCGCGCTCCCCGCCGCCGCCGAGCCGTGCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
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Db   61 GGCGCGCTCCCCGCCGCCGCCGAGCCGTGCTGCTGCGCAGCCACTACCGCGAGGTGCT 120

Qy   121 GCCGCTGGCCACGTTCGTGCGGCGGCCCCTGGGGTCGGTGGCCGGCTGGTCAGGCGCG 180
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Db   121 GCCGCTGGCCACGTTCGTGCGGCGGCCCCTGGGGTCGGTGGCCGGCTGGTCAGGCGCG 180

Qy   181 GGACCCGGCGGCTTCCCGCGCGCCCCGCCCGCCCCCAGTGCCGCGTGGTGCCCTGGACGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACCCGGCGGCTTCCCGCGCGCCCCGCCCGCCCCCAGTGCCGCGTGGTGCCCTGGACGC 240

Qy   241 ACGGCCCGCCCCCGCGCCCCGCGCCCCCCTCCTTCCGCGCAGGGCGGGCGGGGGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACGGCCCGCCCCCGCGCCCCGCGCCCCCCTCCTTCCGCGCAGGGCGGGCGGGGGCCTG 300

Qy   301 CCGAGTGCTGCAGAGGCCGTGCGAGGCCTTCGGCTTCGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGAGTGCTGCAGAGGCCGTGCGAGGCCTTCGGCTTCGC 360

Qy   361 GCTGCTGACGCGGACGGCCCGCCTTCACCACCAGCGTGCGCAGCTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCTGCTGACGCGGACGGCCCGCCTTCACCACCAGCGTGCGCAGCTA 420

Qy   421 CCTGCCAACACGGTGACCGACACGACGCGTGGGGGGCGTGGGGAGCGTGCTGCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTGCCAACACGGTGACCGACACGACGCGTGGGGGGCGTGGGGAGCGTGCTGCG 480

Qy   481 CCCGTGGGGACGACGTGCTGTTCACCTGCTGGTCGCGCGTCTTTGTGCTGT 540
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Db   481 CCCGTGGGGACGACGTGCTGTTCACCTGCTGGTCGCGCGTCTTTGTGCTGT 540

Qy   541 GGCTCCCAGTGCCGCTACCAGGTGTGCGCGCGCGTGTACCAGCTCGGCGCCTCGCCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2881 GCAGAGCGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
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Qy   2941 CGGCTTCAAGGCTGGGAGGAACATGGTCGCAAACTCTTTGGGGTCTTGCGCGTGAAGTG 3000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CGGCTTCAAGGCTGGGAGGAACATGGTCGCAAACTCTTTGGGGTCTTGCGCGTGAAGTG 3000

Qy   3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCCTTCCAGCACGGTGTGCACCAACATCTA 3060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TCACAGCCTGTTTCTGGATTTGCAGTGAACAGCCTTCCAGCACGGTGTGCACCAACATCTA 3060

Qy   3061 CAAGATCCTTCCTGCTGCGTACAGGTTTCACCGCATGTGTGCTGCAGCTCCCATTTCA 3120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CAAGATCCTTCCTGCTGCGTACAGGTTTCACCGCATGTGTGCTGCAGCTCCCATTTCA 3120

Qy   3121 TCAGCAAGTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 TCAGCAAGTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT 3180

Qy   3181 CTGCTACTCCATCCTGAAAGCCAGGATGTCCGCTGGGGGCCAAGGGGCGGCCGGC 3240
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Db   3181 CTGCTACTCCATCCTGAAAGCCAGGATGTCCGCTGGGGGCCAAGGGGCGGCCGGC 3240

Qy   3241 CGGCCCCTCTGCCCTCCGAGCCGTGCAGTGCGTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CGGCCCCTCTGCCCTCCGAGCCGTGCAGTGCGTGTGCCACCAAGCATTCCTGCTCAAGCT 3300

Qy   3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGCA 3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGCA 3360

Qy   3361 GCTGAGTCGGAAGCTCCCGGGACAAGCGTGACTGCCCTGGAGGCCCAGCGAGCCCAACCCGGC 3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCCAGCGAGCCCAACCCGGC 3420

Qy   3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCGCCAGCAGCCAGGCCGA 3480
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Db   3421 ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCGCCAGCAGCCAGGCCGA 3480

Qy   3481 GAGCAGACACCAGCAGCCCTGTCACGCCCGGGCTCCAGGAGGAGGGGGCGGGGC 3540
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Db   3481 GAGCAGACACCAGCAGCCCTGTCACGCCCGGGCTCCAGGAGGAGGGGGCGGGGC 3540

Qy   3541 CACACCCAGGCCCGACCGCCGCACCGTGGGAGTCTGAGGCCTGAGTGTTTGGCCGAGGCCTG 3600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CACACCCAGGCCCGACCGCCGCACCGTGGGAGTCTGAGGCCTGAGTGTTTGGCCGAGGCCTG 3600

Qy   3601 CATGTCCGGCTGAAGGCTGAGGCTGAGGCGTCCGGCTGAGGCTGAGCTGTCCAGCCAAGGGGCT 3660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CATGTCCGGCTGAAGGCTGAGGCTGAGGCGTCCGGCTGAGGCTGAGCTGTCCAGCCAAGGGGCT 3660

Qy   3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCGCGTCTGGCCTCGGCTCCACCCCA 3720
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Db   3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCGCGTCTGGCCTCGGCTCCACCCCA 3720

Qy   3721 GGGCCAGCTTTTCCTCCACCAGGAGCCGGCGTTCCACTCCCCACATAGGAATAGTCCATCC 3780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GGGCCAGCTTTTCCTCCACCAGGAGCCGGCGTTCCACTCCCCACATAGGAATAGTCCATCC 3780

Qy   3781 CCAGATTCGGCCATTGTTCACCCTGCTCCTTTGCCTTTGCCTTCCACCCACCACCATCC 3840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 CCAGATTCGGCCATTGTTCACCCTGCTCCTTTGCCTTTGCCTTCCACCCACCACCATCC 3840

Qy   3841 AGGTGGAGACACAGGCCAGGAGACCCTGGAGTTGGAGTCTGGGAATTGGAGTCATGTGTG 3900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 AGGTGGAGACACAGGCCAGGAGACCCTGGAGTTGGAGTCTGGGAATTGGAGTCATGTGTG 3900

Qy   3901 CCCTGTACACAGGCGAGGAGGACCCCTGCGATGGGGGTCCCCGTGGGGTCAAATTGGGGG 3960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CCCTGTACACAGGCGAGGAGGACCCCTGCGATGGGGGTCCCCGTGGGGTCAAATTGGGGG 3960

Qy   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAATATGAGTTTTTCAGTTTTTGAAAAAA 4015
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GAGGTGCTGTGGGAGTAAAATACTGAATATATGAATATGAGTTTTTCAGTTTTTGAAAAAA 4015

Db   541 GGCTCCAGCTGCGCTACCAGTGTGCGGGCCGCCGCTGTACCAGTCGGCGGCTGCCAC   600

Qy   601 TCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCGGAAGGCGTCTGGGATGCGGAACGGGC 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCGGAAGGCGTCTGGGATGCGGAACGGGC 660

Qy   661 CTGGAACCATAGCGTCAGGGAGGCCGGAGGCGGGGTCCCCTGGGCCTGCCAGCCCGGGTGCGGAG 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGGAACCATAGCGTCAGGGAGGCCGGAGGCGGGGTCCCCTGGGCCTGCCAGCCCGGGTGCGGAG 720

Qy   721 GAGGCGGCGGGGAGCAGTGCCAGCCGAAGTCTGCCGTTGCCGTTGCCCAAGAGGCCCAGGCGTGCCGGC 780
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Qy   1321 AGCCGGTGTCTGGCCCCGGAGAAGTCAGGGCTCTCCCTGGGCGGCCCCCGAGGAGGA 1380
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Qy   2341 CGTCTCTACCTTGACAGACCTCCAGCCGTCGTGGCTCACCTGCAGGA 2400
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Qy   2581 CAGCCTGTGCTACGGCGACATGGGACATGAAGCTGTTTGGGATTCGGCGGGACGGGGCT 2640
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RESULT 10
US-10-044-692-1
; Sequence 1, Application US/10044692
; Publication No. US20030095344A1
; GENERAL INFORMATION:
;  APPLICANT: Cech, Thomas R.
;            Lingner, Joachim
;            Nakamura, Toru
;            Chapman, Karen B.
;            Morin, Gregg B.
;            Harley, Calvin
;            Andrews, William H.
;  TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
;                      THERAPEUTIC METHODS
;  NUMBER OF SEQUENCES: 335
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, 8th Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: United States of America
;   ZIP: 94111
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/044,692
;   FILING DATE: 11-Jan-2002
;   CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/912,951
;   FILING DATE: <Unknown>
;   APPLICATION NUMBER: US 08/854,050
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph T.
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-002600US
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 4015 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 56..3454
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Sequence alignment (Qy / Db), positions 2761–4015:

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Qy  2821  GCCGGCCCACGGCCTATTCCCCTGGTGCGCTGCTGCTGATACCCGGACCCTGAGGT  2880
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Qy  3421  ACTGCCCTCAGACTTCAAGACCATCTGGACTGAGCTGATGGCCACCCGCCCAGCAGGCCGA  3480
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Db  3961  GAGGTGCTGTGGGAGTAAAATACTGAAATATGAGTTTTCAGTTTTGAAAAAAA  4015
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;
;
;
US-10-044-692-1
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OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match   100.0%; Score 4015; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1  GCAGCGCTGCGTCCTGCTGCGCACGTGGAAGCCCTGGCCCCGCCACCCCGCGATGCC   60
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Qy   61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGCGAGGTGCT  120
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Db   61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGCGAGGTGCT  120

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Qy  181  GGACCCGGGGCTTTCCGCGCGCTGGTGCCCCAGTGCCGCCTGGTGTGCCCTGGGACGC  240
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Db  541  GGCTCCCAGCTGCGCCTACCAGGTGCGGGGCCGGCCGCCGCCAAGAGGCCGCTGGCAC  600

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Qy  841  GCGTGGACCGAGTGACCGGTTTCTGTGTGGTCACCTGCCGCCAGACCCGCCAAGAAGC  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  GCGTGGACCGAGTGACCGGTTTCTGTGTGGTCACCTGCCGCCAGACCCGCCAAGAAGC  900

Qy  901  CACCTCTTTGGAGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGCCGCCA  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  901  CACCTCTTTGGAGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGCCGCCA  960

Qy  961  GCACCACGCGGCGGCCGCCCATCCACATCCACGCGGCGGCCGCCCACGTCCCGTTGTCC 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  GCACCACGCGGCGGCCGCCCATCCACATCCACGCGGCGGCCGCCCACGTCCCGTTGTCC 1020

Qy 1021  CCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCCGACAAGGAGCAGCTGCG 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021  CCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCCGACAAGGAGCAGCTGCG 1080

Qy 1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGTGGCTCGTGGA 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGTGGCTCGTGGA 1140

Qy 1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCCAGGGACTCCCCGCGGTTGCCCCGCCT 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCCAGGGACTCCCCGCGGTTGCCCCGCCT 1200

Qy 1201  GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTGGGTGGAACCACGCGCCA 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201  GCCCCAGCGCTACTGGCAAATGCGGCCCCCTGTTTCTGGAGCTGCTGGGTGGAACCACGCGCA 1260

Qy 1261  GTGCCCTACGGGCGTGCTCCTCAAGACGCACTGCCGTGCGAGCTGCGGTGCGCCCCGAGCTGGTGCGC 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261  GTGCCCTACGGGCGTGCTCCTCAAGACGCACTGCCGTGCGAGCTGCGGTGCGCCCCAGC 1320

Qy 1321  AGCCGGTGTCTGTGCGCCCGGAGAAGCGCTCGTGTGGCTGCGGCCCGGAGGAGGA 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321  AGCCGGTGTCTGTGCGCCCGGAGAAGCGCTCGTGTGGCTGCGGCCCGGAGGAGGA 1380

Qy 1381  CACAGACCCCGTGCGCCTGCTGCAGCTGCGCCGCGCCAGCAGCCTGGCAGGTGTA 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381  CACAGACCCCGTGCGCCTGCTGCAGCTGCGCCGCGCCAGCAGCCTGGCAGGTGTA 1440

Qy 1441  CGGCTTCGTGTGCGGGCCGCTGCCTGCCCGGCCTGGGCGGGCTCCCAGGCA 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441  CGGCTTCGTGTGCGGGCCGCTGCCTGCCCGGCCTGGGCGGGCTCCCAGGCA 1500

Qy 1501  CAACGAACGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501  CAACGAACGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

Qy 1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAG 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAG 1620

Qy 1621  GAGCCCAGGGGTTGGCACTGGCGTGTTCCGGGCCCGCAGAGCACCGTCTGCGGGAGATCTGGC 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1621  GAGCCCAGGGGTTGGCACTGGCGTGTTCCGGGCCCGCAGAGCACCGTCTGCGGGAGATCTGGC 1680

Qy 1681  CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTGCTCAGGTGCTCTTTTTA 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681  CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTGCTCAGGTGCTCTTTTTA 1740

Qy 1741  TGTCACGGAGACCACGTTCAAAAGAAACAGGCTCTTTTCTCACCGGAAGAGTGTCGGGAG 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741  TGTCACGGAGACCACGTTCAAAAGAAACAGGCTCTTTTTCTCACCGGAAGAGTGTCGGGAG 1800

Qy 1801  CAAGTTGCAAAGCATTGGAATCAGACGACACTTGAAGAGGTGCAGCTCGCGGGAGCTGTC 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801  CAAGTTGCAAAGCATTGGAATCAGACGACACTTGAAGAGGTGCAGCTCGCGGGAGCTGTC 1860

Qy 1861  GGAAGCAGAGGTCAGGCAGCGCATCGGAAGCCCGCCGCCCGCCCGTCCAGACTCCG 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1861  GGAAGCAGAGGTCAGGCAGCGCATCGGAAGCCCGCCGCCCGCCCGTCCAGACTCCG 1920

Qy 1921  CTTCATCCCCAAGCCTGACGGCGCTGCGGCCGATTGTGAACATGACTCGTGGGAGC 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921  CTTCATCCCCAAGCCTGACGGCGCTGCGGCCGATTGTGAACATGACTCGTGGGAGC 1980

Qy 1981  CAGAACGTTCCGCAGAGAAAAGAGGGCGCGCGTCCTCACCTCGAGGGTGAAGGCACTGTT 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1981  CAGAACGTTCCGCAGAGAAAAGAGGGCGCGCGTCCTCACCTCGAGGGTGAAGGCACTGTT 2040
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Qy  2041  CAGCGTGCTCAACTACGAGGGCGGCGGCGCCTCCTGGGCGCCTCCTGTGCTGGG    2100
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Db  2041  CAGCGTGCTCAACTACGAGGGCGGCGGCGCCTCCTGGGCGCCTCCTGTGCTGGG    2100

Qy  2101  CCTGGACGATATCCACAGGGCCTGGCCGCACCTTCGTGCGCGTGGGGCCCAGGACCC    2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCTGGACGATATCCACAGGGCCTGGCCGCACCTTCGTGCGCGTGGGGCCCAGGACCC    2160

Qy  2161  GCCGCCTGAGCTGTACTTTGTCACGTGGATGGATGTGACGGGCGTACGACACCATCCCCA    2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCCGCCTGAGCTGTACTTTGTCACGTGGATGGATGTGACGGGCGTACGACACCATCCCCA    2220

Qy  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCG    2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCG    2280

Qy  2281  TCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA    2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  TCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA    2340

Qy  2341  CGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGTTCGTGCTCACCTGCAGGA    2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGTTCGTGCTCACCTGCAGGA    2400

Qy  2401  GACCACCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG    2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GACCACCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG    2460

Qy  2461  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG    2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG    2520

Qy  2521  CAAGTCCTACGTCCAGTGCCCAGGGATCCCGCCAGGGCTCCATCCTCTCCACGCTGCTCTG    2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CAAGTCCTACGTCCAGTGCCCAGGGATCCCGCCAGGGCTCCATCCTCTCCACGCTGCTCTG    2580

Qy  2581  CAGCCTGTGTACGGCGACATGGAGAACAAGCGTGTTGCGGGGATTCGGCGGGACGGGGCT    2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CAGCCTGTGTACGGCGACATGGAGAACAAGCGTGTTGCGGGGATTCGGCGGGACGGGGCT    2640

Qy  2641  GCTCCTGCGGTTGGTGGATGATTTCTTTGTGTTGGTGACACCTCACCTCAGGGCCGGAAAAC    2700
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Db  2641  GCTCCTGCGGTTGGTGGATGATTTCTTTGTGTTGGTGACACCTCACCTCAGGGCCGGAAAAC    2700

Qy  2701  CTTCCTTCAGGACCCTTGGTCCGAGGTGCGCTGAGTATGGCGTGCGTGGTGAACTTGCCGGAA    2760
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Db  2701  CTTCCTTCAGGACCCTTGGTCCGAGGTGCGCTGAGTATGGCGTGCGTGGTGAACTTGCCGGAA    2760

Qy  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTGTTCAGAT    2820
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Db  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTGTTCAGAT    2820

Qy  2821  GCCGGCCACGGCCTATTCCCCGTGGTTGCGCGCCTGCTGGCCCTGGATACCCGGAGGT    2880
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Db  2821  GCCGGCCACGGCCTATTCCCCGTGGTTGCGCGCCTGCTGGCCCTGGATACCCGGAGGT    2880

Qy  2881  GCAGAGCGACTACTCCAGCTATGCCCGGCACTTCCATCAGAGCCAGTCTCACCTTCAACCG    2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  GCAGAGCGACTACTCCAGCTATGCCCGGCACTTCCATCAGAGCCAGTCTCACCTTCAACCG    2940

Qy  2941  CGGCTTCAAGGCTGGGAGGAACATGCTCGCCAAAACTCTTTGGGGTCTTGGGGTCTTGCGGCTGAAGTG    3000
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Db  2941  CGGCTTCAAGGCTGGGAGGAACATGCTCGCCAAAACTCTTTGGGGTCTTGGGGTCTTGCGGCTGAAGTG    3000

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Db  3001  TCACAGCCTGTTTCTGGATTGCAGGTGAACAGCCTTCCAGCGTGCACCAACATCTA    3060

Qy  3061  CAAGATCCTCCGTCGCTGCAGGCGGTACAGGTTTTCACCGCATGTGTGCTGCAGTCTCCCATTTCA    3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  CAAGATCCTCCGTCGCTGCAGGCGGTACAGGTTTTCACCGCATGTGTGCTGCAGTCTCCCATTTCA    3120
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Qy  3121  TCAGCAAGTTTGAAGAACCCCACATTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT    3180
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Db  3121  TCAGCAAGTTTGAAGAACCCCACATTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT    3180

Qy  3181  CTGCTACTCCATCTGAAAGCCAGGGATGTCGCTGGGGCGCTGGGGGCCAAGGGCGCCGGC    3240
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Db  3181  CTGCTACTCCATCTGAAAGCCAGGGATGTCGCTGGGGCGCTGGGGGCCAAGGGCGCCGGC    3240

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Db  3241  CGGCCCTGCGCCTCCGAGGCCGTGCAGTGGCGTGCGTGCCACCAAGCATTCTGCTCAAGCT    3300

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Db  3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA    3360

Qy  3361  GCTGAGTCGGAAGCTCCCGGGACGACGTCGACTGACTGCCCTGGAGGCCGCAGCCAACCCCGGC    3420
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Db  3361  GCTGAGTCGGAAGCTCCCGGGACGACGTCGACTGACTGCCCTGGAGGCCGCAGCCAACCCCGGC    3420

Qy  3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGAGGCCACCCGCCCACAGCCAGGCCGA    3480
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Db  3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGAGGCCACCCGCCCACAGCCAGGCCGA    3480

Qy  3481  GAGCAGAGACACCAGCAGCCCTGTCACGTGCCGGGCGCTCACGTCACGGCCTCTACGTCCCAGGAGGGGGCCGCC    3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  GAGCAGAGACACCAGCAGCCCTGTCACGTGCCGGGCGCTCACGTCACGGCCTCTACGTCCCAGGAGGGGGCCGCC    3540

Qy  3541  CACACCCAGGCCGCCCACCCCTGAGGCCTGAGTGAGTGTTGGCCAGGCCTG    3600
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Qy  3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCGTCCAGCCAAGGGCT    3660
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Db  3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCGTCCAGCCAAGGGCT    3660

Qy  3661  GAGTGTCCAGCAGCACCTGCCGTCTTCACTTCACCTGGGAATTGGAGTGACCAAAGGTGTG    3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  GAGTGTCCAGCAGCACCTGCCGTCTCTGCGTCTTCACTTCACCTGGGAATTGGAGTGACCAAAGGTGTG    3720

Qy  3721  GGGCCAGCTTTTCTCCACCAGAGCGCCCGGCTTCCCCACTCCCCCACATAGGAATAGTTCCATCC    3780
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Db  3721  GGGCCAGCTTTTCTCCACCAGAGCGCCCGGCTTCCCCACTCCCCCACATAGGAATAGTTCCATCC    3780

Qy  3781  CCAGATTCGCCATTGTTCACCCCTGCCTTCCACCCCATCC    3840
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Db  3781  CCAGATTCGCCATTGTTCACCCCTCGCCCTTCCACCCCATCC    3840

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Db  3901  CCCTGTACACAGGCCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGG    3960

Qy  3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTCAGTTTTGAAAAAA    4015
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TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335
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ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-044-539-1

Query Match   100.0%;   Score 4015; DB 14; Length 4015;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 4015;   Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GCAGCGCTGCGTCCTGCGTGCGCACGTGGGAAGCCCCTGCCACCCCGCCACCCCGCGATGCC   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCAGCGCTGCGTCCTGCGTGCGCACGTGGGAAGCCCCTGCCACCCCGCCACCCCGCGATGCC   60

Qy   61 GGGCGCTCCCCCGCCGCCAGCCGTGCGCTCCCTGCGCTGCGCCAGCCACTACCGCGAGGTGCT   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGGCGCTCCCCCGCCGCCAGCCGTGCGCTCCCTGCGCTGCGCCAGCCACTACCGCGAGGTGCT   120

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Db   121 GCCCGCTGCCACGTTCGTGCGGGCGCCCTCGGCGCCCCAGGGCGCTGGCGGTGCGCAGCGCGG   180

Qy   181 GGACCCGGCGGCTTTCCGCGCGCTGGTGCGCCAGTGCCCAGTGCTGCTCGCGGTGTGCGCCCTGGGACGC   240
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Db   181 GGACCCGGCGGCTTTCCGCGCGCTGGTGCGCCAGTGCCCAGTGCTGCTCGCGGTGTGCGCCCTGGGACGC   240

Qy   241 ACGGCCGCGCCCCGCGCGCCCCCCTCCTTCGCGCGGCGCGCGCGCCCCCGAAGGAGTGGTGGC   300
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Db   241 ACGGCCGCGCCCCGCGCGCCCCCCTCCTTCGCGCGGCGCGCGCGCCCCCGAAGGAGTGGTGGC   300

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Db   301 CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGGCGCGAAGAACGTGGCCTTCGGCTTCGC   360

Qy   361 GCTCTGGACGGGGCCCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA   420
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Db   361 GCTGCTGGACGGGGCCCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA   420

Qy   421 CCTGCCCACACGTGACCGACCACTGCGGGGGAGCGGGGGCGTGGGGGCTGCTGCGCG   480
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Db   421 CCTGCCCACACGTGACCGACCACTGCGGGGGAGCGGGGGCGTGGGGGCTGCTGCGCG   480

Qy   481 CCGCGTGGCGACGACGTGCTGGTCACCTGGCACGCTGCCGCTCTTTGCTCGT   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCGCGTGGCGACGACGTGCTGGTCACCTGGCACGCTGCCGCTCTTTGTGCTGGT   540

Qy   541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCGCCGCTGTACCAGCTCGGCGCTGCCAC   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCGCCGCTGTACCAGCTCGGCGCTGCCAC   600

Qy   601 TCAGGCCCGGCCCCGCCACACGTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCAGGCCCGGCCCCGCCACACGTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC   660

Qy   661 CTGGAACCATAGCGTCAGGGAGGCCGCGGGGTCCCCGGCCTGCCAGCCGGGGGTGCGAG   720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGGAACCATAGCGTCAGGGAGGCCGCGGGGTCCCCGGCCTGCCAGCCGGGGGTGCGAG   720

Qy   721 GAGGCGCGGGGCAGTGCCAGCCGGAGTCTGCCGTTGCCCGGCGTGGCGC   780
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GAGGCGCGGGGCAGTGCCAGCCGGAGTCTGCCGTTGCCCGGCGTGGCGC   780

Qy   781 TGCCCCTGAGCCGGCGACGCCCGTTGGCGCAGGGTCTGGGCCCACCCGGCAGGAC   840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGCCCCTGAGCCGGCGACGCCCGTTGGCGCAGGGTCTGGGCCCACCCGGCAGGAC   840

Qy   841 GCGTGGACCGAGTGACCGTGGTTTCGTGGTGTCACCTGCCAGACCCCGAAGAAGC   900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCGTGGACCGAGTGACCGTGGTTTCGTGGTGTCACCTGCCAGACCCCGAAGAAGC   900

Qy   901 CACCTCTTTGGAGGGTGCCTCTCGGCACGCGCCACTCCACCCCATCCGTGGGCCGCCA   960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CACCTCTTTGGAGGGTGCCTCTCGGCACGCGCCACTCCACCCCATCCGTGGGCCGCCA   960

Qy   961 GCACCACGCGGCCCCCCCATCCACATCCGCGCCACATCCCTGGACACGCGCCCTGTCC   1020
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Db   961 GCACCACGCGGCCCCCCCATCCACATCCGCGCCACATCCCTGGACACGCGCCCTGTCC   1020

Qy   1021 CCCGGTACGCCGAGACCAAGGACACTTCCTCTACTCCTCCAGGGGACACAAGGAGCAGCTGCG   1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCCGGTACGCCGAGACCAAGGACACTTCCTCTACTCCTCCAGGGGACACAAGGAGCAGCTGCG   1080

Qy   1081 GCCCTCCTCCTACTCAGCTCTCTGAGGCCCTGACTGGCCGTCGGCTCGTGCTCGTGTGGA   1140
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Qy   1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCCGCCCT   1200
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Db   1141 GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCCGCCCT   1200

Qy   1201 GCCCCAGCCTACTGCAAATGCGGGCCCCGTGTTTCTCGGGAGCGTCGGGCTGCGCAGCGCGGG   1260
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Db   1201 GCCCCAGCCTACTGCAAATGCGGGCCCCGTGTTTCTCGGGAGCGTCGGGCTGCGCAGCGCGGG   1260

Qy   1261 GTGCCCTACGGGGTGCTCCTCAAGACGCACTGGCACGCTGCGAGCTGCGAGCGCTCACCCCAGC   1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db  1261  GTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGTCACCCCAGC  1320

Qy  2401  GACCAGCCGCCGCTGAGGGATGCCGCTGCGTCGTCATCGAGCAGCAGAGCTCCTCCCTGAATGAGGCCAG  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GACCAGCCGCCGCTGAGGGATGCCGCTGCGTCGTCATCGAGCAGCAGAGCTCCTCCCTGAATGAGGCCAG  2460

Qy  1321  AGCCGGTGTCGTGCCCGGAGAAGCCCAGGGCTCGTGTGGCGGCCCCCGAGGAGGAGGA  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  AGCCGGTGTCGTGCCCGGAGAAGCCCAGGGCTCGTGTGGCGGCCCCCGAGGAGGAGGA  1380

Qy  2461  CAGTGGCCGCTCTTCGACGTCTTCGACGTCCATGTGCGCATCAGGGGCATCAGGGG  2520
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Db  2461  CAGTGGCCGCTCTTCGACGTCTTCGACGTCCATGTGCGCATCAGGGGCATCAGGGG  2520

Qy  1381  CACAGACCCCGTCGCTCGGTCGTCCGCACAGCAGCCCTGGGCAGGTGTA  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CACAGACCCCGTCGCTCGGTCGTCCGCACAGCAGCCCTGGGCAGGTGTA  1440

Qy  2521  CAAGTCCTACGTCCAGTGCCAGGGGATCCCAGGGGTCCATCCTCTCCACCGTGCTCTG  2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CAAGTCCTACGTCCAGTGCCAGGGGATCCCAGGGGTCCATCCTCTCCACCGTGCTCTG  2580

Qy  1441  CGGCTTCGTGCGGGCCTGCTGCGGCCGGCTGGTGCCCCCAGGGCTGTGGGCTCCAGGCA  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  CGGCTTCGTGCGGGCCTGCTGCGGCCGGCTGGTGCCCCCAGGGCTGTGGGCTCCAGGCA  1500

Qy  2581  CAGCCTGCTACGGCGACACGGCGTTTTGCGGGACGTGTGGCGGCGGACGGGCT  2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CAGCCTGCTACGGCGACACGGCGTTTTGCGGGACGTGTGGCGGCGGACGGGCT  2640

Qy  1501  CAACGAACGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560
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Db  1501  CAACGAACGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560

Qy  2641  GCTCCTGCGTTTGGTGGATGATTTCTTGTTGTGACACCTCACCTCACCGGCGAAAAC  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCTCCTGCGTTTGGTGGATGATTTCTTGTTGTGACACCTCACCTCACCCACGCGAAAAC  2700

Qy  1561  GCTCTCGTGCAGGAGGCTGACGTGAAGATGAGCGTGCGGCTTGGCTGCCGCAG  1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  GCTCTCGTGCAGGAGGCTGACGTGAAGATGAGCGTGCGGCTTGGCTGCCGCAG  1620

Qy  2701  CTTCCTCAGGACCCTGTCCCAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAA  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CTTCCTCAGGACCCTGTCCCAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAA  2760

Qy  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCCGCAGAGCCACCGTTCGTGCTGCGGGAGGATCCTGGC  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCCGCAGAGCCACCGTTCGTGCTGCGGGAGGATCCTGGC  1680

Qy  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGTGGCACGGCGTTTTGTTGTTCAGAT  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGTGGCACGGCGTTTTGTTGTTCAGAT  2820

Qy  1681  CAAGTTCCTGCACTGGCTGTATGCGTCGTGTGCGCTGCTCAGGTCTTTCTTTTA  1740
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Db  1681  CAAGTTCCTGCACTGGCTGTATGCGTCGTGTGCGCTGCTCAGGTCTTTCTTTTA  1740

Qy  2821  GCCGGCCACAGGGCCTATTCCCCTGGTGCGGCGCTCGCTGCTGGATACCGGAGGT  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  GCCGGCCACAGGGCCTATTCCCCTGGTGCGGCGCTCGCTGCTGGATACCGGAGGT  2880

Qy  1741  TGTCACGGACCACGTTTCAAAGAACAGGCTCTTTTTTCTACCGGAAGAGTGTCTGGAG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  TGTCACGGACCACGTTTCAAAAGAACAGGCTCTTTTTTCTACCGGAAGAGTGTCTGGAG  1800

Qy  2881  GCAGAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCACCTTCAACCG  2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  GCAGAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCACCTTCAACCG  2940

Qy  1801  CAAGTTGCAAAGCCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGGAGCTGTC  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  CAAGTTGCAAAGCCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGGAGCTGTC  1860

Qy  2941  CGGCTTCAAGGCTGGGAGGAACATGCTTGGGGTCTTTGGGGTCTTTGGCGGCTGAAGTG  3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  CGGCTTCAAGGCTGGGAGGAACATGCTTGGGGTCTTTGGGGTCTTTGGCGGCTGAAGTG  3000

Qy  1861  GGAAGCAGAGGTCAGGCAGCATCGGGAGACGTCGGCGGCCCGGGCGGGCCGCCCCTCGTGTGCTGCTCCG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  GGAAGCAGAGGTCAGGCAGCATCGGGAGACGTCGGCGGCCCGGGCGGGCCGCCCCTCGTGTGCTGCTCCG  1920

Qy  3001  TCACAGCGTGTTTCTGGATTTGACAGTGTGAACATGTGAACTACGTCGTGGGAGC  3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  TCACAGCGTGTTTCTGGATTTGACAGTGTGAACATGTGAACAGCTGTCACCAACATCTA  3060

Qy  1921  CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACGTCGTGCGGGAGC  1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACGTCGTGCGGGAGC  1980

Qy  3061  CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCCATTTCA  3120
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Db  3061  CAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCCATTTCA  3120

Qy  1981  CAGAACGTTCCGCAGAGAAAGAGGGCCGAGCCGTCTCACCTGAAGGTGAAGGCACTGTT  2040
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Db  1981  CAGAACGTTCCGCAGAGAAAGAGGGCCGAGCCGTCTCACCTGAAGGTGAAGGCACTGTT  2040

Qy  3121  TCAGCAAGTTTGGAAGAACCCCACACATTTCTGCTGCGGCGTCATCTCTGACACGGCTCCCT  3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  TCAGCAAGTTTGGAAGAACCCCACACATTTCTGCTGCGGCGTCATCTCTGACACGGCTCCCT  3180

Qy  2041  CAGGCGTGCTCAACTACGAGGGCCGAGCCGTCTCCCGGCCTCGTGTGCCTGGG  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CAGGCGTGCTCAACTACGAGGGCCGAGCCGTCTCCCGGCCTCGTGTGCCTGGG  2100

Qy  3181  CTGCTACTCCATCCTGAAAAGCCAAGAACGCAGGGATGTCGCTGGGGATGGGCCGCGC  3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  CTGCTACTCCATCCTGAAAAGCCAAGAACGCAGGGATGTCGCTGGGGAGGCGCGCGGC  3240

Qy  2101  CCTGGACGATATCCACAGGGCCGCGCACTTCGTGCTGCCTGCGTGTGCGGGCCAGGACCC  2160
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Db  2101  CCTGGACGATATCCACAGGGCCGCGCACTTCGTGCTGCCTGCGTGTGCGGGCCAGGACCC  2160

Qy  3241  CGGCCCTCTGCCCTCCGAGGCCGTGTCACTGGCTGTGCGCTACGAGTCTTCCTGCTCAAGCT  3300
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Qy  2161  GCCGCCTGAGCCGTACTTTGTCAAGGTGGATGTGACGGCCGGCGTACGACACCATCCCCCA  2220
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Qy  3301  GACTCGTGAGTCACCTACTCCCACTCGTCACTCAGGAGTCACTCAGGAGGCGCCGCCAGACCA  3360
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Db  3301  GACTCGTGAGTCACCTACTCCCACTCGTGCCACTCCTGGGGTCACTCAGGAGGCCCAGACGCA  3360

Qy  2221  GGACAGGCTCACGGAGGTCATCGGCCAGCATCATCAAACCCCAGAAACGTCCCAAGGGCTTGCG  2280
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Qy  3361  GCTGAGTCGGAAGCTCCGGGGACGAGCCTTCAAGAGCCCGCC  3420
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Db  3361  GCTGAGTCGGAAGCTCCGGGGACGAGCCTTCAAGAGCCGGC  3420

Qy  2281  TCGGTATGCCGTGGTCTCCGCAGGACCTTCCAGGACCTTCGCCGCAAGGCCTTCAAGAGCCCA  2340
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Qy  3421  ACTGCCCCTCAGACTTCAAGACCCCTCCTGGACTTGATGCCGGCCAGGCCGA  3480
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Qy  2341  CGTCTCTACCTTGACAGACCTTCCGACACCTGCGTCGTGGCTGACAGTTCGTTGCGTCCACCTGCAGGA  2400
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Db  2341  CGTCTCTACCTTGACAGACCTTCCGACACCTGCGTCGTTGCGTCCACCTGCAGGA  2400
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Db  3481  GAGCAGACACCAGCAGCCCTGTCACGCGGGCTCTACGTCCCAGGGAGGAGGGGCGGCC  3540

Qy  3541  CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGGTGTTGGCCGAGGGCCTG   3600
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Qy  3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCCAAGGGCT          3660
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Db  3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCCAAGGGCT          3660

Qy  3661  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGCGCTCGGCTCCACCCA    3720
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Db  3661  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGCGCTCGGCTCCACCCA    3720

Qy  3721  GGGCCAGCGTTTTCCTCACCAGGAGCCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC  3780
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Db  3721  GGGCCAGCGTTTTCCTCACCAGGAGCCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC  3780

Qy  3781  CCAGATTCGCCATTGTTCACCCCTCGCCCCTCCTTGCCTTCCACCCCACCATCC       3840
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Db  3781  CCAGATTCGCCATTGTTCACCCCTCGCCCCTCCTTGCCTTCCACCCCACCATCC       3840

Qy  3841  AGGTGGAGACCCTGAGAAGGACCCTGGGAGACCCTCTGGAATTTGGAGTGACCAAAGGTGTG  3900
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Db  3841  AGGTGGAGACCCTGAGAAGGACCCTGGGAGACCCTCTGGAATTTGGAGTGACCAAAGGTGTG  3900

Qy  3901  CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGG   3960
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Qy  3961  GAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA       4015
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RESULT 12
US-09-843-676-173
; Sequence 173, Application US/09843676
; Patent No. US2002016478GA1
GENERAL INFORMATION:
  APPLICANT: Cech, Thomas R.
    Lingner, Joachim
    Nakamura, Toru
    Chapman, Karen B.
    Morin, Gregg B.
    Harley, Calvin
    Andrews, William H.
  TITLE OF INVENTION: No. US2002016478GA1e1 Telomerase
  NUMBER OF SEQUENCES: 225
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, 8th Floor
    CITY: San Francisco
    STATE: California
    COUNTRY: United States of America
    ZIP: 94111
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/843,676
    FILING DATE: 26-Apr-2001
    CLASSIFICATION: 536
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/854,050
    FILING DATE: 09-MAY-1997
    APPLICATION NUMBER: US 08/846,017
    FILING DATE: 25-APR-1997
    APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph T.
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 4029 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  FEATURE:
    NAME/KEY:
    LOCATION: 1..4029
    OTHER INFORMATION: /note= "preliminary sequence for
      human TRT cDNA insert of
      plasmid pGRN121"
  SEQUENCE DESCRIPTION: SEQ ID NO: 173:

US-09-843-676-173

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Query Match               95.9%;     Score 3849.2;   DB 10;   Length 4029;
Best Local Similarity     98.5%;     Pred. No. 0;
Matches 3955;  Conservative  0;  Mismatches  53;  Indels  9;  Gaps  8;

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Db  1   GCAGCGCTGCGTCCTGCTCGCGCAGTGGGAAGCCCTGGCCCCGGCCACCCCGGCGATGCC   60

Qy  61  GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCGGGCCCCAGGCCGCTGGCGTGCGCTGGCGGTGTGCGGG  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  121 GCCGCTGGCCAGCGTTCGTGCGCCAGGGCTGGCGGGCGGGCGCTGGTCAGCGCGG   180
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Db  121 GCCGCTGGCCAGCGTTCGTGCGCCAGGGCTGGCGGGCGGGCGCTGGTCAGCGCGG   180

Qy  181 GGACCCGGGGCGCTTCCGCGCGTCGGTGGCCCAGTGCCTGGTGTCGTGCCCTGGGACGC   240
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Db  181 GGACCCGGGGCGCTTCCGCGCGNTGGTGGCCANTGCNTGGTGTCGTGCCCTGGGANGN  240

Qy  241 ACGGCGCCCCCGCCCCTCCTTCCGCCCAGGCTGTCCTGCTCGAAGGAGCTGGTGGCC   300
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Db  301 CCGAGTGCTGCANANGCTGTGCGANCGCGGCGGAANAAACGTGCTGGCCTTCGGCTTCGC  360

Qy  361 GCTGCTGGACGGGGCCCCCCCCGAGGCCTTCACCACCAGCGTGCCCAGCTA        420
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GCTGCTGGACGGGGCCCCCCCCGAGGCCTTCACCACCAGCGTGCCCAGCTA        420

Qy  421 CCTGCCCAACACGGTGACCGACGCCACTGCGGGGCGGCGTGGGGGCTGCGTGCTGCTGCG   480
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Qy  481 CCGCGTGGCGACGACGTGCTGGTTCACCTGCGTGCCACCTGCGTGCCGCCTCTTTGTGCTGTGT  540
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Qy  541 GGCTCCCAGTCGCCGCCTACCAGGTGTGCGGCGGCGTGCCCGTGTACCAGCTCGGCGCCAC  600
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Db  541 GGNTNCCAGTCGCCGCCTACCAGGTGTGCGGCGGCGTGCCCGTGTACCAGCTCGGCGCNAC  600

Qy  601 TCAGGCCCGGCCCCGCCACCACGCTAGTGCAGCGGCGGTCTGGGATGCGGAACGGGC  660
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Db   659 CTGGAACCATAGCGTCAGGAGGCGGGGCGCCCGGGCGTCCCCTGGG-CTGCCAGCCCGGGGTGCGAG           717

Qy   721 GAGGCGGGGGCAGTGCAGCCGGAAGCTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGC                    780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   718 GAGGCGGGGGCAGTGCAGCCGGAAGCTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGC                    777

Qy   781 TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCCACCCGGGCAGGAC                  840
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Db   778 TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCCACCCGGGCAGGAC                  837

Qy   841 GCGTGACCGAGTGACCGTGGTTTCTGTGTGTCACCTGCCAGACCCCGAGGAAGC                         900
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Db   838 GCCTGACCGAGTGACCGTGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC                     897

Qy   901 CACCTCTTTGGAGGGTGCGCTCTCTGGACGCGCCACTCCCACCCATCGTGGGCCGCCA                     960
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Db   898 CACCTCTTTGGAGGGTGCGCTCTCTGGACGCGCCACTCCCACCCATCGTGGGCCGCCA                     957

Qy   961 GCACCACGCGGGGCCCCCCCATCCACATCGCGCCACCACGTCCCTGGGACACGCTTGTCC                   1020
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Db   958 GCACCACGCGGGGCCCCCCCATCCACATCGCGCCACCACGT-CCTGGGACACGCCTTGTCC                  1016

Qy  1021 CCCGGTGTACGGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACGAAGGAGCAGCTGCG                 1080
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Db  1017 CCCGGTGTACGGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACGAAGNA--CACTGCG                 1074

Qy  1081 GCCCTCCTTCCTACTC-AGCTCTCTGAGGGCCCAGCCCTGACTGCGCTCGGAGGCTCGTGG                  1139
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Qy  1140 AGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCCAGGGACTCCCCGCAGGTTGCCCCGCC                  1199
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Qy  1200 TGCCCCAGCGACTACTGGCAAATGCGGCCCGTGTTTCTGGAGCTGCTTGGGAACCACGCGGC                 1259
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Qy  1260 AGTGCCCTACGGGCGTGCTCCTCAAGACGCACTGCCGCTGGCGGTCGCGTGTGG                         1319
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Db  1254 AGTGCCCTACGGGCGTGCTCCTCAAGACGCACTGCCGCTGGCGGTCGCGTGTGG                         1313

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Qy  1439 TACGGCTTCGTGTGGGGTTGGCTGTGTTCCGGCCGCTGGTGCCCCAGGGCCTCTGGGGCTCCAGG            1498
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Qy  1499 CACAACGAACGCCGCTTCCTCAGGAACAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCC            1558
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Db  1494 CACAACGAACGCCGCTTCCTCAGGAACAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCC            1553

Qy  1559 AAGCTCTCGCTGCTGCAGGAGCTGACGCTGGTGGAAGATGAGCCGTGCGGACTGCGCTGCGC              1618
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Db  1554 AAGCTCTCGCTGCTGCAGGAGCTGACGCTGGTGGAAGATGAGCCGTGCGGACTGCGCTGCGC              1613

Qy  1619 AGGAGCCCAGGGGTTGGCTGCGTGTTCCGGCCCGCTGTCTGCGTGCGTGTGAGGAGATCCTG             1678
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1614 AGGAGCCCAGGGGTTGGCTGCGTGTTCCGGCCCGCTGTCTGCGTGCGTGTGAGGAGATCCTG             1673

Qy  1679 GCCAAGTTCCTGCACTGGCTGATGAGTGTACGTCGTCGATGAGCTGCTCGTCAGGTCTTTCTTT           1738
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Qy  1739 TATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTCACCGGAAGAGTGTCTGG     1798
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Qy  1799 AGCAAGTTGCAAAGCATTGGAATCAGACAGCACTGAGAGGTGCAGCTGCGGGAGCTG         1858
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Qy  1859 TCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCCGCCCTGCGACGTCCAGACTC            1918
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Db  2154 CCGCGCCGAGCGTGACTTTGTGCAAGGTGGATGTGACGGGCGCTACGACACCATCCCC        2213

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Qy  2399 GAGACCAGCCCGTCGTGAGGGATGCCGTCGTCATCGAGCAGCAGCAGAGCTCCTGAATGAGGCC  2458
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Qy  2459 AGCAGTGGCCTCTTCGACGTCTTCGACGTCTCATTCGTGTGCCACATGGCCGCCATCAGG      2518
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Db  2454 AGCAGTGGCCTCTTCGACGTCTTCGACGTCTCATTCGTGTGCCACATGGCCGCCATCAGG      2513

Qy  2519 GGCAAGTCCTCCAGTGCCAGTGGGATCCCCGCAGGGCTCCAGGGCTCCTCCCAGCCGCTGCTC    2578
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Qy  2579 TGCAGCCCTGCTGCGACTTCCCTGTAGAGACGAGGGCCCTGGTGGCACGGGCTTTTTGTTCAG   2638
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Qy  2699 ACCTTCCTCAGGACCCTGCTCCCGAGTGTCCCTGAGTATGGCTGCGTGTGAACTTGCGG       2758
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Qy  2819 ATGCCGGCCCACCGGCCTATTCCCCTGGTGCGCCTGCTGGATACCCGGAGACCCTGGAG      2878
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RESULT 13
US-09-438-486-173
; Sequence 173, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
;   APPLICANT: Cech, Thomas R.
;   APPLICANT: Lingner, Joachim
;   APPLICANT: Nakamura, Toru
;   APPLICANT: Chapman, Karen B.
;   APPLICANT: Morin, Gregg B.
;   APPLICANT: Harley, Calvin
;   APPLICANT: Andrews, William H.
;   TITLE OF INVENTION: No. US20030009019A1el Telomerase
;   NUMBER OF SEQUENCES: 223
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, 8th Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: United States of America
;   ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/438,486
;   FILING DATE: 12-NOV-1999
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph T.
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-002931US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4029 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY:
;   LOCATION: 1..4029
;   OTHER INFORMATION: /note= "preliminary sequence for
;   OTHER INFORMATION: human TRT cDNA insert of
;   OTHER INFORMATION: plasmid pGRN121"

Db   2814 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            ATGCCCAGCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAG 2873
Qy |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2879 GTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCGTCCACCTTCAAC 2938
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Qy   2874 GTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCGTCCACCTTCAAC 2933
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Db   2939 CGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAG 2998
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Qy   2994 TGTCACAGCCTGTTCTGGATTTGCAGTTGAACAGCTCCAGAGCGTGTGACCAACATC 3053
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Db   3059 TACAAGATCTCCTGCTGCAGGCGTACAGGTTTCACCGCATGTGTCTGCAGCTCCCATTT 3118
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Qy   3054 TACAAGATCCTCCGCTGCAGGCGTACAGGTTTCACGCATGTGTCTGCAGCTCCCATTT 3113
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Db   3119 CATCAGCAAGTTGGAAGAACCCCACATTTTCCTGCGCGTCATCTCTGACACGCGCCTCC 3178
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Qy   3174 CTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGAGATGTCGCTGCGCTGGGGCCAAGGGGCGCC 3233
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Qy

us-10-054-295-224.rnpb

US-09-438-486-173

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Query Match      95.9%;  Score 3849.2;  DB 11;  Length 4029;
Best Local Similarity 98.5%;  Pred. NO. 0;
Matches 3955;  Conservative  0;  Mismatches 53;  Indels  9;  Gaps  8;
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         |||||||||||| |||||||||| |||| ||||||||||  |||||||||||||
Db   541 GGNTCCCAGTGTGCGCTACCANGTGTGCGGGCCGCCTANGGAT-CCAACGGGGC 600

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Qy   901 CACCTCTTTGAGGGTGCGCTCTGGCACGCGCCACCATCCGTGGGCCGCCA 960
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Qy  1140 AGACCATCTTCTTCGGTTCCAGGCCCTGATGCCAGGGACTCCCCGCCAGGTTGCCCCGCC 1199
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Qy  1559 AAGCTCTCGCTGGAGGAGCTGACGTGGAAGAGATGAGCGTGGCGGACTGCGCTTGGCCTGCGCGC 1618
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Qy   2579 TGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGGGACCTCACCTCACCCACGGG 2638
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CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/10/053,758
   FILING DATE: 18-Jan-2002
   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US/08/854,050
   FILING DATE: 09-MAY-1997
   APPLICATION NUMBER: US 08/851,843
   FILING DATE: 06-MAY-1997
   APPLICATION NUMBER: US 08/846,017
   FILING DATE: 25-APR-1997
   APPLICATION NUMBER: US 08/844,419
   FILING DATE: 18-APR-1997
   APPLICATION NUMBER: US 08/724,643
   FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
   NAME: Apple, Randolph T.
   REGISTRATION NUMBER: 36,429
   REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
   TELEPHONE: (415) 576-0200
   TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 4029 base pairs
   TYPE: nucleic acid
   STRANDEDNESS: single
   TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
   NAME/KEY:
   LOCATION: 1..4029
   OTHER INFORMATION: /note= "preliminary sequence for
      human TRT cDNA insert of plasmid pGRN121"
SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-10-053-758-173

Query Match 95.9%;     Score 3849.2;  DB 14;   Length 4029;
Best Local Similarity 98.5%;  Pred. No. 0;
Matches 3955;  Conservative 0;  Mismatches 53;  Indels 9;  Gaps 8;
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(DNA sequence alignment between Qy and Db strands follows, positions 1–1438)

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Db  2874 GTGCAGAGCGACTACTCCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACCTTCAAC 2933

Qy  2939 CGCGGCTTCAAGGCTGGGAGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTTGCGGCTGAAG 2998
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Db  2934 CGCGGCTTCAAGGCTGGGAGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTTGCGGCTGAAG 2993

Qy  2999 TGTCACGGCCTGTTTCTGCTGGATTTGCAGTGTCAGGTTGTGCTGCAGTGCTGCGAGCTCCAACATC 3058
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2994 TGTCACGGCCTGTTTCTGCTGCGAGGCGTGCAGGTTGCAGTGTCAGCTGCGAGCTCCAACATC 3053

Qy  3059 TACAAGATCTCCTCTGCTGGAGGCGTACAGTTTCGTGCTGTGTGCTGCGAGCTCCCATTT 3118
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3054 TACAAGATCTCCTCTGCTGGAGGCGTACAGTTTCGTGCTGTGTGCTGCGAGCTCCCATTT 3113

Qy  3119 CATCAGCAAGTTTGGAAGAACCCCACCATTTTTCCTGCGCGTCATCTCTGACACGGCCTCC 3178
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3114 CATCAGCAAGTTTGGAAGAACCCCACCATTTTTCCTGCGCGTCATCTCTGACACGGCCTCC 3173

Qy  3179 CTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCCAAGGGCGCC 3238
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3174 CTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCCAAGGGCGCC 3233

Qy  3239 GCCGCGCCCTTGCCCTCCGAGGCCGTGCAGTGGCCGTGTGCCACCAGCATTCCTGCTCAAG 3298
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3234 GCCGCGCCCTTGCCCTCCGAGGCCGTGCAGTGGCCGTGTGCCACCAGCATTCCTGCTCAAG 3293

Qy  3299 CTGACTGCGACACCGTGTCACACGGTGTCACCTAGCTGCCACTCCGGGGCACTCAGGAGCAGCCCAGACG 3358
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3294 CTGACTGCGACACCGTGTCACACGGTGTCACCTAGCTGCCACTCCGGGGCACTCAGGAGCAGCCCAGACG 3353

Qy  3359 CAGGTGAGTGGAAGCTCCCGGGACGCTGCCCTGCCGACTGCACCAGCCGCCCAACCCG 3418
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3354 CAGCTGAGTGGAAGCTCCCGGGACGCTGCCCTGCCGACTGCACCAGCCGCCCAACCCG 3413

Qy  3419 GCACTGCCCTGACTTCAAGACCATCCTGACTGAATGGCACCGCCGCCCACAGCCAGGCC 3478
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3414 GCACTGCCCTGACTTCAAGACCATCCTGACTGAATGGCACCGCCGCCCCACAGCCAGGCC 3473

Qy  3479 GAGAGCAGACCACCAGCAGCCGCTCTACGGCGACGAGGAGGGGCGG 3538
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  3474 GAGAGCAGACCACCAGCAGCCGCTCTACGGCGACGAGGAGGGGCGG 3533

Qy  3539 CCCACACCCAGGGCCCGCACCGCTGGAGTCGACCTGAGGCTCATCAGG 3598
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3534 CCCACACCCAGGGCCCGCACCGCTGGAGTCGACCTGAGGCTCATCAGG 3593

Qy  3599 TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCGTCAAGGG 3658
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                                                 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 173:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 4029 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
     MOLECULE TYPE: cDNA
     FEATURE:
          NAME/KEY:
          LOCATION: 1..4029
          OTHER INFORMATION: /note= "preliminary sequence for
               human TRT cDNA insert of
               plasmid pGRN121"
     SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-10-054-295-173

Query Match       95.9%;  Score 3849.2;  DB 14;  Length 4029;
Best Local Similarity  98.5%;  Pred. No. 0;
Matches 3955;  Conservative 0;  Mismatches 53;  Indels 9;  Gaps 8;

Qy      1 GCAGCGCTGCGCGTCCTGCTGCGCGACGTGGGAAGCCCTGGCCCCGGAAGCCCACCCCCGCCGATGCC  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCAGCGCTGCGCGTCCTGCTGCGCGACGTGGGAAGCCCTGGCCCCGGAAGCCCACCCCCGCCGATGCC  60

Qy     61 GGCGCTCCCCGCGTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCGCTCCCCGCGTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT 120

Qy    121 GCCGCTGCCACGTTCGTGCGGCGCCCTGGGCGGCCTGGCGTGCAGCGCGG 180
          |||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCGCTGCCACGTTCGTGCGGCGCCCTGGGCGGCCTGGCGTGCAGCGCGG 180

Qy    181 GGACCCGCGGCTGTTTCGGCGCCTGGTGGCCAGTGCCTGGTGTGCCCTGGGACGC 240
          |||||||||||||||||| ||||||||||   ||  |||||||||| |
Db    181 GGACCCGCGGCGGCTTTCCGGCGGTGGCCCANTGCNTGGTGTGCCCTGGGANGN 240

Qy    241 ACGGCGCCCCCCGCCCCCCCTCCTTCCGCCAGGTGCTCCTGCCTCCAGGTGTCTCCTGCTGAAGGAGCTGGTGGC 300
          |||  |  |||||||||||||| ||||||||||||||| || |||||
Db    241 ANGGCNGCCCCCGCGCCCCCCTCCTTCCGCCAGGTGTCCTCCTGCCTGCCAGGTGTCTCCTGCTGAANGANCTGGTGGC 300

Qy    301 CCGAGTGCTGCAGAGCGTGTGCGAGCGCGGCGAAGAACGTGCTGGCCTTCCGC 360
          |||||||||| || ||||  |||||||||||||||
Db    301 CCGAGTGCTGCANANGCTGTGCGANCGCGGCGAANAACGTGCTGGCCTTCCGC 360

Qy    361 GCTGCTGACAGGGGCCCGCGGCGGGGCCCTTCACCACCAGCGTGCGCAGCTA 420
          ||||||||||||||| || |||||||| |||||||
Db    361 GCTGCTGACAGGGGCGCGGCGGGGGCCCTTCACCACCAGCGTGCGCAGCTA 420

Qy    421 CCTGCCCAACACGGTGACCGACGCCACTCGGGGGCGTGGGGAGCGTGGGGCTGCTGCGG 480
          |||||||||||||||||||||  ||||||||||||||||||
Db    421 CCTGCCCAACACGGTGACCGACGCCACTCGGGGGGAGCGTGGGGCTGCTGCGG 480

Qy    481 CCCGTGGGCGACGACGTGCTGGTTCACCTGGCACGCTGCGCCTCTTTGTGCTGT 540
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Db    481 CCCGTGGGCGACGACGTGCTGGTTCACCTGGCACGCTGCGCGNTNTTTGTGCTGT 540

Qy    541 GGCTCCAGCTGCGCGTACCAGGTGTGCGGGCCGGCCGCGTGTACCAGCTCGGCGCCTGCCAC 600
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Db    541 GGNTCCCAGCTGCGCCTACCANGTGTGCGGGGCCGGCCGCGTGTACCAGCTCGGCGCCTGCNAC 600

Qy    601 TCAGGCCCCGGCCGGGGGTCAGGAGGCGGTCTGGGATGGAACCGGGGC 660
          ||||||||||  |||||||||||||||||||    ||
Db    601 TCAGGCCCCGGCCGGGGGTCACACGCTANTGGA-CCCGGAANGCGTCTGGGAT-CCAACGGGC 658

Qy    661 CTGGAACCATAGCCTCAGGGAGGCCCGGGTGCGGGCCTCCCAGCCCCGGGTGCGCAG 720
          |||||||||||| |||||||||||||||  -|||||  |||  |||||||||
Db    659 CTGGAACCATAGCCTCAGGGAGGCCCGGGTCCGGGT-CTGCCCAGAGGCCCCAGGGCTGGGGC 717

Qy    721 GAGGCGCGGGGGCAGTGCCAAGTCGCCGAAGTCTGCCGTTGCCCAAGAGAGGGCTGGGGC 780
          ||||||||| |||||||||||||||||||||||||||||||  ||||||||||
Db    718 GAGGCGCGGGGGCAGTGCCAGCCCGAAGTCTGCCGTTGCCCAAGAGAGGGCTGGGGC 777
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Db   3594                                                  |||||||||||||||||||||||||
     3594 TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGTCAGCCAAGGG 3653
Qy   3659 CTGAGTGTCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCCACCC 3718
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3654 CTGAGTGTCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCCACCC 3713
Qy   3719 CAGGGCCCAGCTTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCAT 3778
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3714 CAGGGCCAGCTTTTTCCTCACCAGGAGCCCGGCTTCCCACATAGGAATAGTCCAT 3773
Qy   3779 CCCAGATTCGCCATTGTTCACCCCTCGCCCTCCTTTGCCTTCCACCCCACCAT 3838
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3774 CCCCAGATTCGCCATTGTTCACCCCTCGCCCTCCTTTGCCTTCCACCCCACCAT 3833
Qy   3839 CCAGGTGGGACCCTGAGAAGGACCCTGGGAGGCTCTGGGAATTGGAGTGACCAAAGGTG 3898
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Db   3834 CCAGGTGGGAGACCCTGAGAAGGACCCTGGGAGGCTCTGGGAATTGGAGTGACCAAAGGTG 3893
Qy   3899 TGCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGG 3958
          |||||||||||||||||||||||||||||||||||||||||||||
Db   3894 TGCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGG 3953
Qy   3959 GGGAGGTGCTGTGGGAGGTAAAATACTGAATATATGAGTTTTTGAAAAAAAA 4015
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RESULT 15
US-10-054-295-173
; Sequence 173, Application US/10054295
; Publication No. US2003004953A1
GENERAL INFORMATION:
     APPLICANT: Cech, Thomas R.
          Lingner, Joachim
          Nakamura, Toru
          Chapman, Karen B.
          Morin, Gregg B.
          Harley, Calvin
          Andrews, William H.
     TITLE OF INVENTION: No. US20030044953Alel Telomerase
     NUMBER OF SEQUENCES: 225
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Townsend and Townsend and Crew LLP
          STREET: Two Embarcadero Center, 8th Floor
          CITY: San Francisco
          STATE: California
          COUNTRY: United States of America
          ZIP: 94111
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.30
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/10/054,295
          FILING DATE: 18-Jan-2002
          CLASSIFICATION: 536
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 08/854,050
          FILING DATE: <Unknown>
          APPLICATION NUMBER: US 08/846,017
          FILING DATE: 25-APR-1997
          APPLICATION NUMBER: US 08/844,419
          FILING DATE: 18-APR-1997
          APPLICATION NUMBER: US 08/724,643
          FILING DATE: 01-OCT-1996
     ATTORNEY/AGENT INFORMATION:
          NAME: Apple, Randolph T.
          REGISTRATION NUMBER: 36,429
          REFERENCE/DOCKET NUMBER: 015389-002930US
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: (415) 576-0200

```
Qy   781 TGCCCCTGAGCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCACCGGGCAGGAC  840
         ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   778 TGCCCCTGAGCGGAGCGGACGCCCGTTGGGGCAGGGGTCCTGGGCCACCGGGCAGGAC  837

Qy   841 GGCTGGACGAGTGACCGTGGTTTCTGTGTGTGGTGTCACCTCCACTGCCAGGAGAAGC  900
         |||||||||||  |||||  ||||||||||||||||||||  |||||   ||||||||
Db   838 GCCTGGGACGAGTGACGTGCTGGTTTCTGTGTGTGGTGTCACCTGCCAGGACCGGAAGC  897

Qy   901 CACCTCTTTGGAGGTGCGCTCTCTGGACGCGGCCACTCCACCATCCGTGGCCGCCA    960
         ||||||| |||||||||||||| | |||||||||| ||||||||||| |||||||||
Db   898 CACCTCTTTGGAGGTGCGCTCTCTGCGGACGCGGCCACTCCACCATCCGTGGCCGCCA   957

Qy   961 GCACCACGCGGGACCCCCCATCACACTGCGGCCACCACGTCCTGGGACCACGCCTTGTCC 1020
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Db   958 GCACCACGCGGGACCCCCCATCACCACGTCGGGTCCTGGGACCACGCCTTGCC-     1016

Qy  1021 CCCGGTGTACGGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACGACAAGGAGCAGCTGCG 1080
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Db  1017 CCCGGTGTACGGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACGACAAGA--CACTGCG  1074

Qy  1081 GCCCTCCTTCTACTC-AGTCTCTGAGGCCCAGCCTGACTGCGCTCGGAGGCTCGTGG    1139
         ||||||||||||||| | ||||| || | ||||| |||  |||||  |||  ||| ||
Db  1075 NCCCTCCTTCTACTCAATATATCTCAATATATCTGAGGCCTGACTGCGGTTCGGGAGGTTCCGTG  1134

Qy  1140 AGACCATCTTTCTGGGTTCCAGGCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCGCC   1199
         ||||| |||| |||||||||||||||  || |||| |||| |||||| ||||||||||
Db  1135 GAGACACTTTCTGGGTTCCAGGCCTTGGATGCCAGATTCCCCCGCAGGTTCGGTCCCCCC  1193

Qy  1200 TGCCCCAGCGCTACTGGCCAAATGCGCCCCGTTCTGTTCGGAGCTGCTTGGGAACCACGC  1259
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Db  1194 TGCCCCAGCGNTACTGGCCAAATGCGGCGCGTTCTGTTGGGAGCTGCTGGGAACCACGCGC  1253

Qy  1260 AGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGGAGCGTCGGTCACCCCAG   1319
         ||||||||||||||||| || |||||||||||| |||||||||||||| ||||||||||
Db  1254 AGTGCCCCTACGGGGTGTTCCTCAAGACGCACTGCCCGCTGGAGCGTGGCGTCACCCCAG  1313

Qy  1320 CAGCCGGTGTCTGTGCCCGGGGAAGCCCAGGGCTCGTGTGCGGCCCCCGAGGAGGAG    1379
         ||||||| || ||||||||||||||||||||||| | ||||||||||||||||||||
Db  1314 CAGCCGGTGTCTGTGCCCGGGGAAGCCCAGGGCTCTGTGTGCGGCCCCCGAGGAGGAG   1373

Qy  1380 -ACACAGACCCCCGTGACGCTGCTCCGGCAGCACAGACCCCTGGCCAGTG         1438
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1374 AACACAGACCCCCGTGACGCTGCTCCGGCAGCACAGACCCCTGGCCAGTG         1433

Qy  1439 TACGGCTTCGTGTGGGCGGGCCTGCTGCCGGCGGCCTCCAGGGCTCCAGG        1498
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1434 TACGGCTTCGTGTGGGCGGGCCTGCTGCCGGCGGCCTCCAGGGCTCCAGG        1493

Qy  1499 CACAACGAACGCGGCCGCTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCC 1558
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Db  1494 CACAACGAACGCGGCCGCTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCC 1553

Qy  1559 AAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGCCTCGGACTGCGCGC       1618
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1554 AAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGCCTCGGACTGCGCGC       1613

Qy  1619 AGGAGGCCCAGGGTTGGCTGCTGCTGCTACGGTCGTGTTACGGTGTCTCT        1678
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1614 AGGAGGCCCAGGGTTGGCTGCTGCTGCTACGGTCGTGTTACGGTGTCTCT        1673

Qy  1679 GCCAAGTGTTCCTGCTCACTGCTGTCTCGATGAGTGTCGCTACGGTCGTCAGG      1738
         |||||||||||||||||||||||||  ||| ||||| | ||||||||||||
Db  1674 GCCAAGTGTTCCTGCTCACTGCTGTCTCGATGATGAGTGTCGTACGGTCGTCAGG    1733

Qy  1739 TATGTCACGGAGGACCACGTTCAAAAGAACAGCTCTTTCTTTACCGGAAGAGTGTCTGG    1798
         |||||||||||||||||||||||| |||||| |||||| ||| ||||||||||| |||||
Db  1734 TATGTCACGGAGGACCACGTTGTTCAAAGAACAGCTCTTTTCTTTTCACCGGAAGAGTGTCTGG  1793

Qy  1799 AGGCAAGTTGCAAAGCATTGGAATCAGAGACACTTGAAGAGGTGCAGCTGCGGGGAGCTG  1858
         ||||||||||||||||||||||  |||||| ||||||||||||||||||| |||||| ||
Db  1794 AGGCAAGTTGCAAAGCATTGGAATCAGAGACACTTGAAGAGGTGCAGCTGCGGGGAGCTG  1853

Qy  1859 TCGGAAGCAGAGGTCAGGCAGCATCGGAGGAAGCCGGAAGCCAGGCCCGCTGACGTCCAGACTC 1918
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Db  1854 TCGGAAGCAGAGGTCAGGCAGCATCGGAGGAAGCCGGAAGCCAGGCCCGCTGACGTCCAGACTC 1913
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Db  1854 TCGGAAGCAGAGGTCAGGCAGCATCGGAGGAAGCCGGAAGCCAGGCCCGCTGACGTCCAGACTC 1913
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy  1919 CGGTTCATCCCCAAGCCTCACGGCTGCGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGA 1978
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1914 CGGTTCATCCCCAAGCCTCACGGCTGCGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGA 1973

Qy  1979 GCCAGAAGTTCCGCAGAGAAAAGAGAGGGCCGAGCGTCTCCAGGGTGAAGGCACTG     2038
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1974 GCCAGAAGTTCCGCAGAGAAAAGAGAGGGCCGAGCGTCTCCAGGGTGAAGGCACTG     2033

Qy  2039 TTCAGCGTGCTCAACTACGAGCCGGCGCGCGGCGGCCGGCCCCGGCCTCTGTGCTG      2098
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2034 TTCAGCGTGCTCAACTACGAGCCGGCGCGCGGCGGCCGGCCCCGGCCTCTGTGCTG      2093

Qy  2099 GGCTGGACGATATCCACAGGGCCTGGCCGACTTCGTCGTGCGTGTGGGCCCCAGGAC     2158
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2094 GGGCTGGACGATATCCACAGGGCCTGGCCGACTTCGTCGTGCGTGTGGGCCCCAGGAC    2153

Qy  2159 CCGGCCGCTGAGCTGTACTTGTCAAGGTGACGGGATGTGACGGGCGTACGACACCACCATCCCC 2218
         |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  2154 CCCGGCCGCTGAGCTGTACTTGTCAAGGTGACGGGATGTGACGGGCGTACGACACCACCATCCCC 2213

Qy  2219 CAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAAACACTACTGCGTG    2278
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2214 CAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAAACACTACTGCGTG    2273

Qy  2279 CGTCGGTATGCCGGTGTCCAGGAGGCCACGCCCATGGGCACGTTCGTCTGCAAGAGC     2338
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Db  2274 CGTCGGTATGCCGGTGTCCAGGAGGCCACGCCCATGGGCACGTTCGTCTGCAAGAGC     2333

Qy  2339 CACGTCTCTACCTTGACAGACCTCCAGCCGTCCAGCGGTGACACTGCAGTTCGTGGCTCACCTGCAG 2398
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2334 CACGTCTCTACCTTGACAGACCTCCAGCCGTCCAGCGGTGACACTGCAGTTCGTGGCTCACCTGCAG 2393

Qy  2399 GAGACCAGCCGCGTGAGGGATGCCGCTCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCC 2458
         || || ||||||||||||||||||||  |||||||||||||  ||||||||||||||||
Db  2394 GANAACAGCCGCGTGAGGGATGCCGCTCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCC 2453

Qy  2459 AGCAGTGGCCTCTTCCAGCGTCTTCCACGCTCATGTGCCACCAGGCCGTGCGCATCAGG    2518
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2454 AGCAGTGGCCTCTTCCAGCGTCTTCCACGCTCATGTGCCACCAGGCCGTGCGCATCAGG    2513

Qy  2519 GGCAAGTCCTACGGTCCAGTGCCAGGGGATCCCCAGAGGCTCCATCCTCTCCACGGTGCTC 2578
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Db  2514 GGCAAGTCCTACGGTCCAGTGCCAGGGGATCCCCAGAGGCTCCATCCTCTCCACCGCTGCTC 2573

Qy  2579 TGCAGCCGTGTGCTACGGCCACATGGAGAACAAGCTGTTTGCGGAGATTCGGGGGACGGG  2638
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2574 TGCAGCCGTGTGCTACGGCCACATGGAGAACAAGCTGTTTGCGGGGGATTCGGGGGACGGG 2633

Qy  2639 CTGCTCCTGCGTTTGGTGACTTTGGTGATTTCTTGTGGTGACACCTCACCCAGCCAGCGAAA 2698
         |||||||||| |||||||||||||||| |||||| |||||||||||||||||||||||||||
Db  2634 CTGCTCCTGCGTTTGGTGATGATTCTTGTGGTGACACCTCACCCAGCCAGCGAAA      2693

Qy  2699 ACCTTCCTCAGGACCCTGGTCCCTGTGAACTTCCCGTAGAAGACGAGGCCCTGGTGGTGGAACTTGCGG 2758
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2694 ACCTTCCTCAGGACCCTGGTGTCCCTGTAGAAGACGAGGCCCTGGTGGTGGAACTTGCGG    2753

Qy  2759 AAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGTGGTGGCACGGCTTTTGTTCAG 2818
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  2754 AAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGTGGTGGCACGGCTTTTTCCAG  2813

Qy  2819 ATGGCCGGCCACGGCTATTCCCGGTGCTGCTGCTGGATACCCGGGAGACCCTGGAG     2878
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2814 ATGGCCGGCCACGGCTATTCCCGGTGCTGCTGCTGGATACCCGGGAGACCCTGGAG     2873

Qy  2879 GTGCAGAGCGACTACTCCAGCTACTCCAGCTCAGAGAGCCAGTCTCACCTTCAAC      2938
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2874 GTGCAGAGCGACTACTCCAGCTACTCCAGCTCAGAGAGCCAGTCTCACCTTCAAC      2933

Qy  2939 CGCGGCTTCAAGCGTGGAGGAACATGGGGTTCGCAAAACTCTTGGGGTCTTGCGGCTGAAG 2998
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2939
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`Wed Oct 15 09:29:27 2003   us-10-054-295-224.rnpb

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Db  2934  CGCGGCTTCAAGGCTGGGAGGAACATGCTCGCAAACTCTTTGGGGTCTTGCGGCTGAAG  2993
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2999  TGTCACAGCCTCGTTTCTGGATTTGCAGTGAACAGCCTCCAGACGGTGCACCAACATC  3058
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2994  TGTCACCAGCCCGTTTCTTGGATTTGCAGTGAACAGCCTCCAGACGGTGCACCAACATC  3053

Qy  3059  TACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGTCAGCTCCCATTT  3118
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Db  3054  TACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACCGCATGTGTGCTCGCAGCTCCCATTT  3113

Qy  3119  CATCAGCAAGTTGGAAGAACCCACATTTTTCCTGCGCGTCATCTCTGACACGGGCTCC  3178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3114  CATCAGCAAGTTTGGAAGAACCCACATTTTTCCTGCGCGTCATCCTCTGACACGGGCTCC  3173

Qy  3179  CTCTGCTACTCCATCCTGAAAAGCCAAGAACGCAGGGATGTCCGTGGGGGCCAAGGGCCCC  3238
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3174  CTCTGCTACTCCATCCTGAAAAGCCAAGAACCGCAGGGATGTCCGTGGGGGCCAAGGGCGCC  3233

Qy  3239  GCCGGGCCCTCTGCCCTCCGAGCCGTGCAGTGGCTGCCACCAAGCATTCCTGCTCAAG  3298
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3234  GCCGGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGCCACCAAGCATTCCTGCTCAAG  3293

Qy  3299  CTGACTCGACACCGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACG  3358
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3294  CTGACTCGACACCGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACG  3353

Qy  3359  CAGCTGAGTCGGAAGCTCCCGGGACAGCGCTGACTGCCCTGGAGCGCCAGCCAGCCCG  3418
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3354  CAGCTGAGTCGGAAGCTCCCGGGACAGCGCTGACTGCCCTGGAGCGCCAGCCAACCCG  3413

Qy  3419  GCACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCC  3478
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3414  GCACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGCC  3473

Qy  3479  GAGAGCAGACACCAGCAGCCCTGTCACGCCCGGCTCACGTCCCAGGGAGGGAGGGGCGG  3538
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3474  GAGAGCAGACACCAGCAGCCCTGTCACGCCCGGCTCACGTCCCAGGGAGGGAGGGGCGG  3533

Qy  3539  CCCACACCCAGGCCCGCCACCGGCCCGCCACCCGCTGGGAGTCTCGAGGCCTGAGTGAGTGTTTGGCCGAGGCC  3598
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3534  CCCACACCCAGGCCCGCCACCCGGCCCGCCACCCGCTGGGAGTCTCGAGGCCTGAGTGAGTGTTTGGCCGAGGCC  3593

Qy  3599  TGCATGTCCGGCTGAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGG  3658
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3594  TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGG  3653

Qy  3659  CTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACCAGGCTGGCCGCTCCCACCCC  3718
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3654  CTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACCAGGCTGGCCGCTCCGGCTCCACCCC  3713

Qy  3719  CAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCAT  3778
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3714  CAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCAT  3773

Qy  3779  CCCCAGATTCGGCCATTGTTCACCCCTCGCCCCTTGCCCTTCCACCCCCACCCAT  3838
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Qy  3839  CCAGGTGGGAGACCCTGAGAAGGAGACCCTGGGAGCTCTGGGAATTTGACCCAAGGTG  3898
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3899  TGCCCTGTACACAGGCCAGGAGACCTCGACCTGGATGGGGGTCCCTGTGGGTCAAATTGGG  3958
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3894  TGCCCTGTACACAGGCCAGGAGGACCCTGGATGGGGTCCCTGTGGGTCAAATTGGG  3953

Qy  3959  GGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTGAAAAAAA  4015
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Db  3954  GGGAGGTGCTGTGGGGACTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA  4010
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Job time : 1532 secs

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